

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:26:08 ; Search time 8.93784 Seconds
(without alignments)
9158.169 Million cell updates/sec

Title: US-10-037-182-20
Perfect score: 8527
Sequence: 1 AMDECADEGGRPQRCMPEFV.....EDIKKTLPFGCFNTPSIEKP 1572

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	8460	99.2	1607	1	LMG1_MOUSE	P02468 mus musculus
2	8034	94.2	1609	1	LMG1_HUMAN	P11047 homo sapien
3	3586	42.1	1587	1	LMG3_HUMAN	Q9Y6n6 homo sapien
4	3486.5	40.9	1581	1	LMG3_MOUSE	Q9r0b6 mus musculus
5	3476	40.8	1639	1	LMG1_DROME	P15215 drosophila
6	3176	37.2	1535	1	LML1_CAEEL	Q18823 caenorhabdi
7	2592	30.4	1193	1	LMG2_HUMAN	Q13753 homo sapien
8	2475	29.0	1191	1	LMG2_MOUSE	Q61092 mus musculus
9	1812.5	21.3	3106	1	LMA2_MOUSE	Q60675 mus musculus
10	1790	21.0	3110	1	LMA2_HUMAN	P24043 homo sapien
11	1780.5	20.9	3084	1	LMA1_MOUSE	P19137 mus musculus
12	1735	20.3	3075	1	LMA1_HUMAN	P25391 homo sapien
13	1677	19.7	1786	1	LMB1_HUMAN	P07942 homo sapien
14	1661.5	19.5	1786	1	LMB1_MOUSE	P02469 mus musculus
15	1656.5	19.4	1790	1	LMB1_DROME	P11046 drosophila
16	1569	18.4	1801	1	LMB2_RAT	P15800 rattus norv
17	1541.5	18.1	1798	1	LMB2_HUMAN	P55268 homo sapien
18	1526	17.9	1799	1	LMB2_MOUSE	Q61292 mus musculus
19	1454	17.1	3712	1	LMA_DROME	Q00174 drosophila
20	1384	16.2	3672	1	LML2_CAEEL	Q21313 caenorhabdi
21	1376	16.1	3718	1	LMA5_MOUSE	Q61001 mus musculus
22	1330.5	15.6	3695	1	LMA5_HUMAN	O15230 homo sapien
23	1162.5	13.6	3333	1	LMA3_MOUSE	Q61789 mus musculus
24	1155.5	13.6	606	1	NET1_CHICK	Q90922 gallus gall
25	1140.5	13.4	604	1	NET1_MOUSE	O09118 mus musculus
26	1137	13.3	604	1	NET1_HUMAN	O95631 homo sapien
27	1044.5	12.2	581	1	NET2_CHICK	Q90923 gallus gall
28	986.5	11.6	612	1	UNC6_CAEEL	P34710 caenorhabdi
29	948	11.1	1172	1	LMB3_HUMAN	Q13751 homo sapien
30	903.5	10.6	4391	1	PGBM_HUMAN	P98160 homo sapien
31	902	10.6	1168	1	LMB3_MOUSE	Q61087 mus musculus
32	883	10.4	727	1	NETA_DROME	Q24567 drosophila
33	877.5	10.3	3707	1	PGBM_MOUSE	Q05793 mus musculus

34	841.5	9.9	793	1	NETB_DROME	Q24568 drosophila
35	637.5	7.5	3375	1	UN52_CAEEL	Q06561 caenorhabdi
36	623.5	7.3	539	1	NTG1_MOUSE	Q8r4g0 mus musculus
37	585	6.9	1816	1	LMA4_HUMAN	Q16363 homo sapien
38	574.5	6.7	1816	1	LMA4_MOUSE	P97927 mus musculus
39	560.5	6.6	530	1	NTG2_HUMAN	Q96cw9 homo sapien
40	532	6.2	589	1	NTG2_MOUSE	Q8r4f1 mus musculus
41	514	6.0	1713	1	LMA3_HUMAN	Q16787 homo sapien
42	479	5.6	2470	1	NTC2_MOUSE	O35516 mus musculus
43	477	5.6	2471	1	NTC2_RAT	Q9qw30 rattus norv
44	471	5.5	303	1	LMB1_CHICK	Q01635 gallus gall
45	469.5	5.5	2703	1	NOTC_DROME	P07207 drosophila

ALIGNMENTS

RESULT 1						
LMG1_MOUSE						
ID	LMG1_MOUSE	STANDARD;	PRT;	1607	AA.	
AC	P02468;					
DT	21-JUL-1986 (Rel. 01, Created)					
DT	01-JUL-1989 (Rel. 11, Last sequence update)					
DT	15-MAR-2004 (Rel. 43, Last annotation update)					
DE	Laminin gamma-1 chain precursor (Laminin B2 chain).					
GN	LAMC1 OR LAMC-1 OR LAMB-2.					
OS	Mus musculus (Mouse).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
OX	NCBI_TaxID=10090;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=88059118; PubMed=3680290;					
RA	Sasaki M., Yamada Y.;					
RT	"The laminin B2 chain has a multidomain structure homologous to the					
RT	B1 chain.";					
RL	J. Biol. Chem. 262:17111-17117(1987).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=89000737; PubMed=3167041;					
RA	Durkin M.E., Bartos B.B., Liu S.-H., Phillips S.L., Chung A.E.;					
RT	"Primary structure of the mouse laminin B2 chain and comparison with					
RT	laminin B1.";					
RL	Biochemistry 27:5198-5204(1988).					
RN	[3]					
RP	SEQUENCE OF 1-239 FROM N.A.					
RX	MEDLINE=88228071; PubMed=2836421;					
RA	Ogawa K., Burbelo P.D., Sasaki M., Yamada Y.;					
RT	"The laminin B2 chain promoter contains unique repeat sequences and					
RT	is active in transient transfection.";					
RL	J. Biol. Chem. 263:8384-8389(1988).					
RN	[4]					
RP	SEQUENCE OF 1391-1607 FROM N.A.					
RX	MEDLINE=85051302; PubMed=6209134;					
RA	Barlow D.P., Green N.M., Kurkinen M., Hogan B.L.M.;					
RT	"Sequencing of laminin B chain cDNAs reveals C-terminal regions of					
RT	coiled-coil alpha-helix.";					
RL	EMBO J. 3:2355-2362(1984).					
RN	[5]					
RP	X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 771-932.					
RX	MEDLINE=96196434; PubMed=8648630;					
RA	Stetefeld J., Mayer U., Timpl R., Huber R.;					
RT	"Crystal structure of three consecutive laminin-type epidermal growth					
RT	factor-like (LE) modules of laminin gamma1 chain harboring the					
RT	nidogen binding site.";					
RL	J. Mol. Biol. 257:644-657(1996).					
RN	[6]					
RP	STRUCTURE BY NMR OF 824-881.					
RX	MEDLINE=96196435; PubMed=8648631;					
RA	Baumgartner R., Czisch M., Mayer U., Poeschl E., Huber R.,					
RA	Timpl R., Holak T.A.;					
RT	"Structure of the nidogen binding LE module of the laminin gamma1					
RT	chain in solution.";					

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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:28 ; Search time 42.6441 Seconds
(without alignments)
11631.021 Million cell updates/sec

Title: US-10-037-182-20
Perfect score: 8527
Sequence: 1 AMDECADEGGRPQRCMPEFV.....EDIKKTLPTGCFNTPSIEKP 1572

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	6145	72.1	1593	13 Q8JHV8	Q8jlv6 brachydanio
2	4704	55.2	1007	13 Q90ZN3	Q90zn3 gallus gall
3	3535.5	41.5	1623	5 Q9U3U7	Q9u3u7 anopheles g
4	2583.5	30.3	1196	6 Q867A2	Q867a2 canis famil
5	2579.5	30.3	1190	6 Q8HZI9	Q8hzi9 equus cabal
6	1715	20.1	1785	13 Q8JHV7	Q8jlv7 brachydanio
7	1687	19.8	529	4 Q8N2D6	Q8n2d6 homo sapien
8	1655	19.4	1792	13 Q57484	Q57484 gallus gall
9	1638	19.2	351	11 P97552	P97552 rattus norv
10	1632	19.1	3102	5 O45614	O45614 caenorhabdi
11	1630	19.1	1761	4 Q86XN2	Q86xn2 homo sapien
12	1523	17.9	1799	11 Q8R0Y0	Q8r0y0 mus musculu
13	1502.5	17.6	2731	5 Q9VJT5	Q9vjt5 drosophila
14	1502.5	17.6	3367	5 Q9XZC9	Q9xzc9 drosophila
15	1502.5	17.6	3375	5 Q8IP51	Q8ip51 drosophila
16	1478	17.3	1827	13 Q8JHV6	Q8jlv6 brachydanio

17	1464	17.2	1631	4 Q9Y6U6	Q9y6u6 homo sapien
18	1457	17.1	3712	5 Q9VRW0	Q9vrw0 drosophila
19	1415	16.6	319	4 Q96BH6	Q96bh6 homo sapien
20	1384	16.2	3704	5 P91904	P91904 caenorhabdi
21	1329.5	15.6	3695	4 Q8TDF8	Q8tdf8 homo sapien
22	1173	13.8	1168	5 Q967S8	Q967s8 schistocerc
23	1138.5	13.4	603	13 Q42140	Q42140 brachydanio
24	1138	13.3	604	11 Q924Z9	Q924z9 rattus norv
25	1134.5	13.3	569	13 Q57339	Q57339 xenopus lae
26	1129.5	13.2	602	13 Q42203	Q42203 brachydanio
27	1127.5	13.2	1026	5 Q8SWY0	Q8swy0 drosophila
28	1116.5	13.1	464	11 Q61965	Q61965 mus musculu
29	1107.5	13.0	1069	5 Q9BPS2	Q9bpe2 bombyx mori
30	1081.5	12.7	1086	4 Q8TAS6	Q8tas6 homo sapien
31	1073.5	12.6	1067	5 Q44565	Q44565 caenorhabdi
32	1072	12.6	555	5 Q9NFW6	Q9nfw6 branchiosto
33	1041.5	12.2	1546	4 Q9NS27	Q9ns27 homo sapien
34	1037.5	12.2	1546	4 Q75445	Q75445 homo sapien
35	1029	12.1	610	5 Q96659	Q96659 hirudo medi
36	1003.5	11.8	1461	11 Q9JLP3	Q9jlp3 mus musculu
37	977.5	11.5	984	11 Q8K271	Q8k271 mus musculu
38	970.5	11.4	1512	11 Q8K3K1	Q8k3k1 rattus norv
39	950	11.1	1486	4 Q14637	Q14637 homo sapien
40	926.5	10.9	695	11 Q8C9J2	Q8c9j2 mus musculu
41	922	10.8	1168	11 Q91V90	Q91v90 mus musculu
42	903	10.6	911	11 Q9CRX6	Q9crx6 mus musculu
43	871	10.2	667	5 Q9VY25	Q9vy25 drosophila
44	849	10.0	580	4 Q00634	Q00634 homo sapien
45	842	9.9	580	11 Q9R1A3	Q9r1a3 mus musculu

ALIGNMENTS

RESULT 1

Q8JHV8	ID	Q8JHV8	PRELIMINARY;	PRT;	1593 AA.
AC	Q8JHV8;				
DT	01-OCT-2002 (TremBLrel. 22, Created)				
DT	01-OCT-2002 (TremBLrel. 22, Last sequence update)				
DT	01-JUN-2003 (TremBLrel. 24, Last annotation update)				
DE	Laminin gamma 1.				
GN	LAMC1.				
OS	Brachydanio rerio (Zebrafish) (Danio rerio).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;				
OC	Cyprinidae; Danio.				
OX	NCBI_TaxID=7955;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=22065263; PubMed=12070089;				
RA	Parsons M.J., Pollard S.M., Saude L., Feldman B., Coutinho P.,				
RA	Hirst E.M., Stemple D.L.;				
RT	"Zebrafish mutants identify an essential role for laminins in				
RT	notochord formation."				
RL	Development 129:3137-3146(2002).				
DR	EMBL; AF468048; AAM61766.1; .				
DR	GO; GO:0005578; C:extracellular matrix; IEA.				
DR	GO; GO:0005198; F:structural molecule activity; IEA.				
DR	InterPro; IPR006209; EGF like.				
DR	InterPro; IPR000034; Laminin_B.				
DR	InterPro; IPR002049; Laminin_EGF.				
DR	InterPro; IPR008211; LamNT.				
DR	InterPro; IPR008212; Lam_N2.				
DR	Pfam; PF00052; laminin_B; 1.				
DR	Pfam; PF00053; laminin_EGF; 10.				
DR	Pfam; PF00055; laminin_Nterm; 1.				
DR	PRINTS; PR00011; EGFLAMININ.				
DR	ProDom; PD002082; Lam_N2; 1.				
DR	SMART; SM00180; EGF_Lam; 11.				
DR	SMART; SM00281; LamB; 1.				
DR	SMART; SM00136; LamNT; 1.				
DR	PROSITE; PS00022; EGF_1; 7.				

DR PROSITE; PS01186; EGF 2; 2.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 10.
KW Laminin EGF-like domain.
SQ SEQUENCE 1593 AA; 176218 MW; A501F3A8884AA411 CRC64;

Query Match 72.1%; Score 6145; DB 13; Length 1593;
Best Local Similarity 69.3%; Pred. No. 5.7e-258;
Matches 1091; Conservative 213; Mismatches 268; Indels 2; Gaps 2;

QY 1 AMDECADEGGRPQRCMPPEFNAAFNVTVATNTCTTPPEEYCVQGTGVTGKTSCHLADAG 60
Db 20 AMDECADEGGRPQRCMPPEFNAAFNVTVATNTCTTPPEEYCVQGTGVTGKTSCHLADAG 79

QY 61 QHLOHGAFLTDYNNQADITWQSQOTMLAGVQYVNSINLTLLHKGAFDITYVRLKFHTS 120
Db 80 DPLRHGAFLTDYNNQADITWQSQOTMLAGVQYVNSINLTLLHKGAFDITYVRLKFHTS 139

QY 121 RPESFAIKRTREDGPWIPYQYSGSCENTYSKANRGFIRTGDEQALCTDEFSDISPL 180
Db 140 RPESFAIKRTREDGPWIPYQYSGSCENTYSKANRGFIRTGDEQALCTDEFSDISPL 199

QY 181 TGGNVAFTLEGRPSAYNFNSPVLQEWVTATDIRVTLNRLNTFGDEVENDPKVLKSYVY 240
Db 200 YGGNVAFTLEGRPSAYNFNSPVLQEWVTATDIRVTLNRLNTFGDEVENDPKVLKSYVY 259

QY 241 AISDFAVGGRCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPFNDPWRRTAAS 300
Db 260 AISDFAVGGRCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPFNDPWRRTAAS 319

QY 301 ASECLPCDNGRSQECYFDPPELYRSTGHGHTCNCRDNTDGAKECERENFFRLGNTZAC 360
Db 320 PNECLPCDNGRSQECYFDPPELYRSTGHGHTCNCRDNTDGAKECERENFFRLGNTZAC 379

QY 361 SPCHCSPVGLSTQCDYSGRCKPGVMGDKCDRCOPGFHSLTEAGRCPCSDPSGSTDE 420
Db 380 LSCGCPVGLSTQCDYSGRCKPGVMGDKCDRCOPGFHSLTEAGRCPCSDPSGSTDE 439

QY 421 CNVETGRVCCKDNVEGFNCERCKPGFFNFLESNPKGCTPCFCFHSVCTNAVGYSVYDI 480
Db 440 CDVQTRGCKCKENVDGFCNCRCKLGYFNLDPQNPQCGCTPCFCFHSVCTNAVGYSVYDI 499

QY 481 SSTFQIDEGWRVEQDRGSEASLEWSSDRQYIAVSDSYFPRYFIAPVKFLGNQVLSYGQ 540
Db 500 TSTFDRDDEGWRVEQDRGSEASLEWSSDRQYIAVSDSYFPRYFIAPVKFLGNQVLSYGQ 559

QY 541 NLSFSFRVDRDRRLSAEDLVLEGAGLRVSVPLIAQGNYSYSETTVKYIFRLHEATDYPW 600
Db 560 NLTLNFRIRQHRDARLSAEDLVLEGAGLRVSVPLIAQGNYSYSETTVKYIFRLHEATDYPW 619

QY 601 RPALSPFEQKLLNLTSLIKRTGYSERSAGYLDVLTQSRPGRPGVPATVWESCTCPVG 660
Db 620 RPTIKHADFOKLLNLTSLIKRTGYSERSAGYLDVLTQSRPGRPGVPATVWESCTCPVG 679

QY 661 YGGQFCETCLPGYRRPESLPGYSPCVLCTCNHSETCDPETGVCDNRDNTAGPHCEKCS 720
Db 680 YLGQHCEQCDQGFRRSRPELRREFTCERCNCNGHSDTCDPETGMCMCNCOHNTAGLSCERCK 739

QY 721 DGYGDSLTGTSDDCQPCPCPGSSCAIVPKTKVEVCTHCPTGTAGKRCCLDDGYFGDP 780
Db 740 DGYGDSLTGTSDDCQPCPCPGSSCAIVPKTKVEVCTHCPTGTAGKRCCLDDGYFGDP 799

QY 781 LGSNGPVRLCRPPCQNDNIDPNAVGNCRNLTGECCLKCIYNTAGFYCDRCCKEGFFGNPLAP 840
Db 800 LGEKGPVRACRACSCNNIEFNAVGNCRNLTGECCLKCIYNTAGFYCDRCCKEGFFGNPLAP 859

QY 841 NPADKCKACACN-YGTVOQSSCNPTVTGQCQCLPHVSGRDCGTCDPGYVNLQSGQCERC 899
Db 860 NVADKCKPCSPYGTVDRTQACSVTGTGQCQCLPHVSGRDCGTCDPGYVNLQSGQCERC 919

QY 900 DCHALGSTNGQCDIRTGQCECQPGITGQHCERCETNHFGFEGPCKPCDCHHGSLSLQC 959
Db 920 NCNPIGSTNGQCDIRTGQCECQPGITGQHCERCETNHFGFEGPCKPCDCHHGSLSLQC 979

QY 960 KDDGRCECREGVGNRCDCQCEENFYNRSWPGCQECPCYRLVKDAAAEHRVKLOELES 1019
Db 980 KEDGRCHCRPGFVSGRCDCMCEENFYNRSTPQCCQPCYSLVRDKVNCQKQLDLQNL 1039

QY 1020 IANLGTGDDMTDQAFEDRLKEAREVTDLLREAEQVQKVDQNLMDRLQVRNSSLHSQIS 1079
Db 1040 IDSLDNTETTVSDKAFEDRLKEAREVTDLLREAEQVQKVDQNLMDRLQVRNSSLHSQIS 1099

QY 1080 RLQIRNTIETGILAEARARSVESTEQIEIASRELEKAKMA-ANVSITQPESTGEPNN 1138
Db 1100 RLQIRNTIETGILAEARARSVESTEQIEIASRELEKAKMA-ANVSITQPESTGEPNN 1159

QY 1139 MTLAAEARRLAERHKEADDIVRVAKTANETSABAYNLLRLTAGENOTALEIEELNRK 1198
Db 1160 MTLAAEARRLAERHKEADDIVRVAKTANETSABAYNLLRLTAGENOTALEIEELNRK 1219

QY 1199 YEOAKNISODLEKQARVHEBAKRAQKAVIYASVAQLTPVDSEALENEANKIKKEAAD 1258
Db 1220 YLEAKDLAKNLEKQAAKVHAEAEAGNKAALKIYANLTSLPPTKTLEDDANKIKKEAAD 1279

QY 1259 LDRIDQKLDYEDLRDMRGKEHEVKNLLEKGAEOQTADQQLARADAALAEAEAAK 1318
Db 1280 LDKLIDKTEKEYNLREDLRGKETEVRLKLDKGKTEQQTADQQLARADAALAEAEAAK 1339

QY 1319 GRSTLQEAANDILNLDKDFRRVNDKTAEEALRRIPAINRTIAEANEKTRAEALGNA 1378
Db 1340 GKSTFQEAODILNLDKDFRRVNDKTAEEALRRIPAINRTIAEANEKTRAEALGNA 1399

QY 1379 AADATEAKNKAHEAERIAAOKNATSTKADAERTFGEVTDLDNEVNGMLRQLEAEENEL 1438
Db 1400 AADATEAKNKAHEAERIAAOKNATSTKADAERTFGEVTDLDNEVNGMLRQLEAEENEL 1459

QY 1439 KRQDDADQDMMAGMASQAQAEALNAPKAKNSVSSLLSQNLNLLDQGLDQVLDLNL 1498
Db 1460 EKKAQEAADTMMAGMASQAQAEALNAPKAKNSVSSLLSQNLNLLDQGLDQVLDLNL 1519

QY 1499 NEIEGSLNKADEKASDLDRKVSDESARKQEAAMVYNRDIAEIIKDIHNEIDIKKT 1558
Db 1520 NQIDNALKDAKDMAGSELDRLKELNDIAKQEDMISDYDQIQEIRADIANLNDIKNT 1579

QY 1559 LPTGCFNTPSIEKP 1572
Db 1580 LPTGCFNTPSIEKP 1593

RESULT 2

Q90ZN3 PRELIMINARY; PRT; 1007 AA.
AC Q90ZN3;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Laminin gamma 1 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Halfter W., Dong S., Balasubramani M., Bier M.E.;
RT "Aberrant histogenesis after temporary disruption of the retinal basal
lamina.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF373841; AAK55397.1; -.
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR000034; Laminin B.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR008211; LamNT.
DR Pfam; PF00052; laminin_B; 1.
DR Pfam; PF00053; laminin_EGF; 9.

QY	1259	LDRLIDQKLDYEDLRSDMRGKEHEVKNLLEKGAEQQTADQLLARADAAKALAEBAACK	1318
DB	1294	LDRLIDQKLDYEDLRSDMRGKEHEVKNLLEKGAEQQTADQLLARADAAKALAEBAACK	1353
QY	1319	GRSTLQEAANDILNLLKDFDRRVNDNKTAEEALRRIPAINRTIAEANEKTREQAALGNA	1378
DB	1354	GRSTLQEAANDILNLLKDFDRRVNDNKTAEEALRRIPAINRTIAEANEKTREQAALGNA	1413
QY	1379	AADATEAKNKAHEAERIAASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAENEL	1438
DB	1414	AADATEAKNKAHEAERIAASAVQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAENEL	1473
QY	1439	KRKQDDADQDMMWAGMASQAAQAEALNARKAKNSVSSLLSQLNLLDQLGQLDVTDLNKL	1498
DB	1474	KRKQDDADQDMMWAGMASQAAQAEALNARKAKNSVSSLLSQLNLLDQLGQLDVTDLNKL	1533
QY	1499	NEIEGSLNKAKDEMKASDLDRKVSDDLESEARKQEAAMIDYNRDIAEIIKDIHNLEDIKKT	1558
DB	1534	NEIEGSLNKAKDEMKASDLDRKVSDDLESEARKQEAAMIDYNRDIAEIIKDIHNLEDIKKT	1593
QY	1559	LPTGCFNTPSIEKP	1572
DB	1594	LPTGCFNTPSIEKP	1607

RESULT 2

MMHUB2
laminin gamma-1 chain precursor - human
N;Alternate names: laminin chain B2
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text change 10-Dec-1999
C;Accession: S13548; A28158; S13549; B34961; S14664; S23567
R;Kallunki, T.; Ikonen, J.; Chow, L.T.; Kallunki, P.; Tryggvason, K.
J. Biol. Chem. 266, 221-228, 1991
A;Title: Structure of the human laminin B2 chain gene reveals extensive divergence from
A;Reference number: S13548; MUID:91093128; PMID:1985895
A;Accession: S13548
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1609 <KAL>
A;Cross-references: GB:M55217; NID:g186937
A;Note: the nucleotide sequence was submitted to GenBank, February 1991
R;Pikkarainen, T.; Kallunki, T.; Tryggvason, K.
J. Biol. Chem. 263, 6751-6758, 1988
A;Title: Human laminin B2 chain. Comparison of the complete amino acid sequence with the
A;Reference number: A28158; MUID:88198245; PMID:3360804
A;Accession: A28158
A;Molecule type: mRNA
A;Residues: 1-211, 'I', 213-1609 <PIK>
A;Cross-references: EMBL:J03202; NID:g186916; PIDN:AAA59488.1; PID:g307107
R;Fukushima, Y.; Pikkarainen, T.; Kallunki, T.; Eddy, R.L.; Byers, M.G.; Haley, L.L.; He
Cytogenet. Cell Genet. 48, 137-141, 1988
A;Title: Isolation of a human laminin B2 (LAMB2) cDNA clone and assignment of the gene to
A;Reference number: S13549; MUID:89169663; PMID:3234037
A;Accession: S13549
A;Molecule type: mRNA
A;Residues: 1393-1609 <FUK>
A;Cross-references: EMBL:M27654; NID:g186923; PIDN:AAA59489.1; PID:g186924
R;Olson, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki,
Lab. Invest. 60, 772-782, 1989
A;Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 cha
A;Reference number: A34961; MUID:89280632; PMID:2733383
A;Accession: B34961
A;Molecule type: mRNA
A;Residues: 868-1551, 'N', 1553-1609 <OLS>
R;Santos, C.L.S.; Sabbaga, J.; Brentani, R.
DNA Seq. 1, 275-277, 1991
A;Title: Differences in human laminin B2 sequences.
A;Reference number: S14664; MUID:92216129; PMID:1806043
A;Accession: S14664
A;Molecule type: mRNA
A;Residues: 1282-1609 <SAN>
A;Cross-references: EMBL:X13939; NID:g342237; PIDN:CAA32122.1; PID:g34238

Db 396 SSCHCSPVGLSTQCDSYGRCSCKPGVMGDKCDRCQPGFPHSLTEAGCRPCSCDPSGSIDE 455

Qy 421 CNVETGRCVKDQNVGEGNCERCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGSVYDI 480

Db 456 CNVETGRCVKDQNVGEGNCERCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGSVYSI 515

Qy 481 SSTFOIDEDGWRVZQRDSEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYGQ 540

Db 516 SSTFOIDEDGWRAEQRDSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSYGQ 575

Qy 541 NLSFSFRVDRDRTRLSAEDLVLEGAGLRVSVPPLIAQNSYSPSETTVKYIFRLHEATDYPW 600

Db 576 NLSFSFRVDRDRTRLSAEDLVLEGAGLRVSVPPLIAQNSYSPSETTVKYIFRLHEATDYPW 635

Qy 601 RPALSPFEFQKLLNLTSLKIRGTYSERSAGYLDVTLQSRPQPGVDPATWVESCTCPVG 660

Db 636 REALTPFEFQKLLNLTSLKIRGTYSERSAGYLDVTLASARPQPGVDPATWVESCTCPVG 695

Qy 661 YGGQFCETCLPGYRRRETSLGPYSPCVLCTCNHGHSETCDPETGVCDRCRNTAGPHCEKCS 720

Db 696 YGGQFCMCLSGYRRRETPLGPYSPCVLCAACNHGHSETCDPETGVCCNCRDNTAGPHCEKCS 755

Qy 721 DGYGDSLTGTSSDCQPCPCPGSSCAIVPKTKKEVVCTHCPTGTAGKRCCLCDDGYFGDP 780

Db 756 DGYGDSLTGTSSDCQPCPCPGSSCAVVPKTKKEVVCTNCPTGTTGKRCELCDGDFGDP 815

Qy 781 LGSNGPVRLCRPCQCNNDIDNAVGNCRNLGTGELCKIYNTAGFYCDRCKEGFFGNPLAP 840

Db 816 LGRNBPVRLCRLCQCSNIDNAVGNCRNLGTGELCKIYNTAGFYCDRCXGDFGNPLAP 875

Qy 841 NPADCKKACACN-YGTVQQQSSCNPVTCQCCPLPHVSGRDCGTCDPGYYNLQSGGQCERC 899

Db 876 NPADCKKACNCPYGTMTKQSSCNPVTCQCCPLPHVSGRDCGTCDPGYYNLQSGGQCERC 935

Qy 900 DCHALGSTNGQCDIRTGQCECOPGITGQHCCERCETNHFPGPEGCKPCDCHHGSLSLQC 959

Db 936 DCHALGSTNGQCDIRTGQCECOPGITGQHCCERCETNHFPGPEGCKPCDCHHGSLSLQC 995

Qy 960 KDDGRCEGREGFVGNRCDCQCEENFYNRSWPGQCECPACVRLVKDKAAEHRVKLQELSL 1019

Db 996 KDDGRCEGREGFVGNRCDCQCEENFYNRSWPGQCECPACVRLVKDKVADHRVKLQELSL 1055

Qy 1020 IANLGTGDDMVTDOAFEDRLKEAREVTDLLREAQEVKDQNDQNLMDRLQRVNSSLHSQIS 1079

Db 1056 IANLGTGDEMVTDOAFEDRLKEAREVMDLLREAQDVKDQNDQNLMDRLQRVNSSLSSQIS 1115

Qy 1080 RLQNIQNTIETGILAEARARSRVESTEQLEIEIASRELEKAKM-AANVSITQPESTGEPNN 1138

Db 1116 RLQNIQNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAANVSITQPESTGDPNN 1175

Qy 1139 MTLAEEARRLAERHKQEAADDIVRVAKTANETSAAEYNLLRLTLAGENQTALEIEELNRK 1198

Db 1176 MTLAEEARKLAERHKQEAADDIVRVAKTANDTSTEAYNLLRLTLAGENQTAFAIEELNRK 1235

Qy 1199 YEQAKNISQLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAAD 1258

Db 1236 YEQAKNISQLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPLDSETLENEANNIKNEAEN 1295

Qy 1259 LDRLIDQKLKDYEDLREDMRGKEHEVKNLLEKGAEQQTADQLLARADAAKALAEBAKK 1318

Db 1296 LEQLIDQKLKDYEDLREDMRGKELEVKNLLEKGTQEQQTADQLLARADAAKALAEBAKK 1355

Qy 1319 GRSTLQEANDILNNLKDFFRRVNDNKTAAEEALRRIPAINRTIAEANEKTRQAQLALGNA 1378

Db 1356 GRDTLQEANDILNNLKDFFRRVNDNKTAAEEALRKIPAINQITTEANEKTRQAQALGSA 1415

Qy 1379 AADATEAKNKAHEAERIAASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAENEL 1438

Db 1416 AADATEAKNKAHEAERIAASAVQKNATSTKAAEARTFAEVTDLNEVNNMLKQLQEAKEKL 1475

Qy 1439 KRKQDDADQDMMAGMASQAQAEALNARKAKNSVSLLSQLNNLLDQLGQDVTDLNKL 1498

Db 1476 KRKQDDADQDMMAGMASQAQAEALNARKAKNSVTSLLSIINDLLEQLGQDVTDLNKL 1535

RESULT 3

MMFFB2

laminin gamma-1 chain precursor - fruit fly (Drosophila melanogaster)

N:Alternate names: laminin chain B2

C:Species: Drosophila melanogaster

C>Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text_change 16-Jun-2000

C:Accession: A31483; A33737; S01733; A40502

R:Chi, H.C.; Hui, C.F.

J. Biol. Chem. 264, 1543-1550, 1989

A:Title: Primary structure of the Drosophila laminin B2 chain and comparison with human,

A:Reference number: A31483; MUID:89109164; PMID:2912972

A:Accession: A31483

A:Molecule type: mRNA

A:Residues: 1-1639 <CHI>

A:Cross-references: EMBL:M25063; NID:g157803; PIDN:AAA28664.1; PID:g157804

R:Montell, D.J.; Goodman, C.S.

J. Cell Biol. 109, 2441-2453, 1989

A:Title: Drosophila laminin: sequence of B2 subunit and expression of all three subunits

A:Reference number: A33737; MUID:90037237; PMID:2808533

A:Accession: A33737

A:Molecule type: mRNA

A:Residues: 1-39, 'T', '41-891, 'L', 893-1106, 'T', 1108-1459, 'HV', 1462-1581, 'G', 1583-1639 <MON

A:Note: 831-Tyr was also found

R:Chi, H.C.; Hui, C.F.

Nucleic Acids Res. 16, 7205-7206, 1988

A:Title: cDNA and amino acid sequences of Drosophila laminin B2 chain.

A:Reference number: S01733; MUID:88303364; PMID:3405777

A:Accession: S01733

A:Molecule type: mRNA

A:Residues: 344-1639 <CH2>

A:Cross-references: EMBL:X07806; NID:g8179; PIDN:CAA30665.1; PID:g1335618

A:Note: the authors translated the codon GGC for residue 409 as Phe

R:Chi, H.C.; Juminaga, D.; Wang, S.Y.; Hui, C.F.

DNA Cell Biol. 10, 451-466, 1991

A:Title: Structure of the Drosophila gene for the laminin B2 chain.

A:Reference number: A40502; MUID:91299161; PMID:1840513

A:Accession: A40502

A:Molecule type: DNA

A:Residues: 1-891, 'L', 893-1639 <CH3>

A:Cross-references: GB:M58417; NID:g157805; PIDN:AAA28665.1; PID:g157806

C:Genetics:

A:Gene: lamB2

A:Cross-references: FlyBase:FBgn0002528

A:Map position: 3L 67C

A:Introns: 65/3; 110/2; 153/1; 358/1; 495/2; 1357/2; 1469/3; 1570/1

C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin

C:Function:

A:Description: interact with cells and with other basement membrane proteins to promote

C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology

C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular

F:1-33/Domain: signal sequence #status predicted <SIG>

F:34-1639/Product: laminin gamma-1 chain #status predicted <MAT>

F:34-297/Domain: VI <DOM6>

F:298-528/Domain: V <DOM5>

F:299-356/Domain: laminin-type EGF-like homology <LE01>

F:359-411/Domain: laminin-type EGF-like homology <LE02>

F:414-458/Domain: laminin-type EGF-like homology <LE03>

F:461-511/Domain: laminin-type EGF-like homology <LE04>

F:514-523/Domain: laminin-type EGF-like homology #status atypical <LE05>

F:529-705/Domain: IV <DOM4>

F:706-1057/Domain: III <DOM3>

F:710-741/Domain: laminin-type EGF-like homology #status atypical <LE06>

F:744-790/Domain: laminin-type EGF-like homology <LE07>

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:58 ; Search time 14.4672 Seconds
(without alignments)
10452.141 Million cell updates/sec

Title: US-10-037-182-20
Perfect score: 8527
Sequence: 1 AMDECADEGGRPQRCMPFV.....EDIKKTLPTGCFNTPSIEKP 1572

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8460	99.2	1607	1 MMMSB2	laminin gamma-1 ch
2	8034	94.2	1609	1 MMHUB2	laminin gamma-1 ch
3	3469	40.7	1639	1 MMFFB2	laminin gamma-1 ch
4	3193	37.4	1557	2 T28811	hypothetical prote
5	2591	30.4	1193	2 A44018	laminin B2t chain
6	2400.5	28.2	1192	2 S69000	laminin gamma 2 ch
7	1812.5	21.3	3106	1 S53868	laminin alpha-2 ch
8	1780.5	20.9	3084	1 MMMSA	laminin alpha-1 ch
9	1735	20.3	3075	2 S14458	laminin alpha-1 ch
10	1677	19.7	1786	1 MMHUB1	laminin beta-1 cha
11	1661.5	19.5	1786	1 MMMSB1	laminin beta-1 cha
12	1655.5	19.4	1790	1 MMFFB1	laminin beta-1 cha
13	1632	19.1	2823	2 T23064	hypothetical prote
14	1632	19.1	2823	2 F87908	protein T22A3.8 [i
15	1632	19.1	3102	2 T43291	laminin alpha chai
16	1620.5	19.0	1808	2 T15099	hypothetical prote
17	1569	18.4	1801	1 MMRTS	laminin beta-2 cha
18	1547.5	18.1	1798	2 S53869	laminin beta-2 cha
19	1457	17.1	1797	2 A55677	laminin beta-2 cha
20	1454	17.1	3712	2 S18253	laminin alpha-1 ch
21	1384	16.2	3672	2 T23433	hypothetical prote
22	1384	16.2	3704	2 T37316	probable laminin a
23	1347.5	15.8	3635	2 T10053	laminin alpha 5 ch
24	1155.5	13.6	606	2 A54665	netrin-1 precursor
25	1044.5	12.2	581	2 B54665	netrin-2 precursor
26	986.5	11.6	612	2 JH0799	laminin-related pr
27	938	11.0	1170	2 A53612	laminin B1k chain
28	903.5	10.6	4391	2 A38096	perlecan precursor
29	903	10.6	1168	2 I56985	kalinin B1 - mouse

30	877.5	10.3	3707	2 S18252	heparan sulfate pr
31	637.5	7.5	1160	2 F88369	protein unc-52 [im
32	637.5	7.5	2295	2 C88369	protein unc-52 [im
33	637.5	7.5	3375	2 T19821	hypothetical prote
34	619	7.3	1751	1 MMHUMH	laminin alpha-2 ch
35	588	6.9	1620	2 T27283	hypothetical prote
36	586	6.9	1816	1 S68960	laminin alpha-4 ch
37	555.5	6.5	1574	2 T13954	MEGF6 protein - ra
38	551	6.5	1111	2 T26972	hypothetical prote
39	514	6.0	1713	2 A55347	adhesive ligand ep
40	490	5.7	400	2 T46383	hypothetical prote
41	477	5.6	2471	2 A49128	cell-fate determin
42	471	5.5	303	2 B45067	laminin B1 chain -
43	466.5	5.5	2703	1 A24420	notch protein - fr
44	466	5.5	2318	2 S45306	notch 3 protein -
45	459.5	5.4	2352	2 T30201	Notch homolog prot

ALIGNMENTS

RESULT 1

MMMSB2
laminin gamma-1 chain precursor - mouse
N;Alternate names: laminin chain B2
C;Species: Mus musculus (house mouse)
C;Date: 28-Feb-1986 #sequence revision 30-Jun-1991 #text change 10-Dec-1999
C;Accession: A28469; A27729; A28082; S02680; S05327; S02037; A02870; S13544; S14552
R;Sasaki, M.; Yamada, Y.
J. Biol. Chem. 262, 17111-17117, 1987
A;Title: The laminin B2 chain has a multidomain structure homologous to the B1 chain.
A;Reference number: A28469; MUID:88059118; PMID:3680290
A;Accession: A28469
A;Molecule type: mRNA
A;Residues: 1-1607 <SAS>
A;Cross-references: EMBL:J03484; NID:G198694; PIDN:AAA39405.1; PID:G293688
R;Durkin, M.E.; Bartos, B.B.; Liu, S.H.; Phillips, S.L.; Chung, A.E.
Biochemistry 27, 5198-5204, 1988
A;Title: Primary structure of the mouse laminin B2 chain and comparison with laminin B1
A;Reference number: A27729; MUID:89000737; PMID:3167041
A;Accession: A27729
A;Molecule type: mRNA
A;Residues: 1-263, 'D', 265-336, 'C', 338-446, 'PS', 449-661, 'S', 663-885, 887-1155, 1157-1433, 'A'
A;Cross-references: EMBL:J02930; NID:G198702; PIDN:AAA39408.1; PID:G293691
A;Note: the authors translated the codon TAT for residue 544 as Asp and GCG for residue 5
R;Ogawa, K.; Burebello, P.D.; Sasaki, M.; Yamada, Y.
J. Biol. Chem. 263, 8384-8389, 1988
A;Title: The laminin B2 chain promoter contains unique repeat sequences and is active in
A;Reference number: A28082; MUID:88228071; PMID:2836421
A;Accession: A28082
A;Molecule type: DNA
A;Residues: 1-215, 'A', 217-239 <OGA>
A;Cross-references: EMBL:J03749; NID:G198704; PIDN:AAA39409.1; PID:G554184
R;Fujiwara, S.; Shinkai, H.; Deutzmann, R.; Paulsson, M.; Timpl, R.
Biochem. J. 252, 453-461, 1988
A;Title: Structure and distribution of N-linked oligosaccharide chains on various domains
A;Reference number: S02678; MUID:88326259; PMID:2458101
A;Accession: S02680
A;Molecule type: protein
A;Residues: 227-238 <FUJ>
R;Hartl, L.; Oberbaumer, I.; Deutzmann, R.
Eur. J. Biochem. 173, 629-635, 1988
A;Title: The N terminus of laminin A chain is homologous to the B chains.
A;Reference number: S00624; MUID:88225080; PMID:3267223
A;Accession: S05327
A;Molecule type: protein
A;Residues: 227-238;387-393, 'F', 395-405;881-912;1022-1034 <HAR>
R;Deutzmann, R.; Huber, J.; Schmetz, K.A.; Oberbaumer, I.; Hartl, L.
Eur. J. Biochem. 177, 35-45, 1988
A;Title: Structural study of long arm fragments of laminin. Evidence for repetitive C-ter
A;Reference number: S01790; MUID:89030693; PMID:3181157
A;Accession: S02037
A;Molecule type: protein

A;Residues: 1362-1377,'X',1379-1392,'X',1394-1406 <DEU>
R;Barlow, D.P.; Green, N.M.; Kurkinen, M.; Hogan, B.L.M.
EMBO J. 3, 2355-2362, 1984
A;Title: Sequencing of laminin B chain cDNAs reveals C-terminal regions of coiled-coil a
A;Reference number: A02870; MUID:85051302; PMID:6209134
A;Accession: A02870
A;Molecule type: mRNA
A;Residues: 1391-1474,'K',1476-1575,'N',1577-1607 <BAR>
A;Cross-references: EMBL:X05211; NID:G52862; PIDN:CAA28838.1; PID:9817975
R;Paulsson, M.; Deutzmann, R.; Timpl, R.; Dalzoppo, D.; Odermatt, E.; Engel, J.
EMBO J. 4, 309-316, 1985
A;Title: Evidence for coiled-coil alpha-helical regions in the long arm of laminin.
A;Reference number: S13543; MUID:85257455; PMID:3848400
A;Accession: S13544
A;Molecule type: protein
A;Residues: 1506-1523,'X',1525 <PAU>
R;Olson, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki,
Lab. Invest. 60, 772-782, 1989
A;Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 cha
A;Reference number: A34961; MUID:89280632; PMID:2733383
A;Accession: S14552
A;Molecule type: protein
A;Residues: 881-912;1022-1034;1364-1377;1379-1392;1394-1409;1506-1525;1593-1606 <OLS>
C;Genetics:
A;Gene: Lamb-2
A;Map position: 1
A;Introns: 138/1; 239/3
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C;Function:
A;Description: interact with cells and with other basement membrane proteins to promote
C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular
F;1-33/Domain: signal sequence #status predicted <SIG>
F;34-1607/Product: laminin gamma-1 chain #status predicted <MAT>
F;34-283/Domain: VI <DOM6>
F;284-502/Domain: V <DOM5>
F;284-337/Domain: laminin-type EGF-like homology #status atypical <LE01>
F;340-393/Domain: laminin-type EGF-like homology <LE02>
F;396-440/Domain: laminin-type EGF-like homology <LE03>
F;443-490/Domain: laminin-type EGF-like homology <LE04>
F;493-502/Domain: laminin-type EGF-like homology #status atypical <LE05>
F;503-687/Domain: IV <DOM4>
F;688-1032/Domain: III <DOM3>
F;688-719/Domain: laminin-type EGF-like homology #status atypical <LE06>
F;722-768/Domain: laminin-type EGF-like homology <LE07>
F;771-823/Domain: laminin-type EGF-like homology <LE08>
F;826-879/Domain: laminin-type EGF-like homology <LE09>
F;882-930/Domain: laminin-type EGF-like homology <LE10>
F;933-978/Domain: laminin-type EGF-like homology <LE11>
F;981-1026/Domain: laminin-type EGF-like homology <LE12>
F;1033-1607/Domain: II/I <DOM2>
F;1033-1607/Region: heptad repeats
F;38-48/Disulfide bonds: #status predicted
F;58,132,574,648,1020,1105,1159,1173,1203,1221,1239,1437/Binding site: carbohydrate (Asn
F;1029,1032/Disulfide bonds: interchain #status predicted
F;1378,1393/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;1598/Disulfide bonds: interchain (to chain B1) #status experimental

Query Match

Best Local Similarity 99.2%; Score 8460; DB 1; Length 1607;

Mismatches 1565; Conservative 2; Indels 2; Gaps 2;

QY	1	AMDECADEGGRPQRCMPEFVNAAFNVVATNTCGTPPBEYCVQGTGVTGKSchLCDAG 60
Db	34	AMDECADEGGRPQRCMPEFVNAAFNVVATNTCGTPPBEYCVQGTGVTGKSchLCDAG 93
QY	61	QOHLQHGAFLTDYNNQADTTWQSQTMLAGVQYPSNLTLLHLGKAFDITYVRLKFHTS 120
Db	94	QOHLQHGAFLTDYNNQADTTWQSQTMLAGVQYPSNLTLLHLGKAFDITYVRLKFHTS 153
QY	121	RPESFAIYKRTREDGPWIPYQYSSGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDISPL 180
Db	154	RPESFAIYKRTREDGPWIPYQYSSGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDISPL 213

QY	181	TGQNVAFSTLEGRPSAYNFNDNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSYYY 240
Db	214	TGQNVAFSTLEGRPSAYNFNDNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSYYY 273
QY	241	AISDFAVGGRCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPFFNDRPWRATAES 300
Db	274	AISDFAVGGRCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPFFNDRPWRATAES 333
QY	301	ASECLPCDCNGRSQECYFDPPELYRSTGHGGHCTNCRDNTDGAKCERCRENFRGLNTEAC 360
Db	334	ASESLPCDCNGRSQECYFDPPELYRSTGHGGHCTNCRDNTDGAKCERCRENFRGLNTEAC 393
QY	361	SPCHCSPVGSLSLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLSLTAAGCRPCSCDPSGSTDE 420
Db	394	SPCHCSPVGSLSLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLSLTAAGCRPCSCDPSGSTDE 453
QY	421	CNVETGRVCVKDNVEGFNCERCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGSYVYDI 480
Db	454	CNVETGRVCVKDNVEGFNCERCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGSYVYDI 513
QY	481	SSTFQIDEDGWRVEQRDGSEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYGQ 540
Db	514	SSTFQIDEDGWRVEQRDGSEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYGQ 573
QY	541	NLSFSFRVDRRDLRLSAEDLVLEGAGLRVSVPLIAQNSYPSSETTVKYIFRLHEATDYPW 600
Db	574	NLSFSFRVDRRDLRLSAEDLVLEGAGLRVSVPLIAQNSYPSSETTVKYIFRLHEATDYPW 633
QY	601	RPALSPFEFQKLLNLTSLKIRGTYSERSAGYLDVTLQOSARPGPGVPATWVESCTCPVG 660
Db	634	RPALSPFEFQKLLNLTSLKIRGTYSERTAGYLDVTLQOSARPGPGVPATWVESCTCPVG 693
QY	661	YGGQFCETCLPGYRRRETPSLGPYSPCVLCTCNHSHSTCDPETGVCDNRDNTAGPHCEKCS 720
Db	694	YGGQFCETCLPGYRRRETPSLGPYSPCVLCTCNHSHSTCDPETGVCDNRDNTAGPHCEKCS 753
QY	721	DGYVGDSTLTGTSDDCQPCPCPGGSSCAIVPKTKVVVCHTCTGTAGKRCCLCDGYYFGDP 780
Db	754	DGYVGDSTLTGTSDDCQPCPCPGGSSCAIVPKTKVVVCHTCTGTAGKRCCLCDGYYFGDP 813
QY	781	LGSNGPVRLCRPCQCNDNIDPNAVGNCRNLTGECCLKIYNTAGFYCDRCCKEGFGNPLAP 840
Db	814	LGSNGPVRLCRPCQCNDNIDPNAVGNCRNLTGECCLKIYNTAGFYCDRCCKEGFGNPLAP 873
QY	841	NPADKCKACACN-YGTVQQSSCNPNVTGQCQCLPHYSGRDCGTCDPGYYNLQSGGCERC 899
Db	874	NPADKCKACACNPGYTVQQSSCNPNVTGQCQCLPHYSGRDCGTCDPGYYNLQSGGCERC 933
QY	900	DCHALGSTNGQCDIRTGQCECPGIGTGHCHCERCETNHFHGFGECKPCDCHHEGSLQOC 959
Db	934	DCHALGSTNGQCDIRTGQCECPGIGTGHCHCERCETNHFHGFGECKPCDCHHEGSLQOC 993
QY	960	KDGRCECREGFGVGNRCDCQCEENYFYNRSWPGQCECPACRYLVKDKAAEHRVKLQLESL 1019
Db	994	KDGRCECREGFGVGNRCDCQCEENYFYNRSWPGQCECPACRYLVKDKAAEHRVKLQLESL 1053
QY	1020	IANLGTGDDMVTDQAFEDRLKAEAREVTDLLREAEQVQDVQDQNLMDRLQRVNSSLHSQIS 1079
Db	1054	IANLGTGDDMVTDQAFEDRLKAEAREVTDLLREAEQVQDVQDQNLMDRLQRVNSSLHSQIS 1113
QY	1080	RLQNTIRNTIETGILAEARARSVESTEQLEIEIASRELEKAKM-AANVSITQPESTGEPPN 1138
Db	1114	RLQNTIRNTIETGILAEARARSVESTEQLEIEIASRELEKAKMAANVSITQPESTGEPPN 1173
QY	1139	MTLLAEERARRLAERHKQEAADDIVRVAKTANETSAEAYNLLRTLAGENQTALEIEELNRK 1198
Db	1174	MTLLAEERARRLAERHKQEAADDIVRVAKTANETSAEAYNLLRTLAGENQTALEIEELNRK 1233
QY	1199	YEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAAD 1258
Db	1234	YEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAAD 1293

Query Match		99.2%;	Score 8460;	DB 1;	Length 1607;
Best Local Similarity		99.4%;	Pred. No. 2.1e-310;		
Matches 1565;		Conservative	2;	Mismatches	5;
		Indels		2;	Gaps
				2;	
QY	1	AMDECADEGGRRPQRCMPEFVNAAFNVTVATNTCGTPPEYCVQGTGVTGKSHLCDAG	60		
Db	34	AMDECADEGGRRPQRCMPEFVNAAFNVTVATNTCGTPPEYCVQGTGVTGKSHLCDAG	93		
QY	61	QQLHQGAFLTDYNNQADTTWQSQTMLAGVQYVNSINLTLHLGKAFDITYVRLKFHTS	120		
Db	94	QQLHQGAFLTDYNNQADTTWQSQTMLAGVQYVNSINLTLHLGKAFDITYVRLKFHTS	153		
QY	121	RPEFAIYKRTREDGPWIPYQYVSGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDISPL	180		
Db	154	RPEFAIYKRTREDGPWIPYQYVSGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDISPL	213		
QY	181	TGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTEFGEVENDPKVLKSYYY	240		
Db	214	TGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTEFGEVENDPKVLKSYYY	273		
QY	241	AISDFAVGRCKCNCHGASHCEVCNKEPDKLMCNCKHNTYGVDCCKLPPFNDRPWRRATAES	300		
Db	274	AISDFAVGRCKCNCHGASHCEVCNKEPDKLMCNCKHNTYGVDCCKLPPFNDRPWRRATAES	333		
QY	301	ASECLPCDCNGRSQECYFDPPELYRSTGHGGHCTNCRDNTDGAKCERCRENFFRLGNTEAC	360		
Db	334	ASESLPCDCNGRSQECYFDPPELYRSTGHGGHCTNCRDNTDGAKCERCRENFFRLGNTEAC	393		
QY	361	SPCHCSPVGSLSLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSTDE	420		
Db	394	SPCHCSPVGSLSLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSTDE	453		
QY	421	CNVETGRVCCKDNVEGFNCERCCKPGFNLESNPCKGCTPCFCFGHSSVCTNAVGSYVIDI	480		
Db	454	CNVETGRVCCKDNVEGFNCERCCKPGFNLESNPCKGCTPCFCFGHSSVCTNAVGSYVIDI	513		
QY	481	SSTFQIDEDGWRVEQRDGEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYGQ	540		
Db	514	SSTFQIDEDGWRVEQRDGEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYGQ	573		
QY	541	NLSFSFRVDRDRTRLAEDLVLEGAGLRVSVPLIAQNSYPSSETTVKYIFRLHEATDYPW	600		
Db	574	NLSFSFRVDRDRTRLAEDLVLEGAGLRVSVPLIAQNSYPSSETTVKYIFRLHEATDYPW	633		
QY	601	RPALSPFEFQKLLNNLTSIKIRGTYSERSAGYLDVTLQSAHPGPGVPATWVESCTCPVG	660		
Db	634	RPALSPFEFQKLLNNLTSIKIRGTYSERTAGYLDVTLQSAHPGPGVPATWVESCTCPVG	693		
QY	661	YGGQFCETCLPGYRRETPSLGPYSPCVLCTCNHGHSETCDPETGVCDCRDNTAGPHCEKCS	720		
Db	694	YGGQFCETCLPGYRRETPSLGPYSPCVLCTCNHGHSETCDPETGVCDCRDNTAGPHCEKCS	753		
QY	721	DGYYGDSITLGTSSDCQPCPCPGGSSCAIVPKTEVVCVTHCPTGTAGKRCCLCDDGYFGDP	780		
Db	754	DGYYGDSITLGTSSDCQPCPCPGGSSCAIVPKTEVVCVTHCPTGTAGKRCCLCDDGYFGDP	813		
QY	781	LGSNGPVRLCRQCNDNIDPNVAGVNCNRLTGECLKCIYNTAGFYCDRCKEGFFGNPLAP	840		
Db	814	LGSNGPVRLCRQCNDNIDPNVAGVNCNRLTGECLKCIYNTAGFYCDRCKEGFFGNPLAP	873		
QY	841	NPADKCKACACN-YGTVQQQSSCNPVTTGQCQCLPHVSGRDCGTCDPGYYNLQSGQGGERC	899		
Db	874	NPADKCKACACNPGYGTVQQQSSCNPVTTGQCQCLPHVSGRDCGTCDPGYYNLQSGQGGERC	933		
QY	900	DCHALGSTNGQCDIRTGQCECQPGITGQHCCERCETNHFHFGPEGCKPCDCHHEGSLSLQC	959		
Db	934	DCHALGSTNGQCDIRTGQCECQPGITGQHCCERCETNHFHFGPEGCKPCDCHHEGSLSLQC	993		
QY	960	KDDGRCECREGFGVGNRCQDCEENYFYNRSPWPGCQCECPACRYLVKDKAAEHRVKLQLESL	1019		
Db	994	KDDGRCECREGFGVGNRCQDCEENYFYNRSPWPGCQCECPACRYLVKDKAAEHRVKLQLESL	1053		

QY	1020	IANLGTGDDMVTDQAFEDRLKEAREVTDLLREAEQVKVDQNLMDRLQVNSSLSHSQIS	1079
Db	1054	IANLGTGDDMVTDQAFEDRLKEAREVTDLLREAEQVKVDQNLMDRLQVNSSLSHSQIS	1113
QY	1080	RLQNRNTIETTGILAEARARSRVESTEQLIEIASRELEKAKM-AANVSITQPESTGEPNN	1138
Db	1114	RLQNRNTIETTGILAEARARSRVESTEQLIEIASRELEKAKMAANVSITQPESTGEPNN	1173
QY	1139	MTLLAEERRLAERHKQAEADDIVRVAKTANETSAAEAYNLLRLLAGENQTALEIEELNRK	1198
Db	1174	MTLLAEERRLAERHKQAEADDIVRVAKTANETSAAEAYNLLRLLAGENQTALEIEELNRK	1233
QY	1199	YEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALEANEANKIKKEAAD	1258
Db	1234	YEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALEANEANKIKKEAAD	1293
QY	1259	LDRLIDQKLDYEDLREDMRGKEHEVKNLLEKGAEQQTADQQLLARADAATAKALAEAAKK	1318
Db	1294	LDRLIDQKLDYEDLREDMRGKEHEVKNLLEKGAEQQTADQQLLARADAATAKALAEAAKK	1353
QY	1319	GRSTLQEAANDILNNLKDFDRRVNDNKTAAEEALRRIPAINRTIAEANEKTREAOALGNA	1378
Db	1354	GRSTLQEAANDILNNLKDFDRRVNDNKTAAEEALRRIPAINRTIAEANEKTREAOALGNA	1413
QY	1379	AADATEAKNKAHEAERIAASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAENEL	1438
Db	1414	AADATEAKNKAHEAERIAASAVQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAENEL	1473
QY	1439	KRKQDDADQDMMAGMASQAAQAEELNARKAKNSVSSLLSQNLNLLDQQLGQDQDQDQDQD	1498
Db	1474	KRKQDDADQDMMAGMASQAAQAEELNARKAKNSVSSLLSQNLNLLDQQLGQDQDQDQDQD	1533
QY	1499	NEIEGSLNKADEMKAASDLDRKVSDESEARKQEAAMDYNRDIAEIIKDHNLEDIKKT	1558
Db	1534	NEIEGSLNKADEMKAASDLDRKVSDESEARKQEAAMDYNRDIAEIIKDHNLEDIKKT	1593
QY	1559	LPTGCFNTPSIEKP	1572
Db	1594	LPTGCFNTPSIEKP	1607

RESULT 2
LMG1_HUMAN
ID LMG1_HUMAN STANDARD; PRT; 1609 AA.
AC P11047;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Laminin gamma-1 chain precursor (Laminin B2 chain).
GN LAMC1 OR LAMB2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91093128; PubMed=1985895;
RA Kallunki T., Ikonen J., Chow L.T., Kallunki P., Tryggvason K.;
RT "Structure of the human laminin B2 chain gene reveals extensive
RT divergence from the laminin B1 chain gene."
RL J. Biol. Chem. 266:221-228(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88198245; PubMed=3360804;
RA Pikkarainen T., Kallunki T., Tryggvason K.;
RT "Human laminin B2 chain. Comparison of the complete amino acid
RT sequence with the B1 chain reveals variability in sequence homology
RT between different structural domains."
RL J. Biol. Chem. 263:6751-6758(1988).
RN [3]
RP SEQUENCE OF 1393-1609 FROM N.A.
RX MEDLINE=89169663; PubMed=3234037;
RA Fukushima Y., Pikkarainen T., Kallunki T., Eddy R.L., Byers M.G.,

RA Haley L.L., Henry W.M., Tryggvason K., Shows T.B.;
RT "Isolation of a human laminin B2 (LAMB2) cDNA clone and assignment of
RL the gene to chromosome region 1q25-->q31.";
RN Cytogenet. Cell Genet. 48:137-141(1988).
[4]
RP SEQUENCE OF 1282-1609 FROM N.A.
RX TISSUE=Endothelial cells;
RY MEDLINE=22660472; PubMed=12754519;
RA Zhang H., Li X.-J., Martin D.B., Aebersold R.;
RT "Identification and quantification of N-linked glycoproteins using
RL hydrazide chemistry, stable isotope labeling and mass spectrometry.";
RN Nat. Biotechnol. 21:660-666(2003).
CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components.
CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC different polypeptide chains (alpha, beta, gamma), which are bound
CC to each other by disulfide bonds into a cross-shaped molecule
CC comprising one long and three short arms with globules at each
CC end. The gamma-1 chain is a subunit of laminin-1 (EHS laminin),
CC laminin-2 (merosin), laminin-3 (S-laminin), laminin-4 (S-merosin),
CC laminin-6 (K-laminin) and laminin-7 (KS-laminin).
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Found in the basement membranes (major
CC component).
CC -!- DOMAIN: The alpha-helical domains I and II are thought to interact
CC with other laminin chains to form a coiled coil structure.
CC -!- DOMAIN: Domains VI and IV are globular.
CC -!- SIMILARITY: Contains 1 laminin N-terminal domain.
CC -!- SIMILARITY: Contains 11 laminin EGF-like domains.
CC -!- SIMILARITY: Contains 1 laminin IV domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M55210; AAA59492.1; JOINED.
DR EMBL; M55217; AAA59492.1; JOINED.
DR EMBL; M55201; AAA59492.1; JOINED.
DR EMBL; M55211; AAA59492.1; JOINED.
DR EMBL; M55212; AAA59492.1; JOINED.
DR EMBL; M55213; AAA59492.1; JOINED.
DR EMBL; M55214; AAA59492.1; JOINED.
DR EMBL; M55215; AAA59492.1; JOINED.
DR EMBL; M55216; AAA59492.1; JOINED.
DR EMBL; M55192; AAA59492.1; JOINED.
DR EMBL; M55193; AAA59492.1; JOINED.
DR EMBL; M55194; AAA59492.1; JOINED.
DR EMBL; M55195; AAA59492.1; JOINED.
DR EMBL; M55196; AAA59492.1; JOINED.
DR EMBL; M55197; AAA59492.1; JOINED.
DR EMBL; M55198; AAA59492.1; JOINED.
DR EMBL; M55199; AAA59492.1; JOINED.
DR EMBL; M55200; AAA59492.1; JOINED.
DR EMBL; M55202; AAA59492.1; JOINED.
DR EMBL; M55203; AAA59492.1; JOINED.
DR EMBL; M55204; AAA59492.1; JOINED.
DR EMBL; M55205; AAA59492.1; JOINED.
DR EMBL; M55206; AAA59492.1; JOINED.
DR EMBL; M55207; AAA59492.1; JOINED.
DR EMBL; M55208; AAA59492.1; JOINED.
DR EMBL; M55209; AAA59492.1; JOINED.

DR EMBL; J03202; AAA59488.1; --
DR EMBL; M27654; AAA59489.1; --
DR EMBL; X13939; CAA32122.1; --
DR PIR; S13548; MTHUB2.
DR HSSP; P02468; 1TLE.
DR Genew; HGNC:6492; LAMC1.
DR MIM; 150290; --
DR GO; GO:0005604; C:basement membrane; TAS.
DR GO; GO:0007492; P:endothelium development; TAS.
DR GO; GO:0006461; P:protein complex assembly; TAS.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR008212; Lam_N2.
DR InterPro; IPR000034; Laminin B.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR008211; LamNT.
DR Pfam; PF00052; laminin_B; 1.
DR Pfam; PF00053; laminin_EGF; 9.
DR Pfam; PF00055; laminin_Nterm; 1.
DR PRINTS; PR00011; EGF_LAMININ.
DR ProDom; PD002082; Lam_N2; 1.
DR SMART; SM00180; EGF_Lam; 8.
DR SMART; SM00281; LamB; 1.
DR SMART; SM00136; LamNT; 1.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 11.
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal; Polymorphism.
FT SIGNAL 1 33
FT CHAIN 34 1609 LAMININ GAMMA-1 CHAIN.
FT DOMAIN 34 285 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 286 341 LAMININ EGF-LIKE 1.
FT DOMAIN 342 397 LAMININ EGF-LIKE 2.
FT DOMAIN 398 444 LAMININ EGF-LIKE 3.
FT DOMAIN 445 494 LAMININ EGF-LIKE 4.
FT DOMAIN 495 504 LAMININ EGF-LIKE 5 (N-TERMINAL).
FT DOMAIN 505 689 LAMININ DOMAIN IV.
FT DOMAIN 690 723 LAMININ EGF-LIKE 6.
FT DOMAIN 724 772 LAMININ EGF-LIKE 7.
FT DOMAIN 773 827 LAMININ EGF-LIKE 8.
FT DOMAIN 828 883 LAMININ EGF-LIKE 9.
FT DOMAIN 884 934 LAMININ EGF-LIKE 10.
FT DOMAIN 935 982 LAMININ EGF-LIKE 11.
FT DOMAIN 983 1030 DOMAIN II AND I.
FT DOMAIN 1030 1609 COILED COIL (POTENTIAL).
FT DOMAIN 1038 1609 BY SIMILARITY.
FT DISULFID 286 295 BY SIMILARITY.
FT DISULFID 288 305 BY SIMILARITY.
FT DISULFID 307 316 BY SIMILARITY.
FT DISULFID 319 339 BY SIMILARITY.
FT DISULFID 342 351 BY SIMILARITY.
FT DISULFID 344 367 BY SIMILARITY.
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FT DISULFID 418 427 BY SIMILARITY.
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FT DISULFID 445 456 BY SIMILARITY.
FT DISULFID 447 463 BY SIMILARITY.
FT DISULFID 465 474 BY SIMILARITY.
FT DISULFID 477 492 BY SIMILARITY.
FT DISULFID 724 733 BY SIMILARITY.
FT DISULFID 726 740 BY SIMILARITY.
FT DISULFID 742 751 BY SIMILARITY.
FT DISULFID 754 770 BY SIMILARITY.
FT DISULFID 773 781 BY SIMILARITY.
FT DISULFID 775 792 BY SIMILARITY.
FT DISULFID 795 804 BY SIMILARITY.
FT DISULFID 807 825 BY SIMILARITY.
FT DISULFID 828 842 BY SIMILARITY.
FT DISULFID 830 849 BY SIMILARITY.
FT DISULFID 852 861 BY SIMILARITY.

FT	DISULFID	864	881	BY SIMILARITY.
FT	DISULFID	884	898	BY SIMILARITY.
FT	DISULFID	886	905	BY SIMILARITY.
FT	DISULFID	907	916	BY SIMILARITY.
FT	DISULFID	919	932	BY SIMILARITY.
FT	DISULFID	935	947	BY SIMILARITY.
FT	DISULFID	937	954	BY SIMILARITY.
FT	DISULFID	956	965	BY SIMILARITY.
FT	DISULFID	968	980	BY SIMILARITY.
FT	DISULFID	983	995	BY SIMILARITY.
FT	DISULFID	985	1001	BY SIMILARITY.
FT	DISULFID	1003	1012	BY SIMILARITY.
FT	DISULFID	1015	1028	BY SIMILARITY.
FT	DISULFID	1031	1031	INTERCHAIN (PROBABLE).
FT	DISULFID	1034	1034	INTERCHAIN (PROBABLE).
FT	DISULFID	1600	1600	INTERCHAIN (PROBABLE).
FT	CARBOHYD	60	60	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	134	134	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	576	576	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	650	650	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1022	1022	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1107	1107	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1161	1161	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1175	1175	N-LINKED (GLCNAC. . .) (POTENTIAL).
Query Match 94.2%; Score 8034; DB 1; Length 1609;				
Best Local Similarity 93.3%; Pred. No. 2e-294;				
Matches 1468; Conservative 56; Mismatches 48; Indels 2; Gaps 2				
QY	1	AMDECADEGRRPQRCMP	EFVNAAFNVTVATNTCGTTPPEEYCVQGTGVTKSCHLCDAG	60
Db	36	AMDECTDEGRRPQRCMP	EFVNAAFNVTVATNTCGTTPPEEYCVQGTGVTKSCHLCDAG	95
QY	61	QOHLQHGAAFLTDYNNQ	ADTTWQSQOTMLAGVQYPN	INLT
Db	96	QPHLQHGAAFLTDYNNQ	ADTTWQSQOTMLAGVQYPS	INLT
QY	121	RPESFAIYKRTREDGP	WIPYQYYSGSCENTYSKANRGFIR	TGGDEQQALCTDEFS
Db	156	RPESFAIYKRTREDGP	WIPYQYYSGSCENTYSKANRGFIR	TGGDEQQALCTDEFS
QY	181	TGGNVAFTSLIEGR	PSAYNFNDSPLVQEWVTATDIRVT	LNRLNTFGDEVNDPKVLK
Db	216	TGGNVAFTSLIEGR	PSAYNFNDSPLVQEWVTATDIRVT	LNRLNTFGDEVNDPKVLK
QY	241	AISDFAVGGRCKNGHASE	CVKNEFDKLMCNCKHNTYGVDC	CKCLPFFNDRPWR
Db	276	AISDFAVGGRCKNGHASE	CMKNEFDKLVNCKHNTYGVDC	CKCLPFFNDRPWR
QY	301	ASECLPCDCNGRSQECY	FDPPELYRSTGHGGHCTNCRDNTD	GAKCERC
Db	336	ASECLPCDCNGRSQECY	FDPPELYRSTGHGGHCTNCQDNTD	GAHCERC
QY	361	SPCHCSPVGSLS	TQCDSYGRCSCKPGVMGDKCDRCQ	PGFHS
Db	396	SSCHCSPVGSLS	TQCDSYGRCSCKPGVMGDKCDRCQ	PGFHS
QY	421	CNVETGRVCCKDNVEGF	NCERCKPGFFENLESSNPKGCTPC	FCF
Db	456	CNVETGRVCCKDNVEGF	NCERCKPGFFENLESSNPRGCTPC	FCF
QY	481	SSTFQIDEDGWRVEQR	DGEASLEWSSDRQYIAVIS	DSYFP
Db	516	SSTFQIDEDGWRAEQR	DGEASLEWSSERQDIAVIS	DSYFP
QY	541	NLSFSFRVDRRDR	TRL	SAEDLV
Db	576	NLSFSFRVDRRDR	TRL	SAEDLV
QY	601	RPALSPFEFQKLNNLT	SIKIRGTYSERSAGY	LDVTLQ
Db	636	RPALTPEFQKLNNLT	SIKIRGTYSERSAGY	LDVTLA

QY	661	YGGQFCETCLPGYRRETSLGPYSPCVLCTCNHGHSETCDPBTGVCD	CRDNTAGPHCEKCS	720
Db	696	YGGQFCMCLSGYRRETENLGPYSPCVLACNGHSETCDPBTGVCNCRDNTAGPHCEKCS	755	
QY	721	DGYYGDSSTLTGTSSDCQPCPCPGSSCAIVPKTKVVCTHCTPTGTAGKRCCEL	CDDGYFGDP	780
Db	756	DGYYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKVVCTNCTPTGTTGKRCCEL	CDDGYFGDP	815
QY	781	LGSNGPVRLCRPCQCNNDNIDPNAVGN	CNRLTGECLKCIYNTAGFYCDRCKEGFFGNPLAP	840
Db	816	LGRNGPVRLCRLCQCSNDNIDPNAVGN	CNRLTGECLKCIYNTAGFYCDRCKDGF	875
QY	841	NPADKCKACACN - YGTVQOSSCN	PVTGQCQCLPHVSGRDCGTCDPGYYNLQSGQGCERC	899
Db	876	NPADKCKACNPNYGTMKQOSSCN	PVTGQCECLPHVTGQDCGACDPGFYNLQSGQGCERC	935
QY	900	DCHALGSTNGQCDIR	TGQCEBQPGITGOHCERCETNHFGEFGECKPCDCHHEGSL	959
Db	936	DCHALGSTNGQCDIR	TGQCEBQPGITGOHCERCEVNHFGFGECKPCDCHPEGSL	995
QY	960	KDDGRCECREGFVGN	RCDQCEENYFYNRSWPGCQECPCYRLVKDKAAEHRVKLQ	1019
Db	996	KDDGRCECREGFVGN	RCDQCEENYFYNRSWPGCQECPCYRLVKDKVADHRVKLQ	1055
QY	1020	IANLGTGDDMVT	DQAFEDRLKEAREVTDLLREAEQVDQNDLMDRLQ	1079
Db	1056	IANLGTGDEMVT	DQAFEDRLKEAREVMDLLREAQVDQNDLMDRLQ	1115
QY	1080	RLQNRNTIETGILAEAR	SRVSTEQ	1138
Db	1116	RLQNRNTIETGNLAEQ	ARAHVENTERLIEIASRELEKAKVAAANVSVTQ	1175
QY	1139	MTLLAEAEARRLAE	RHKQEA	1198
Db	1176	MTLLAEAEARKLAE	RHKQEA	1235
QY	1199	YEQAKNISQ	DLKQAA	1258
Db	1236	YEQAKNISQ	DLKQAA	1295
QY	1259	LDRLIDQKL	KDYEDLREDMRGKEHEVKNLLEKGAEQQTADQLLARADA	1318
Db	1296	LEQLIDQKL	KDYEDLREDMRGKEHEVKNLLEKKGTEQQTADQLLARADA	1355
QY	1319	GRSTLQ	EANDILNNLKDFDRRVNDNKTAAEEALRRIPAINRTIAEANEK	1378
Db	1356	GRDTLQ	EANDILNNLKDFDRRVNDNKTAAEEALRKIPAINQITTEANEK	1415
QY	1379	AADATEAKNKAHEA	ERIASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEA	1438
Db	1416	AADATEAKNKAHEA	ERIASAVQKNATSTKAAERTFAEVTDLNEVNNMLKQLEAEK	1475
QY	1439	KRKQDDADQDMM	MAGMASQAAQAEALNARKAKNSVSSLLSQNLNLLDQLGLD	1498
Db	1476	KRKQDDADQDMM	MAGMASQAAQAEALNARKAKNSVTSLLSIINDLLEQLGLD	1535
QY	1499	NEIEGSLNKA	DEMKA	1558
Db	1536	NEIEGTLNKA	DEMKVSDLRKVS	1595
QY	1559	LPTGCFNT	PSIEKP	1572
Db	1596	LPSCGFNT	PSIEKP	1609

RESULT 3
LMG3_HUMAN
ID_LMG3_HUMAN STANDARD; PRT; 1587 AA.
AC_Q9Y6N6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Laminin gamma-3 chain precursor (Laminin 12 gamma 3).

GN LAMC3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=99242614; PubMed=10225960;
RA Koch M., Olson P.F., Albus A., Jin W., Hunter D.D., Brunken W.J.,
RA Burgeson R.E., Champlaud M.F.;
RT "Characterization and expression of the laminin gamma3 chain: a novel,
RT non-basement membrane-associated, laminin chain.";
RL J. Cell Biol. 145:605-618(1999).
CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components.
CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC different polypeptide chains (alpha, beta, gamma), which are bound
CC to each other by disulfide bonds into a cross-shaped molecule
CC comprising one long and three short arms with globules at each
CC end. The gamma-3 chain is a subunit of laminin-12.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Broadly expressed in: skin, heart, lung, and
CC the reproductive tracts.
CC -!- DOMAIN: The alpha-helical domains I and II are thought to interact
CC with other laminin chains to form a coiled coil structure.
CC -!- DOMAIN: Domain IV is globular.
CC -!- SIMILARITY: Contains 1 laminin N-terminal domain.
CC -!- SIMILARITY: Contains 1 laminin EGF-like domains.
CC -!- SIMILARITY: Contains 1 laminin IV domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; AF041835; AAD36991.1; -.
CC HSSP; P02468; 1TLE.
CC Genew; HGNC:6494; LAMC3.
CC MIM; 604349; -.
CC GO; GO:0005578; C:extracellular matrix; TAS.
CC GO; GO:0016020; C:membrane; TAS.
CC GO; GO:0005198; F:structural molecule activity; TAS.
CC InterPro; IPR006209; EGF_like.
CC InterPro; IPR008212; Lam_N2.
CC InterPro; IPR000034; Laminin_B.
CC InterPro; IPR002049; Laminin_EGF.
CC InterPro; IPR008211; LamNT.
CC Pfam; PF00052; laminin_B; 1.
CC Pfam; PF00053; laminin_EGF; 9.
CC Pfam; PF00055; laminin_Nterm; 1.
CC PRINTS; PR00011; EGF_LAMININ.
CC ProDom; PD002082; Lam_N2; 1.
CC SMART; SM00180; EGF_Lam; 9.
CC SMART; SM00136; LamNT; 1.
CC PROSITE; PS00022; EGF_1; 7.
CC PROSITE; PS01186; EGF_2; 2.
CC PROSITE; PS01248; LAMININ_TYPE_EGF; 10.
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 1587 LAMININ GAMMA-3 CHAIN.
FT DOMAIN 20 270 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 271 326 LAMININ EGF-LIKE 1.
FT DOMAIN 327 382 LAMININ EGF-LIKE 2.
FT DOMAIN 383 429 LAMININ EGF-LIKE 3.
FT DOMAIN 430 479 LAMININ EGF-LIKE 4.
FT DOMAIN 480 489 LAMININ EGF-LIKE 5 (N-TERMINAL).

FT	DOMAIN	490	672	DOMAIN	LAMININ DOMAIN IV.
FT	DOMAIN	673	706	DOMAIN	LAMININ EGF-LIKE 5 (C-TERMINAL).
FT	DOMAIN	707	754	DOMAIN	LAMININ EGF-LIKE 6.
FT	DOMAIN	755	809	DOMAIN	LAMININ EGF-LIKE 7.
FT	DOMAIN	810	865	DOMAIN	LAMININ EGF-LIKE 8.
FT	DOMAIN	866	916	DOMAIN	LAMININ EGF-LIKE 9.
FT	DOMAIN	917	964	DOMAIN	LAMININ EGF-LIKE 10.
FT	DOMAIN	965	1013	DOMAIN	LAMININ EGF-LIKE 11.
FT	DOMAIN	1014	1587	DOMAIN	DOMAIN II AND I.
FT	DOMAIN	1071	1141	COILED COIL	(POTENTIAL).
FT	DOMAIN	1200	1229	COILED COIL	(POTENTIAL).
FT	DOMAIN	1424	1504	COILED COIL	(POTENTIAL).
FT	DOMAIN	1535	1579	COILED COIL	(POTENTIAL).
FT	SITE	1059	1061	CELL ATTACHMENT SITE	(POTENTIAL).
FT	CARBOHYD	87	87	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	119	119	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	295	295	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	328	328	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	631	631	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	837	837	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	980	980	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	1185	1185	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	1518	1518	N-LINKED (GLCNAC. .)	(POTENTIAL).
SQ	SEQUENCE	1587 AA;	172051 MW;	3CB6E09B5F203319	CRC64;
Query Match					
Best Local Similarity		42.1%;		Score 3586; DB 1; Length 1587;	
Matches 700;		Conservative 258;		Pred. No. 1.3e-127;	
				Mismatch 568; Indels 72; Gaps 23;	
Qy	2	MDECADEGGRPQRCMPFVNAFNTVATNTGTPPEEYCVQTVGTGVTSKCHLCDAGQ	61		
Db	22	MGACYDGAGRQRCPLPVFENAFRLAQASHTCGSPDEDFCPHVGAAGAHQRCDAAD	81		
Qy	62	QHLOHGAFLTDYNNQADTTWQSQTMLAGVOYPSINLTLLHGLKAFDITYVRLKFTSR	121		
Db	82	QRHNASYLTDFHSQDESTWQSPSMAGVQYPTSVNITRLGKAYEITYVRLKFTSR	141		
Qy	122	PESFAIKRTREDGPMIPYQYSGSCENTYSKANRGFI RTGGDEQALCTDEFSDISPLT	181		
Db	142	PESFAIKRSRADGPWPYQFYASACQKTYGRPEGQYLRGDERVAFTSEFSDISPLS	201		
Qy	182	GGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVNDPKVLKSYVA	241		
Db	202	GGNVAFSTLEGRPSAYNFEESPLQEWVTSTELLISLDRNLNTFGDIFKDPKVLQSYVA	261		
Qy	242	ISDFAVGGRCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPFPNDRPWRATAESA	301		
Db	262	VSDFSVGRCKNGHASECGPDVAGQLACRCQHNTTGTDCERCLPFFQDRPWARGTAAEA	321		
Qy	302	SECLPCDCNGRSQECYFDPPELYRSTGHGHCNCRDNTDGAKCERCENFFRLGNTEACS	361		
Db	322	HECLPCNCSGRSECTFDRELFRSTGHGHCNCRDHTAGHCHRCQENFYHWDPRMPCQ	381		
Qy	362	PCHCSPVGLSTQCDSDYGRCSCKPGVMGDKDRCPGFHSLTEAGRCPCSCDPSGSTDEC	421		
Db	382	PCDCQSAGSLHLQCDTGTGTCACKPTVTGWKCDRLCPGFHSLSEGGCRPCTCNPAAGSLDTC	441		
Qy	422	NVETGRVCCKDNVEGFNCERCKPGFFNLESNNPKGCTPCFCFHSVCTNAVGSVYDIS	481		
Db	442	DPKSGRCPCKENVEGNLDCRCRPGTFLNLPHPNAGCSCFCYGHSKVCACASTAQFQVHHIL	501		
Qy	482	STFQIDEDGWRVBEQDSEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYGN	541		
Db	502	SDFHQAGGWARSVGGSEHSPQWSPN----GVLLSPEDEBELTAPGKFLGDQRFSGOP	557		
Qy	542	LSFSFRVDRDRTRLSAEDLVLEGAGLRVSVPLIAQGNYSYBSETTVKYIFRLH---EATDY	598		
Db	558	LILTRVPPGDSPLPVQ-LRLEGTGLALS--LRHSSLSGPDARASQGGRAQVPLQETSE	614		
Qy	599	PWRPALSPFEFOKLLNNLTSLKIRGTYSERSAG--YLDVDTLQISARPGGVPATWVESCT	656		
Db	615	DVAPPLPPFHFQRLANLTSLRLRVSPGSPAGVPVFLTEVRLTSARPLSPASWVEICS	674		

OM protein - protein search, using sw model

Run on: May 18, 2004, 14:56:24 ; Search time 39.9931 Seconds
(without alignments)
10937.572 Million cell updates/sec

Title: US-10-037-182-20
Perfect score: 8527
Sequence: 1 AMDECADEGGRPQRCMPEFV.....EDIKKTLPTGCFNTPSIEKP 1572

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
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13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8527	100.0	1572	14	US-10-037-182-20 Sequence 20, Appl
2	8527	100.0	1605	14	US-10-037-182-18 Sequence 18, Appl
3	8460	99.2	1607	9	US-09-938-275-10 Sequence 10, Appl
4	8038	94.3	1576	14	US-10-037-182-16 Sequence 16, Appl
5	8038	94.3	1609	14	US-10-037-182-14 Sequence 14, Appl
6	8038	94.3	1609	14	US-10-299-058-12 Sequence 12, Appl
7	8034	94.2	1609	9	US-09-938-275-11 Sequence 11, Appl
8	8034	94.2	1609	15	US-10-372-683-36 Sequence 36, Appl
9	3586	42.1	1587	9	US-09-845-583-10 Sequence 10, Appl
10	3586	42.1	1587	12	US-10-262-839-210 Sequence 210, App
11	3583	42.0	1575	12	US-10-262-839-212 Sequence 212, App
12	3193	37.4	1557	15	US-10-369-493-6816 Sequence 6816, Ap
13	2592	30.4	1193	12	US-10-392-113-14 Sequence 14, Appl
14	2592	30.4	1193	14	US-10-171-311-115 Sequence 115, App
15	2592	30.4	1193	14	US-10-053-662A-31 Sequence 31, Appl

16	2592	30.4	1193	15	US-10-295-027-390 Sequence 390, App
17	2592	30.4	1193	15	US-10-295-027-1269 Sequence 1269, Ap
18	2592	30.4	1193	16	US-10-188-832-147 Sequence 147, App
19	2591	30.4	1193	9	US-09-756-071B-13 Sequence 13, Appl
20	2591	30.4	1193	14	US-10-227-738-13 Sequence 13, Appl
21	2591	30.4	1193	15	US-10-603-725-26 Sequence 26, Appl
22	2584	30.3	1172	15	US-10-603-725-28 Sequence 28, Appl
23	2583	30.3	1193	15	US-10-603-725-30 Sequence 30, Appl
24	2577.5	30.2	1190	14	US-10-053-662A-2 Sequence 2, Appli
25	2576	30.2	1172	15	US-10-603-725-32 Sequence 32, Appl
26	2477.5	29.1	1111	12	US-10-392-113-15 Sequence 15, Appl
27	2476.5	29.0	1111	9	US-09-756-071B-15 Sequence 15, Appl
28	2476.5	29.0	1111	14	US-10-227-738-15 Sequence 36, Appl
29	2400.5	28.2	1171	15	US-10-603-725-36 Sequence 12, Appl
30	2400.5	28.2	1192	12	US-10-392-113-12 Sequence 32, Appl
31	2400.5	28.2	1192	14	US-10-053-662A-32 Sequence 34, Appl
32	2400.5	28.2	1192	15	US-10-603-725-34 Sequence 7, Appli
33	1790	21.0	3070	10	US-09-961-403-7 Sequence 4, Appli
34	1780.5	20.9	3084	9	US-09-938-275-4 Sequence 2, Appli
35	1780.5	20.9	3084	14	US-10-262-670-2 Sequence 5, Appli
36	1735	20.3	3075	9	US-09-938-275-5 Sequence 8, Appli
37	1677	19.7	1765	14	US-10-037-182-8 Sequence 113, App
38	1677	19.7	1786	9	US-09-873-676-113 Sequence 6, Appli
39	1677	19.7	1786	9	US-09-938-275-6 Sequence 6, Appli
40	1677	19.7	1786	14	US-10-037-182-6 Sequence 7, Appli
41	1661.5	19.5	1786	9	US-09-938-275-7 Sequence 10, Appl
42	1661.5	19.5	1786	14	US-10-037-182-10 Sequence 12, Appl
43	1637.5	19.2	1725	14	US-10-037-182-12 Sequence 5220, Ap
44	1632	19.1	2823	15	US-10-369-493-5220 Sequence 5221, Ap
45	1632	19.1	2823	15	US-10-369-493-5221

ALIGNMENTS

RESULT 1
US-10-037-182-20
; Sequence 20, Application US/10037182
; Publication No. US20030044899A1
; GENERAL INFORMATION:
; APPLICANT: tryggvason, Karl
; APPLICANT: Doi, Masayuki
; APPLICANT: Thyboll, Jill
; TITLE OF INVENTION: Recombinant Laminin 10
; FILE REFERENCE: 99-274-F
; CURRENT APPLICATION NUMBER: US/10/037,182
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,449
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/279,282
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 1572
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-037-182-20

Query Match	100.0%;	Score 8527;	DB 14;	Length 1572;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1572;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
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QY	121	RPESFAIYKRTREDGPWIPQYYSGSCENTYSKANRGFI RTGGDEQALCTDEFSDISPL	180	

QY 301 ASECPCDCNRSQCYFDPELYRSTGHGHTNCRDNTDGAKCERENFFRLGNTEAC 360
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QY 361 SPCHCSPVGSLSSTQCDSYGRCSCKPGVMGDKDRCPGFHSLTEAGCRPCSDPSGSTDE 420
Db 394 SPCHCSPVGSLSSTQCDSYGRCSCKPGVMGDKDRCPGFHSLTEAGCRPCSDPSGSTDE 453
QY 421 CNVETGRCVCNDNVEGFNCERCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGSYVDI 480
Db 454 CNVETGRCVCNDNVEGFNCERCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGSYVDI 513
QY 481 SSTFQIDEDGWRVEQDGESEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYGQ 540
Db 514 SSTFQIDEDGWRVEQDGESEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYGQ 573
QY 541 NLSFSFRVDRRDLRLSAEDLVLEGAGLRVSVPLIAQGSYSPSETTVKYIFRLHEATDYPW 600
Db 574 NLSFSFRVDRRDLRLSAEDLVLEGAGLRVSVPLIAQGSYSPSETTVKYIFRLHEATDYPW 633
QY 601 RPALSPFEFQKLLNLTISKIRGTYSERSAGYLDVLTQ SARPGPGVPATVWESCTCPVG 660
Db 634 RPALSPFEFQKLLNLTISKIRGTYSERSAGYLDVLTQ SARPGPGVPATVWESCTCPVG 693
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QY 1141 LLABEARRLAERHKQAEADDIVRVAKTANETSAAEYNLLRLTLAGENQTALEIEELNRKYE 1200
Db 1174 LLABEARRLAERHKQAEADDIVRVAKTANETSAAEYNLLRLTLAGENQTALEIEELNRKYE 1233
QY 1201 QAKNISQDLEKQAA RVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLD 1260
Db 1234 QAKNISQDLEKQAA RVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLD 1293
QY 1261 RLTDQKLKDYEDLREDMRGKEHEVNKLLKGAEQQTADQLLARADA AKALABEAAKKGR 1320
Db 1294 RLTDQKLKDYEDLREDMRGKEHEVNKLLKGAEQQTADQLLARADA AKALABEAAKKGR 1353
QY 1321 STLOEANDILNLLKDFDRRVNDNKTAAEALRRIPAINRTIAEANECTREAOALGNAAA 1380
Db 1354 STLOEANDILNLLKDFDRRVNDNKTAAEALRRIPAINRTIAEANECTREAOALGNAAA 1413

QY 1381 DATEAKNKAHEAERIAAQAQKQATSTKADAERTFGEVTDLDNEVNGMLRQLEEAENELKR 1440
Db 1414 DATEAKNKAHEAERIAAQAQKQATSTKADAERTFGEVTDLDNEVNGMLRQLEEAENELKR 1473
QY 1441 KQDDADQDMMAGMASQAQAQAEALNARKAKNSVSSLLSQNLNLLDQLGQDQDVTDLNKLNE 1500
Db 1474 KQDDADQDMMAGMASQAQAQAEALNARKAKNSVSSLLSQNLNLLDQLGQDQDVTDLNKLNE 1533
QY 1501 IEGLNKA KAKDEMKA SLDLDRKVS DLESEARKQEAAIMDYNRDIAEIIKDIHNLEDIKKTLP 1560
Db 1534 IEGLNKA KAKDEMKA SLDLDRKVS DLESEARKQEAAIMDYNRDIAEIIKDIHNLEDIKKTLP 1593
QY 1561 TGCFTNTPSIEKP 1572
Db 1594 TGCFTNTPSIEKP 1605

RESULT 3
US-09-938-275-10
; Sequence 10, Application US/09938275
; Patent No. US20020111309A1
; GENERAL INFORMATION:
; APPLICANT: Gerardo Castillo
; APPLICANT: Alan Snow
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications
; TITLE OF INVENTION: of Laminin and Laminin-Derived Protein Fragments
; FILE REFERENCE: PROTEO.P03
; CURRENT APPLICATION NUMBER: US/09/938,275
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1607
; TYPE: PRT
; ORGANISM: Mus Musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Swissprot P02468
; DATABASE ENTRY DATE: 1989-07-01
US-09-938-275-10

Query Match 99.2%; Score 8460; DB 9; Length 1607;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1565; Conservative 2; Mismatches 5; Indels 2; Gaps 2;

QY 1 AMDECADEGGRPQRCMPPEFNAAFNVTVATNTCGTPPEEYCVQGTGVTGKSKHLCDAAG 60
Db 34 AMDECADEGGRPQRCMPPEFNAAFNVTVATNTCGTPPEEYCVQGTGVTGKSKHLCDAAG 93
QY 61 QQHLOHGAAFLTDYNNQADTTWQSQTMLAGVQYPNSINLTHLGKAFDITYVRLKPHTS 120
Db 94 QQHLOHGAAFLTDYNNQADTTWQSQTMLAGVQYPNSINLTHLGKAFDITYVRLKPHTS 153
QY 121 RPESFAIYKRTREDGPGWIPYQYYSGCSENTYSKANRGFIRTTGGDEQQAALCTDEFSDISPL 180
Db 154 RPESFAIYKRTREDGPGWIPYQYYSGCSENTYSKANRGFIRTTGGDEQQAALCTDEFSDISPL 213
QY 181 TGGNVAFSTLEGPRPSAYNFDNSPVLQEWVTATDIRVTLNRLNTFGDEVFNDPKVLKSYYY 240
Db 214 TGGNVAFSTLEGPRPSAYNFDNSPVLQEWVTATDIRVTLNRLNTFGDEVFNDPKVLKSYYY 273
QY 241 AISDPAVGGRCCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKCLPFFNDRPWRATAES 300
Db 274 AISDPAVGGRCCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKCLPFFNDRPWRATAES 333
QY 301 ASECLPCDCNRSQCYFDPBELYRSTGHGHTNCRDNTDGAKCERENFFRLGNTEAC 360
Db 334 ASECLPCDCNRSQCYFDPBELYRSTGHGHTNCRDNTDGAKCERENFFRLGNTEAC 393
QY 361 SPCHCSPVGSLSSTQCDSYGRCSCKPGVMGDKDRCPQGFHSLTEAGCRPCSDPSGSTDE 420
Db 394 SPCHCSPVGSLSSTQCDSYGRCSCKPGVMGDKDRCPQGFHSLTEAGCRPCSDPSGSTDE 453
QY 421 CNVETGRCVCNDNVEGFNCERCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGSYVDI 480

Db 543 NLSFSFRVDRDRTRLAEDLVLEGAGLRVSVPLIAQGNVPSETTVKYVRLHEATDYPW 602
Qy 601 RPALSPFEFQKLLNNLTSIKIRGTYSERSAGYLDVTLQSRPGPGVPATWVESCTCPVG 660
Db 603 RPALTPEFQKLLNNLTSIKIRGTYSERSAGYLDVTLASARPGPGVPATWVESCTCPVG 662
Qy 661 YGGQFETCLPGYRRETPLSGPSPCVLCTCNHSETCDPETGVCDNRDNTAGHCEKCS 720
Db 663 YGGQFCMCLSGYRRETPLNLGPSPCVLCACNGHSETCDPETGVCDNRDNTAGHCEKCS 722
Qy 721 DGYGDSLTGSSDCQPCPCPGSSCAIVPKTKEVVCTHPTGTAGRCCELCDDGYFGDP 780
Db 723 DGYGDSLTGSSDCQPCPCPGSSCAVVPKTKEVVCTNPTGTTGRCCELCDDGYFGDP 782
Qy 781 LGSNGPVRLCRPCQCNNDNIDPNAVGNCRNLTGECCLKCIYNTAGFYCDRCCKEGFFGNPLAP 840
Db 783 LGRNGPVRLCRLCQCSNDNIDPNAVGNCRNLTGECCLKCIYNTAGFYCDRCCKDGFFGNPLAP 842
Qy 841 NPADKCKACACN-YGTVQQSSCNPVGTGQCCLPHVSGRDCGTCDPGYYNLQSGQCERC 899
Db 843 NPADKCKACNCPYGTMKQQSSCNPVGTGQCECLPHVTGQCGACDPGFYNLQSGQCERC 902
Qy 900 DCHALGSTNGQCDIRTGQCECQPGITGQHCHERCETNHFHFGPEGCKPCDCHHEGSLSLQC 959
Db 903 DCHALGSTNGQCDIRTGQCECQPGITGQHCHERCCEVNHFGPEGCKPCDCHPEGSLSLQC 962
Qy 960 KDDGRCECREGFVGNRCDQCEENFYNRSWPGCQECPCYRLVKDKAAEHRVKLQLESL 1019
Db 963 KDDGRCECREGFVGNRCDQCEENFYNRSWPGCQECPCYRLVKDKVADHRVKLQLESL 1022
Qy 1020 IANLGTGDDMVTDQAFEDRLKEAREVTDLLREAOEVKDVQDNLMDLRQVRNSSLHSQIS 1079
Db 1023 IANLGTGDEMVTQAFEDRLKEAREVMDLLREAOQVKDVQDNLMDLRQVRNNTLSSQIS 1082
Qy 1080 RLQNIPTNIEETGILAEARARSVESTEQLEIEIASRELEKAKN-AANVSITQPESTGEPNN 1138
Db 1083 RLQNIPTNIEETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSITQPESTGDPNN 1142
Qy 1139 MTLAEEARRLAERHKEADDIRVAKTANETSAAVNNLLRTRLAGENQTALEIEELNRK 1198
Db 1143 MTLAEEARKLAERHKEADDIRVAKTANDTSTEAYNLLRTRLAGENQTALEIEELNRK 1202
Qy 1199 YEQAKNISQDLEKQAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAAD 1258
Db 1203 YEQAKNISQDLEKQAARVHEEAKRAGDKAVEIYASVAQLSPDSETLENEANNIKMEAEEN 1262
Qy 1259 LDRLIDOKLDYEDLREDMRGHEVKNLLEKGAEQQTADQLLARADAAKALAEAAKK 1318
Db 1263 LEQLIDOKLDYEDLREDMRGHEVKNLLEKGTQEQQTADQLLARADAAKALAEAAKK 1322
Qy 1319 GRSTLQEBANDILNNLKDFRRVNDNKTAAEEALRRIPAINRTIAEANEKTRQAQLALGNA 1378
Db 1323 GRDTLQEBANDILNNLKDFRRVNDNKTAAEEALRKIPAINQTITEANEKTRQAQALGSA 1382
Qy 1379 AADATEAKNKAHEAERIAASAVQKNATSTKADAERTFEVTDLDNEVNGMLRQLEAEANEL 1438
Db 1383 AADATEAKNKAHEAERIAASAVQKNATSTKAAERTFAEVTDLNEVNNMLKQLQEAKEKEL 1442
Qy 1439 KRKQDDADQDMMWAGMASQAQBAELNARKAKNSVSSLISQLNNLLDQLGQLDVTVDLNL 1498
Db 1443 KRKQDDADQDMMWAGMASQAQBAEINARKAKNSVTSLSLSIINDLLEQLGQLDVTVDLNL 1502
Qy 1499 NEIEGSLNKADEMKAASDLDRKVSDESEARKQOEAAIMDYNRDIAEIIKDIHNLEDIKKT 1558
Db 1503 NEIEGTLNKADEMKVSDLDLRKVSDDLNEAKQOEAAIMDYNRDIEEIMKDIRNLEDIRKT 1562
Qy 1559 LPTGCCFNTPSIEKP 1572
Db 1563 LPSGCCFNTPSIEKP 1576

RESULT 5
US-10-037-182-14

; Sequence 14, Application US/10037182
; Publication No. US20030044899A1
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Doi, Masayuki
; APPLICANT: Thybøll, Jill
; TITLE OF INVENTION: Recombinant Laminin 10
; FILE REFERENCE: 99-274-F
; CURRENT APPLICATION NUMBER: US/10/037,182
; PRIOR APPLICATION NUMBER: 60/257,449
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/279,282
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 1609
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-037-182-14

Query Match 94.3%; Score 8038; DB 14; Length 1609;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;

Qy 1 AMDECADEGGRPQRCMPFVNAFNVVATNTCGTPPEEYCVQTGVTGVTKSCHLCDAG 60
Db 36 AMDECTDEGGRPQRCMPFVNAFNVVATNTCGTPPEEYCVQTGVTGVTKSCHLCDAG 95
Qy 61 QHQLQHGAFLTDYNNQADTTWQSQTMLAGVQYPSINLTLHLGKAFDITYVRLKEFHTS 120
Db 96 QHQLQHGAFLTDYNNQADTTWQSQTMLAGVQYPSINLTLHLGKAFDITYVRLKEFHTS 155
Qy 121 RPESFAIKRTREDGPWIPYQYISGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDISPL 180
Db 156 RPESFAIKRTREDGPWIPYQYISGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDISPL 215
Qy 181 TGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLNLTFGDEVFNDPKVLKSYYY 240
Db 216 TGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLNLTFGDEVFNDPKVLKSYYY 275
Qy 241 AISDFAVGGRCKCNHGHASECVKNEFDKLMCNCKHNTYGVDCCKCLPFENDRPWRRATAES 300
Db 276 AISDFAVGGRCKCNHGHASECMKNEFDKLVNCKHNTYGVDCCKCLPFENDRPWRRATAES 335
Qy 301 ASECLPCDCNNGRSQECYFDPPELYRSTGHGHCTNCRDNTDGAHCRCRNFRLGNTEAC 360
Db 336 ASECLPCDCNNGRSQECYFDPPELYRSTGHGHCTNCRDNTDGAHCRCRNFRLGNNEAC 395
Qy 361 SPCHCSPVGSLSLTCQDSYGRCSCKPGVMGDKCDRCQPGHSLTEAGCRPCSCDPSGSTDE 420
Db 396 SSCHCSPVGSLSLTCQDSYGRCSCKPGVMGDKCDRCQPGHSLTEAGCRPCSCDPSGSIDE 455
Qy 421 CNVETGRVCVCKDNVEGFNCERCCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGSVYDI 480
Db 456 CNVETGRVCVCKDNVEGFNCERCCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGSVYSI 515
Qy 481 SSTFQIDEDGWRVEQRDGESEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYGQ 540
Db 516 SSTFQIDEDGWRVEQRDGESEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSYGQ 575
Qy 541 NLSFSFRVDRDRTRLAEDLVLEGAGLRVSVPLIAQGNVPSETTVKYIFRLHEATDYPW 600
Db 576 NLSFSFRVDRDRTRLAEDLVLEGAGLRVSVPLIAQGNVPSETTVKYIFRLHEATDYPW 635
Qy 601 RPALSPFEFQKLLNNLTSIKIRGTYSERSAGYLDVTLQSRPGPGVPATWVESCTCPVG 660
Db 636 RPALTPEFQKLLNNLTSIKIRGTYSERSAGYLDVTLASARPGPGVPATWVESCTCPVG 695
Qy 661 YGGQFCETCLPGYRRETPLSGPYSPCVLCTCNHSETCDPETGVCDNRDNTAGHCEKCS 720
Db 696 YGGQFCMCLSGYRRETPLNLGPYSPCVLCAACNGHSETCDPETGVCDNRDNTAGHCEKCS 755

RESULT 6
US-10-299-058-12
; Sequence 12, Application US/10299058
; Publication No. US20030103975A1
; GENERAL INFORMATION:
; APPLICANT: JONES, JONATHAN C.R.
; APPLICANT: GONZALES, MEREDITH
; TITLE OF INVENTION: MODULATION OF ANGIOGENESIS AND ENDOTHELIALIZATION
; FILE REFERENCE: 1720-1-002 CIP
; CURRENT APPLICATION NUMBER: US/10/299,058
; CURRENT FILING DATE: 2002-11-18

Query Match		94.3%;	Score 8038;	DB 14;	Length 1609;
Best Local Similarity		93.3%;	Pred. No. 0;		
Matches 1469;		Conservative	56;	Mismatches	47; Indels 2; Gaps 2;
Qy	1	AMDECADEGGRPQRCMPEFVNAAFNVTVVATNTCGTPPEEYCVQGTGVTGVTKSCHLCDAG	60		
Db	36	AMDECTDEGGRPQRCMPEFVNAAFNVTVVATNTCGTPPEEYCVQGTGVTGVTKSCHLCDAG	95		
Qy	61	QQLHQGAFLTDYNNQADTTWWQSQTMLAGVQYPNSINTLHLGKAFDITYYRLKFHTS	120		
Db	96	QPHLQGAFLTDYNNQADTTWWQSQTMLAGVQYPSSINTLHLGKAFDITYYRLKFHTS	155		
Qy	121	RPEFSAIYKRTREDGPWIPYQYYSGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDISPL	180		
Db	156	RPEFSAIYKRTREDGPWIPYQYYSGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDISPL	215		
Qy	181	TGGNVAESTLEGRRPSAYNFDNSPVLQEWVTATDIRVTLNRLNTFGDEVNDEPKVLKSYYY	240		
Db	216	TGGNVAESTLEGRRPSAYNFDNSPVLQEWVTATDIRVTLNRLNTFGDEVNDEPKVLKSYYY	275		
Qy	241	AISDFAVGRCKCNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPFFNDRPWRATAES	300		
Db	276	AISDFAVGRCKCNGHASECMKNEFDKLVNCKHNTYGVDCCKLPFFNDRPWRATAES	335		
Qy	301	ASECLPCDCNGRSQECYFDPPELYRSTGHGHCNTCRDNTDGAKCERCENFRFLGNTEAC	360		
Db	336	ASECLPCDCNGRSQECYFDPPELYRSTGHGHCNTCQDNTDGAHCERCENFRFLGNNEAC	395		
Qy	361	SPCHCSPVGSLSLSTQCDYSYGRCSCKPGVMGDKCDRCQPGFHSLSLTEAGCRPCSCDPSGSTDE	420		
Db	396	SSCHCSPVGSLSLSTQCDYSYGRCSCKPGVMGDKCDRCQPGFHSLSLTEAGCRPCSCDPSGSIDE	455		
Qy	421	CNVETGRVCCKDNVEGFNCERCCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGYSVYDI	480		
Db	456	CNVETGRVCCKDNVEGFNCERCCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGYSVYSI	515		
Qy	481	SSTFQIDEDGWVEQRDGEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYGQ	540		
Db	516	SSTFQIDEDGWRAEQRDGEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSYGQ	575		
Qy	541	NLSFSFRVDRDTRLRSAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYIFRLHEATDYPW	600		
Db	576	NLSFSFRVDRDTRLRSAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYVFRLHEATDYPW	635		
Qy	601	RPALSPFEFQKLLNNLTSIKIRGTYSERSAGYLDVLTQSARPGPGVPATWVESCTCPVG	660		
Db	636	RPALTPFEFQKLLNNLTSIKIRGTYSERSAGYLDVLTLASARPGPGVPATWVESCTCPVG	695		
Qy	661	YGGQFCETCLPGYRRETPLSGPYSPCVLCTCNHSETCDPETGVCDCRNTAGPHCEKCS	720		
Db	696	YGGQFCMCLSGYRRETPLNLGPYSPCVLCACNHSETCDPETGVCNCRDNTAGPHCEKCS	755		
Qy	721	DGYYGDSLGTSSDCQPCPCPGGSSCAIVPKTKXVWCTHCPTGTAGKRCCLCDDGYFGDP	780		
Db	756	DGYYGDSLGTSSDCQPCPCPGGSSCAVVPKTKXVWCTNCPTGTTGKRCCLCDDGYFGDP	815		
Qy	781	LGSNGPVRLLRQCQNDNIDPNAVGNCRNLTGECCLKCIYNTAGFYCDRCCKEGFFGNPLAP	840		
Db	816	LGRNGPVRLLRCLCQSDNIDPNAVGNCRNLTGECCLKCIYNTAGFYCDRCCKDGFNPLAP	875		
Qy	841	NPADKCKACACN-YGTVQQQSSCNPNVTGQCQCLPHVSGRDCGTCDPQYINLQSGQCERC	899		

Db 1176 MTLAEEARKLAERHKQEAADDIVRAKTAANDTSTAYNLLRLTAGENQTAFEIENLRK 1235
QY 1199 YEOAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAAD 1258
Db 1236 YEOAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDSETLENEANNIKWEAEN 1295
QY 1259 LDRLLDQKLKDYEDLREDMRGKEHEVKNLLEKGAEOQTADQQLARADAAKALAEBAKK 1318
Db 1296 LEQLIDQKLKDYEDLREDMRGKEHEVKNLLEKGAEOQTADQQLARADAAKALAEBAKK 1355
QY 1319 GRSTLOEANDILNNLKDFDRRVNDNKTAAEEALRRIPAINRTIAEANEKTRQAQALGNA 1378
Db 1356 GRDTLOEANDILNNLKDFDRRVNDNKTAAEEALRKIPAINQITAEANEKTRQAQALGSA 1415
QY 1379 AADATEAKNKAHEAERIAASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEBAENEL 1438
Db 1416 AADATEAKNKAHEAERIAASAVQKNATSTKAEARTFAEVTDLNNEVNNMLKQLEAEKEL 1475
QY 1439 KRKQDDADQDMMAGMASQAAQAEALNARKAKNSVSSLLSOLNNLLDQLGQDQDVTDLNKL 1498
Db 1476 KRKQDDADQDMMAGMASQAAQAEALNARKAKNSVTSLLSINDLLLEQLGQDQDVTDLNKL 1535
QY 1499 NEIEGSLNKADEMKAASDLDRKVSLESEARKQEAAMIDYNRDIAEIIKDIHNLEDIKKT 1558
Db 1536 NEIEGTLNKADEMKVSDLDLRKVSLENEAKKQEAAMIDYNRDIEEIMKDIRNLEDIRKT 1595
QY 1559 LPTGCFNTPSIEKP 1572
Db 1596 LPSGCFNTPSIEKP 1609

RESULT 9

US-09-845-583-10
; Sequence 10, Application US/09845583
; Patent No. US20020142954A1
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Brunken, William Joseph
; APPLICANT: Champliand, Marie-France
; APPLICANT: Hunter, Dale
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
; FILE REFERENCE: 10287-056001
; CURRENT APPLICATION NUMBER: US/09/845,583
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/200,863
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1587
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-845-583-10

Query Match 42.1%; Score 3586; DB 9; Length 1587;
Best Local Similarity 43.8%; Pred. No. 3.6e-200;
Matches 700; Conservative 258; Mismatches 568; Indels 72; Gaps 23;
QY 2 MDECADEGGRPQRCMPEFVNAAFNVTVVATNTCGTPPEEYCVQTVGTGVTKSCHLCDAGQ 61
Db 22 MGACYDAGRPQRCPLPVFENAAFGRLAQASHTCGSPPEDFCPHVGAAGAGAHQCQRCDAAD 81
QY 62 QHLOHGAFLTDVNNQADTTWQSQTMLAGVOYPNSINLTLHLGKAFDITYVRLKFTSR 121
Db 82 PQRHNASYLTDFHSQDSESTWQSPSMAFGVQYPTSVNITLRLGKAYEITYVRLKFTSR 141
QY 122 PESFAIKRTRDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQALCTDEFSDISPLT 181
Db 142 PESFAIKRSRADGPWEPIQFYSASQKTYGRPEGQYLRPGEDEVAFCTSEFSDISPLS 201
QY 182 GGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTILNRLNTEFGDEVNDPKVLKSYIYA 241

Db 202 GGNVAFSTLEGRPSAYNFEESPGLOEWVSTSTELLISLORLNTFGDDIFKDPKVLQSYIYA 261
QY 242 ISDFAVGGRCCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPFFNDRPWRRATAESA 301
Db 262 VSDFSVGGRCCKNGHASECGPDVAGQLACRCQHNTTGTDCERCLPFFQDRPWARGTAEAA 321
QY 302 SECLPCDNGRSQECYFDPPELYRSTGHGGHCTNCRDNTDGAKECRKRENFRLGNTEACS 361
Db 322 HECLPCNCSGRSEECTFDRELFRSTGHGRCHHCRDHTAGPHCERQENFYHWDPRMPCQ 381
QY 362 PCHCSPVGSLSLTCDSYGRCSCKPGVMGDKDCRCQPGFHSLTEAGRCPCSDPSGSTDEC 421
Db 382 PCDCQSAGSLHLQCDTGTCAKPTVTGWKCDRLPGFHSLSSEGGRCPCPCNPAGSLDTC 441
QY 422 NVETGRVCVCKDNVEGFNCERCKPGFFENLESSNPKGCTPCFCFGHSSVCTNAVGSVYDIS 481
Db 442 DPRSGRCPCKENVEGNLDCRCRPGTENLQPHNPAGCSSCFYGHKVKVCASTAQFQVHHIL 501
QY 482 STFQIDEDGWRVEQDGSSEASLEWSSDRQYIAVISDSYFPRFYFIAPVKFLGNQVLSYQN 541
Db 502 SDFHQAGEGWARSVGGSEHSPQWSPN----GVLLSPEDEEBELTAPGKFLGDQRFSGQP 557
QY 542 LSFSEFRVDRDTRLAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYIFRLH--EATDY 598
Db 558 LILTRVPPGDSPLPVQ-LRLEGTGLALS--LRHSSLSGPQDARASQGGRAQVPLQETSE 614
QY 599 PWRPALSPFERQKLLNNLTSIKIRGIYSERSAG--YLDVTVLQSAAPPGPVPATWVESCT 656
Db 615 DVAPPLPPFHFORLLANLTSRLRVSPGSPAGVPVFLTEVRLTSARPPGLSPASWVEICS 674
QY 657 CPVYGGQFCETCLPGYRRTPSLGYSPCVLCTCNHGHSETCDPEIGVCDORDNTAGPHC 716
Db 675 CPTGYTGQFCESCAPGYKREMPQGGPYASCVPTCNQHG-TCDPNTGICVCSHHTGPPSC 733
QY 717 EKCSGYGSDTLGTSSDCQPCPCPGSSCAIVPKTKEVVTCHCTPTAGKRCCELDDGY 776
Db 734 ERCLPGFYGNPPAGQADDQPCPCPGQSACTTIPESGEVVTCHCPGQRRRCCEVDDGF 793
QY 777 FGDPLGNSGVPVRLCRPCQCNNDIDPNAVGNCRNLTEGLCKIYNTAGFYCDRCCKEGFFGN 836
Db 794 FGDPLGLFGHPQCHQCQCSGNVDPNAVGNCDPLSGHCLRLCHNLTGDDHCEHCQEGFYS 853
QY 837 PLAPNPADKCKACACN-YGTVOQQSSCNVPTGQCQCLPHVSGRDCGTGDPGYYNLQSGQG 895
Db 854 ALAPRPADKCMPCSCHPQGSVSEQMPCDPVTGQCSCLPHVTARDCSRCPYGFDFLQPRG 913
QY 896 CERCDHALGSTNGQCDIRTGQCECQPGITGQHCHERCETNHFQFEGCKPCDCHHEGSL 955
Db 914 CRSCCKHPLGSQEDQCHPKTGCTCRPGVTGQACDRCOLGFFGSSIKGCRACRCSPLGAA 973
QY 956 SLQCKDDGRCECREGFGVGNRCDQCEENFYFNRSWPGCQECPCYRLVKDKAAEHRVKLQE 1015
Db 974 SAQCHYNGTVCVRPGFEGYKCDRCHYNFELTADGTHCQCPSCYALVKEETAKLKLTL 1033
QY 1016 LESLIANLGTG-----DMVTDQAFEDRLKEAEREVTDLLREAQEVKDVQNLMDRLQRV 1070
Db 1034 TEGWLQSDCGSPWGLDILLGEAPRGDVYQGH-----LLPGAREA-----FLEQMMGL 1083
QY 1071 NSSLHSQISRLQINRTIETGILAEARARSVESTEQLEIASRE-LEKAKMAANVSITQ 1129
Db 1084 EGAVKAAREQLRLNKGARCAQAGSQKTCQLADLEAVLESSEEEILHAAAILASLEIPQ 1143
QY 1130 PESTGEPNNMTLLAEHARRLAERHKQEAADDIVRVAKTANETSAAEAYNLLRLTAGENQTA 1189
Db 1144 -EGPSQPTKWSHLAEARALARSHRDTATKIAATAWRALLASNTSYALLWNLL--EGRVA 1200
QY 1190 LEIE-ELNRKYEQAKNISQDLEKQAAARVHEBAKRAQDKAVEIYASVAQL----- 1237
Db 1201 LETQDLEDRYQEVQAAQKALRTAVEVLPEAE-----SVLATVQQVGADTAPYLALL 1253
QY 1238 -----TPVDEA--LENEANKIKKEAADLRLDQKLKDYEDLRE-DMRGKHEVKNLLE 1289
Db 1254 ASFGALPQKSRADLGLKAKALEKTIVASWQHMAATEAARTLQTAQAATLRQTE---PLTMA 1310

QY 1290 KGKAEQQTADQQLARADAAKALAEAAKGRSTLQEAANDILNNLKDFDRRVNDNKTAEE 1349
Db 1311 RSRITATFASQLHQGARAALTQASSVQAATVTVMGARTLLADLEGMKLQFPRPKDQAAL 1370
QY 1350 ALRRIPAINRTIAEANEKTRBAQALGNAADATEAKNKAHEAERIAAQAQKATSTKAD 1409
Db 1371 QRKADSVSDRLADTRKTKQAERMLGNAAPLSSSAKCKGREAEVLAKDSAKLAKALLRE 1430
QY 1410 AERTFGEVTDLDNEVNGMLRQL-EEAENELKQKQDADQDMMAGMASQAQAEEAELNARK 1468
Db 1431 RKQAHRRASRLTSQTQATLQASQQVLASEARROELEEAEVAGLS-----EMEQQIRE 1485
QY 1469 AKNSVSSLLSQLNLLDQLGQDLD--VDLNKLNIEGSLNKAKDEM-KASDLDRKVSLE 1525
Db 1486 SRISLEKDIETSELLARLGLSLDTHQAPAAQALNETQWALERLRLQLGSPGSLQKLSLE 1545
QY 1526 SEARKQEAAMIDYNRDIAEIIKDIHNLEDIKTLPTGC 1563
Db 1546 QESQQELQIQGFESDLAIBRADKQNLKONLEAILHSLPENC 1583
RESULT 10
US-10-262-839-210
; Sequence 210, Application US/10262839
; Publication No. US20040038877A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, John,
; APPLICANT: Anderson, David W.,
; APPLICANT: Boldog, Ferenc,
; APPLICANT: Burgess, Catherine,
; APPLICANT: Catterton, Elina,
; APPLICANT: Edinger, Shlomit,
; APPLICANT: Ellerman, Karen,
; APPLICANT: Gerlach, Valerie,
; APPLICANT: Gorman, Linda,
; APPLICANT: Guo, Xiaojia,
; APPLICANT: Ji, Weizhen,
; APPLICANT: Kekuda, Ramesh,
; APPLICANT: Leach, Martin,
; APPLICANT: Li, Li,
; APPLICANT: Miller, Charles,
; APPLICANT: Patturajan, Meera,
; APPLICANT: Reiger, Daniel,
; APPLICANT: Rothenberg, Mark,
; APPLICANT: Shimkets, Richard,
; APPLICANT: Smithson, Glenda,
; APPLICANT: Spytek, Kimberly,
; APPLICANT: Taupier, Raymond, jr.,
; APPLICANT: Vernet, Corine,
; APPLICANT: Voss, Edward,
; APPLICANT: Zerhusen, Brian,
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-462A
; CURRENT APPLICATION NUMBER: US/10/262,839
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,101
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/371,972
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/327,342
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/328,044
; PRIOR FILING DATE: 2001-10-09

; PRIOR APPLICATION NUMBER: 60/328,849
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/374,738
; PRIOR FILING DATE: 2002-04-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 367
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 210
; LENGTH: 1587
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-839-210
Query Match 42.1%; Score 3586; DB 12; Length 1587;
Best Local Similarity 43.8%; Pred. No. 3.6e-200;
Matches 700; Conservative 258; Mismatches 568; Indels 72; Gaps 23;
QY 2 MDECADEGGRPQRCMPEFVNAAFNVTVATNTCTGTPPEEYCVQGTGVTGKSLCDAGQ 61
Db 22 MGACYDGAGRPQRCPLPVFENAAFGRLAQASHTCGSPEDFCPHVGAAGAGAGACQRCDAAD 81
QY 62 QHLQGAFLTDYNNQADTTWQSQTMLAGVQYFNSINLTLLHKGAFDITYVRLKFHTSR 121
Db 82 PQRHNASYLTDFHSQDESTWQSPSMAFGVQYPTSNITLRLGKAYEITYVRLKFHTSR 141
QY 122 PESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTGDEQALCTDEFSDISPLT 181
Db 142 PESFAIYKRSRADGPWEYQYFYSASQKTYGRPEGQYLRPGEDERVAFTSEFSDISPLS 201
QY 182 GGNVAFSTLEGRPSAYNFDSNVPVLEWVTATDIRVTNLNLTFGDEVNDPKVLKSYIA 241
Db 202 GGNVAFSTLEGRPSAYNFESPGLEWVTSTELLISLDRLNTFGDDIFKDPKVLQSYIA 261
QY 242 ISDFAVGGRCKNGHASECVKNEFFKLMCNCKNTYGVDCCKLPFFNDRPWRRTAESA 301
Db 262 VSDFSVGRCKNGHASECGPDVAGQLACRCQNTGTGDCERCLPFFQDRPWARGTAEA 321
QY 302 SECLPCDNGRSQECYFDPBLYRSTGHGCHCTNCRDNTDGAKCERCENPFRLGNTACS 361
Db 322 HECLPCNCSGRSEECTFDRLEFRSTGHGGRCHCRDHTAGPHCERCENFYHWDPRMPCQ 381
QY 362 PCHCSPVGSLSLTCDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSDPSGSTDEC 421
Db 382 PCDCOSAGSLHLQCDTGTGACAKPTVTGWKCDRCPLPGFHSLSGEGCRPCTCNPAGSLDTC 441
QY 422 NVETGRVCCKDNVEGFNCERCKPGFFNLESSNPKGCTPCFCFHSVSVCTNAVGSYDIS 481
Db 442 DPRSGRCPCKENVEGNLCDCRCPGTFTNLQPHNPAGSCSCFCYGHSKVCASTAQFQVHHIL 501
QY 482 STFQIDEDGWRVEQRDGEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYQON 541
Db 502 SDFHQAEGWARSVVGSEHSPQWSPN---GVLLSPEDEEELTAPGKFLGDQRFQSYGQP 557
QY 542 LSFSPRVDRDRTRLSAEDLVLEGAGLRVSVPLIAQGNISYPSSETTVKIFRLH---EATDY 598
Db 558 LILFRVPPGDSPLPVQ-LRLEGTGLALS--LRHSSLSGPQDARASQGGRAQVPLQETSE 614
QY 599 PWRPALSPPFEFQKLLNLTSLKIRGTYSERSAG--YLDVDTLQSAARPGVGPATWVESCT 656
Db 615 DVAPPLPFFHFQRLANLTSLRLRVSPGSPAGPVFLTEVRLTSARPLSPPASWVEICS 674
QY 657 CPVGYGGQFCETCLPGYRRETPLSLGYSVPCVLTCTCNHGHSETCDPETGVCDCRDNTAGPHC 716
Db 675 CPTGYTGQFCESCAPGYKREMPQGGPYASCVFCTCNQHG--TCDPNTGICVCSHHTEGPSC 733
QY 717 EKCSGYYGDSLTGTSDDCQPCPCPGGSSCAIVPKTKVVTCHCTGTAGKRCCELDDGY 776
Db 734 ERCLPGFYGNPFAGQADDCQPCPCPGQSACTTIPESGEVVTCHCPGQRRRCRCEVDDGF 793
QY 777 FGDPLGNSGVPVRLCRQCQNDNIDPNAVGNCRNLTGEBCLKCIYNTAGFYCDRCCKEGFFGN 836
Db 794 FGDPLGLFHPQPCHQCQCSGNVDFNAVGNCDPLSGHCLRLHNTTGDHCEHCQEGFYGS 853

QY 837 PLAPNPADKCKACACN-YGTVQQSSCNPVTCQCCLPHVSGRDCGTCDPGYNNLQSGQG 895
Db 854 ALAPRPADKCMPCSCHPQGSVEQMPCDPVTGQCSCLPHVTARDCSRCPGFFDLQPGRG 913
QY 896 CERCDCHALGSTNGQCDIRTHQCECQPGITGQHCHERCETHFGFGPEGCKPCDCHHEGSL 955
Db 914 CRSCCKHPLGSEQEDQCHPKTGQCTCRPGVTGQACDRCLQGGFFGSSIKGCRACRCSPLGAA 973
QY 956 SLOCKDDGRCECREGFGVGNRCDOCEENYFYNRSMWPGQECPCACYRLVKDKAEHRVKLQE 1015
Db 974 SAQCHYNGTCVCRPGFEGYKCDRCHYNFFLTADGTHCQOCPCSCYALVKEETAKLKARLTL 1033
QY 1016 LESLIANLGTGD----DMVTDOAFEDRLKEAEREVTDLLREAEQVKVDQNLMDRLQRV 1070
Db 1034 TEGWLGSDCGSPWGPLDILLGEAPRGDVYQGH-----LLPGAREA-----FLEQMMGL 1083
QY 1071 NSSLSQISRLQIRNTIETGILAEARSRVESTEQLEIASRE-LEKAKMAANVSITQ 1129
Db 1084 EGAVKAAREQLORLNKGARCAQAGSQKCTCTQLADLEAVLESSEEEILHAAAILASLEIPQ 1143
QY 1130 PESTGEPNMTLLAAEEARRLAEHRHKEADDIIVRVAKTANETSAAEYNLLRLTLAGENQTA 1189
Db 1144 -EGPSQPTKWSHLAIEARALARSHRDTATKIAATAPFALLASNTSYALLWNLL--EGRVA 1200
QY 1190 LEIE-ELNRKYEQAKNISQDLEKQAARVHEEAKRAGDKAVEIYASVAQL----- 1237
Db 1201 LETQDLEDRYQEVQAAQKALRTAVAEVLPEAE-----SVLATVQOVGADTAPYLALL 1253
QY 1238 -----TPVDSEA--LENEANKIKKEAADLRLIDQKLKDYEDLRE-DMRGKEHEVKNLLE 1289
Db 1254 ASPGALPQKSRAEDLGLKAKALEKTIVASQWQMATEAARTLQTAQAATLRQTE---PLTMA 1310
QY 1290 KGKABQQTADQOLLARADAAKALAEAAKKGRSTLQEAANDILNNLKDFDRRVNDNKTAAEE 1349
Db 1311 RSRLTATFASQLHQGARAALTQASSSVQAAATVTVMGARTLLADLEGMKLQFFRPKQQAAL 1370
QY 1350 ALRRIPAINRTIAEANECTREQLALGNAAADATEAKNKAHEAEARIAASAAQKATSTKAD 1409
Db 1371 QRKADSVDRLLADTRKTKQAERMLGNAAPLSSAKKKGREAEVLAKDSAKLAKALLRE 1430
QY 1410 AERTFGEVTDLDNEVNGMLRL-EEAENELKRKQDDADQDMMAGMASQAAQAEELNARK 1468
Db 1431 RKQAHRRASRLTSQTQATLQQAQQVLASEARRQEELEAEAEVAGLS-----EMEQQIRE 1485
QY 1469 AKNSVSSLLSQLNNLLDQLGLDT--VDLNKLNIEIGSLNKADEM-KASDLDRKVSdle 1525
Db 1486 SRISLEKDIETLSSELLARGLSLDTHQAPAAQALNETQWALERLRLQLGSPGSLQRLKLSLE 1545
QY 1526 SEARKQEAAIMDYNRDIAEIIKDIHNLEDIKKTLPTGC 1563
Db 1546 QESQQLQIQGFESDLAEIRADKQNLAILHSLPENC 1583
RESULT 11
US-10-262-839-212
; Sequence 212, Application US/10262839
; Publication No. US2004003877A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, John,
; APPLICANT: Anderson, David W.,
; APPLICANT: Boldog, Ferenc,
; APPLICANT: Burgess, Catherine,
; APPLICANT: Catterton, Elina,
; APPLICANT: Edinger, Shlomit,
; APPLICANT: Ellerman, Karen,
; APPLICANT: Gerlach, Valerie,
; APPLICANT: Gorman, Linda,
; APPLICANT: Guo, Xiaojia,
; APPLICANT: Ji, Weizhen,
; APPLICANT: Kekuda, Ramesh,
; APPLICANT: Leach, Martin,
; APPLICANT: Li, Li,
; APPLICANT: Miller, Charles,

; APPLICANT: Patturajan, Meera,
; APPLICANT: Reiger, Daniel,
; APPLICANT: Rotherberg, Mark,
; APPLICANT: Shinkets, Richard,
; APPLICANT: Smithson, Glennda,
; APPLICANT: Spytek, Kimberly,
; APPLICANT: Taupier, Raymond, jr.,
; APPLICANT: Vernet, Corine,
; APPLICANT: Voss, Edward,
; APPLICANT: Zerhusen, Brian,
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD.
; FILE REFERENCE: 21402-462A
; CURRENT APPLICATION NUMBER: US/10/262,839
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,101
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/371,972
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/327,342
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/328,044
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,849
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/374,738
; PRIOR FILING DATE: 2002-04-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 367
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 212
; LENGTH: 1575
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-839-212

Query Match 42.0%; Score 3583; DB 12; Length 1575;
Best Local Similarity 44.3%; Pred. No. 5.3e-200;
Matches 704; Conservative 249; Mismatches 570; Indels 66; Gaps 23;

QY 2 MDECADEGGRPQRCMPEFVNAFNVTVATNTCGTPPEEYVQTGVTGKTSCHLCDAGQ 61
Db 22 MGACYDGAAGRPQRCPLPVFENAAFGRLAQASHTCGSPPEDFCPHVGAAGAGAHQORCDAAD 81
QY 62 QHLQHGAFLTDYNNQADTTWWQSQTMLAGVQYPNSINTLHLGKAFDITYVRLKFTISR 121
Db 82 QQRHNASYLTDFHSQDESTWWQSPSMAFGVQYPTSVNITLRLGKAYEITYVRLKFTISR 141
QY 122 PESFAIYKTRREDGPPWIPYQYVSGSCENTYSKANRGFIRTGDEQQALCTDEFSDISPLT 181
Db 142 PESFAIYKSRADGPPWEPYQFYASQKTYGRPEGQYLRPGEDERVAFTSEFSDISPLS 201
QY 182 GGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLNRLNTFGDEVFNDPKVLKSYYYA 241
Db 202 GGNVAFSTLEGRPSAYNFEESPGLOEWWVTSTELLISLDRLNTFGDDIFKDPKVLQSYYYA 261
QY 242 ISDFAVGGRCCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKLCPFFNDRPWRRATAESA 301
Db 262 VSDFSVGGRCCKNGHASECGPDVAGQLACRCQHNTTGTDCERCCLPFFQDRPWARGTAEAA 321
QY 302 SECLPCDCNGRSQECYFDPELYRSTGHGHCNCRDNTDGAKCERENFFRLGNTEACS 361
Db 322 HECLPCNCSGRSEECTFDRELFRSTGGGRCHCRDHTAGPHCERCQENFYHWDPRMPCQ 381
QY 362 PCHCSPVGSLSLSTQCDSYGRCSCKPGVMGDKDCRCQPGFHSLSLTEAGCRPCSCDPSGSTDEC 421

Db 382 PCDCQAGSLHLQCDTGTCACTPTVTGWKCDRLPGFHSLSSEGGRPCCTCNPAAGSLDTC 441
QY 422 NVETGRVCVCKDNVEGNCERCKPGFFNLESNPKGCTPCFCFHSVCTNAVGSVYDIS 481
Db 442 DPRSGRCPCENVEGNLDCRCRPGTFNLOPHNPAGSCSCFCYCHSKVCASTAQFQVHIL 501
QY 482 STFQIDEDGWRVEQRDSEASLEWSSDRQYIAVISDSYFFPRYFTAPVKFLGNQVLSYGN 541
Db 502 SDFHQAGWARSVSGSEHSPQWSPN---GVLLSPDEDEELTAPGKFLGDQRFSGYGP 557
QY 542 LSPFRVDRDRRLSADLVLEGAGLRVSVPLIAQNSYPSSETTVKVIYFRLH---EATDY 598
Db 558 LILTRVPPGDSPLPQ-LRLEGTGLALS--LRHSSLSGPDARASQGGRAQVPLQETSE 614
QY 599 PWRPALSPFEFQKLLNNLTSIKIRGTYSERSAG--YLDVTLQSAARPGPGVATWVESCT 656
Db 615 DVAPPLPPFHFQRLANLTSRLRVSPGSPAGPVFLTEVRLTSARPLSPASWVICS 674
QY 657 CPVGYGGQFCETCLPGYRRETSLGYPSPCVLCTCNHSETCDPETHGVCDCRDNATAGPHC 716
Db 675 CPTGYTGFCESCAPGYKREMPQGGPYASCPVCTCNQHG-TCDPNTGICVCHRTGSPSC 733
QY 717 EKCSDDGYGDTLGTSSDCQPCPCPGSSCAIVPKTKEVVCTHCPTGTAGKRCCLCDDGY 776
Db 734 ERCLPGFYGNPFRAGQADDCQPCPCPGQSACTIPESGEVCTHCPGQGRRCRCEVDDGF 793
QY 777 FGDPLGNGPVRCLRPCQCNNDIDPNVAGNRLTGECLKCTYNTAGFYCDRCKEGFFGN 836
Db 794 FGDPLGLFGHPQCHQCQSGNVDPNAVGNCDPLSGHCLRLHNTGDHCEHCQEGFYGS 853
QY 837 PLAPNPADKCKACACN-YGTVQQSSCNBVTGQCCLPHVSGRDCGTCDPGYVNLQSGQG 895
Db 854 ALAPRPADKCMPCSHPGQSVSEQMPCPDVTGQCSCLPHVTARDCSRCPYGFDDLPQGRG 913
QY 896 CERCDHALGSTNGQDIRTGQCECQPGITGQHCCERCTNHFPGEGPKPCDCHHEGSL 955
Db 914 CRSCCHPLGSDQCHPKTGQCTCRPGVTGQACDRCLGFFGSSIKGCRACRCSPLGAA 973
QY 956 SLQCKDDGRCEBGFVGNRCQCEENFYNRSPGQCECPACRYLVKDKAAEHRVKLQE 1015
Db 974 SAQCHYNGTCVCRPGFEGYKCDRCHYNFFLTADGTHCQCCPSYALVKEETAKLKLTL 1033
QY 1016 LESLIANLGTGD---DMVTDQAFEDRLKEAREVTDLLRBAQEVKDVQDNLMDRLQRV 1070
Db 1034 TEGWLOQSDCGSPWGLDILLGEAPRGDVGHH---LLPGAREA-----FLEQMMGL 1083
QY 1071 NSSLSQISRLQNRNTIETGILAEARSRVSTEQILIEIASRE-LEKAKMAANVSITQ 1129
Db 1084 EGAVKAAREQOLRINKGARCAQAGSKTCTQLADLEAVLESSEEEILHAAAILASLEIPQ 1143
QY 1130 PESTGEPNNMTLLAEAEARRLAERHKQEAADDIVRVAKTANETSABAYNLLRLTLAGENQTA 1189
Db 1144 -EGPSQPTKWSHLAEARALARSHRDTATKIAATAWRALLASNTSYALLWNL--EGRVA 1200
QY 1190 LEIE-ELNRKYEAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQL---TPVDSEA 1244
Db 1201 LETQDLEDRYQEVQAAQKALRTAVAEVLPEAE-----SVLATVQVQVADTAPYLALL 1253
QY 1245 LENEANKIKKEADLRLIDQKLKDYEDLREDMRGKEHEVKNLLEKGAEQQTADQ--- 1300
Db 1254 ASPGALPKSRAEDL---GLKAKALEKTVASWQHMAATEARTLQ--TAAQATLRQTEPL 1307
QY 1301 --LLARADAALAEAAKGRSTLQEAANDILNNLKDFDRVNDNKTAAEEALRRIPAIN 1358
Db 1308 TKLHQEARAALTQASSSVQAATVTVMGARTLLADLEGMKLQFPPRPKDQAAALQKADSVSD 1367
QY 1359 RTIAEANEKTRQAALGNAADATEAKNKAHEAERIAAGAKQVATSTKADABERTFGEVT 1418
Db 1368 RLLADTRKTKQAERMLGNAAPLSSSAKKKGREAELVAKDSAKLAKALLRERQAARRAS 1427
QY 1419 DLDNEVNGMLRLQ--EEAENELKRRKQDDADQDMMAGMASQAQAEALNARKAKNSVSL 1477

Db 1428 RLTSQTQATLQOASQVLAASEARRQEEAERVGAGLS-----EMEQIRESRISLEKDI 1482
QY 1478 SOLNNLLDQLGQDLD--VDLNKLNEIEGSLNKADEM-KASDLDRKVSDESEARKQEA 1534
Db 1483 ETLSELLARLGLDTHQAPALNETQWALERLRLQLGSPGSLQRLSLLEQESQQQLQ 1542
QY 1535 IMDVNRDIAELIKDIHNLIEDIKKTLPTGC 1563
Db 1543 IQGFESDLAEIRADKQNLKLEAILHSLPENC 1571

RESULT 12
US-10-369-493-6816
; Sequence 6816, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6816
; LENGTH: 1557
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6816

Query Match 37.4%; Score 3193; DB 15; Length 1557;
Best Local Similarity 38.2%; Pred. No. 2.9e-177;
Matches 626; Conservative 289; Mismatches 543; Indels 180; Gaps 30;
QY 5 CADEGGR-PQRCMPEFVNAFNVTVATNTGTP-PEEYCVQTVGTGVTKSCHLCDAGQ 62
Db 25 CYDRATRPQRCVPDFVNAFNVTVATNTGTPKTKFCVQSGHTGQSVCECTCDRHE 84
QY 63 HLOHGAFLTDYNNQADTTWQSQTMLAGVQVPSINLTLHLKAFDITYVRLKFTSRP 122
Db 85 GESHAPKYLTDENVGNNTWQSDTMQEGQYPTTNTLTLVGLKSFDTYVRLKFISRP 144
QY 123 ESFAIKRTREDGPIWYQYVYSGSCENTYKANKRGFIRTTGGDEQALCTDEFSDISPLTG 182
Db 145 ESTIYKTHTDSEWEPWQFYSGSCRATYGLSDRAPI-LPGNEATAQCTKEFSDISPTG 203
QY 183 GNVAFTLEGPRSAYNFNDNSPVLOEWTATDIRVTLNLTNLTGDEVFNDPKVLKSYIYAI 242
Db 204 GNIAFTLEGPRSAHAFAEESVQLQKWTASAIRISLNRMTFGDEVFKDPQVLSYIYAI 263
QY 243 SDFAVGRCCKNGHASECVKNEF---DKLMCNCKHNTYGVDCCKCLPFFNDRPWRATA 298
Db 264 SDFAVGRCCKNGHASECVGSSSVVDGENRLVCRCEHNTQAGDCNECLPFFNDRPWRSGTS 323
QY 299 ESASECLPCDCNRSQECYFDPPELYRSTGHGHCNTCRDNTDGAKECERENFFRLGNT 358
Db 324 VEANEICACNSQLSNRCYFDQLFEETGHGHCIDCQGNTOGVHCEQCIANHWRRPGEN 383
QY 359 ACSPPCHCSPVGLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSILTEAGCRPCSCDPSGST 418
Db 384 YCVACGCNEIGSLSTQCDNEGKCKQKPGVTGRFCQCLDGLDFSTNGCKNCGCETSGSL 443
QY 419 D---ECNVETGRVCCKDNVEGNCERCKPGFFNLESNPKGCTPCFCFHSVCTNAVGY 475
Db 444 NNQPRCDSSSGSCCKLNVEGRQCDKCKPGYFDLSTENQFGCTPCFCFHSVCTNAVGY 503
QY 476 SVYDISSTFQIDEGWRVEQRDGEASLEWSSDRQYIAVISDSYFFPRYFIAPVKFLGNQV 535

Db 504 FAMNVSVFDDQKQWAGQNRIGLQ-DTQWAEALDKAVAVSDTNDSPVYFVAPEQFLGDQR 562
QY 536 LSYGQNLFSFRVDRDRRLSAEDLVLEGAGLR-VSVPLIAQGNYSFSETTVKYIFRLHE 594
Db 563 SSYNQDLVFTLKVAKHVTNQDVKDIIVGADRQELSTSTITAQGNFPFTEAQTFRFRVHA 622
QY 595 ATDYPWRPALSPFEFQKLNNLTSIKIRGYTSERSAGYLDVTLQSRPQGV---PAT 650
Db 623 DPFYGWYPRINELDFIGILSNITAIKIRGYTSYKIDYLSNVNLGAVGAPSAANPKQAT 682
QY 651 WVBESCTCPVGYGGQFCETCLPGYRRETSLGYPSPCVLCTCNHSHSETCDPETGVCDGRDN 710
Db 683 WIEHCECLPGFVGQFCESCEGFRRETQKFGFPNHCICKDCHNHSNCEAESGSCICEHN 742
QY 711 TAGPHCEKSDGYGDLTGTSSDCQPCPCPGSSCAIVPKTKEVVTCHTCTGTAGKRC 770
Db 743 TAGDTCERCARGYGDALQGTEDCQKPCPNQGPC-ILHADGDVICTECPNGYTGRRCD 801
QY 771 LCDDGYFGDPLGNSGPNVRLCRPCQCNNDNIDPNAVGNCRNLGTGECILKIYNTAGFYCDRCK 830
Db 802 ECSDBGYFGNPKDGTGTE---CVEACSGNTDPSIGNCDKITGECKKCFINTHGFNCENCK 857
QY 831 EGFFGNPLAPNPADKCKACACNYGTVQQQSS-----CNPVTGQCCQLPHVSGRDCGTC 884
Db 858 PGYMGDALI-EPKGNCQSCGCAAGTRRRPNNDYTLLECNCQDQGGCDCLPNVIGIQDQCA 916
QY 885 PGYNLQSGQGCERCDCGHALGSTNGQCDIRTCQCECQPGITGQHCERCETNHFQFEGC 944
Db 917 HGFYNITSLGCGQECNCDPLGSEGTCDVNTGQCCQKPGVTGQRCDCADYHFGFSANGC 976
QY 945 KPCDCHHEGSLSLQCK-DDGRCECREGFGVGNRCQCEENYFNRSPWPGCQECPCACVRLVK 1003
Db 977 QPCDCEYIGSENQCDVNSGQCLCKENVEGRRCQCAENRY--GITQGLPCDDCYTLIQ 1034
QY 1004 DKAAEHRVKLQLESILIANLGTGDDMTDQAFEDRLKEAREVTDLLREA-QEVKDVQDN 1062
Db 1035 SRVNVFREKVKSLDNTLQEIENPAPVNDTKFDEKVKETSRASEVWEAVKQKTEGGGT 1094
QY 1063 LMDRLQRVNSSLHQSRLQNRNTIETGILAEARSRSVSTEQLEIASREL----- 1116
Db 1095 IKTKSKAIKDEIVAALKLTSIDESVAQAKVGADAAENDMKRWEIENARREIENVLHY 1154
QY 1117 -----EKAKMAANVSITQPESTGEPN-NMTLLAEARRLAERHKEADDIVRAKTANE 1169
Db 1155 LETEGERAQIAYNAS---QKYGEQSKRMSELASGTREAEKHLKQASEIEQLSEQAIA 1210
QY 1170 TSAEAYNLLRLTAGENQTALEIEELNRYEQ-A-KNISQLEKQAAARVHEEAKAGDKAV 1228
Db 1211 NATQANKEASDAIYGEQISKOIAELKEKQNLNESIHRITLD-----LAEEQKKSADAN 1265
QY 1229 EIYA-----SVAQLTPVDSEALENEANKIKKEAADLRLDQKLKD---YEDLREDMRG 1279
Db 1266 NLAASVLTNVEAVKIPSVDPKELRNDVAGVLEES---ENLVDSSVKENSANDELDFEVNR 1322
QY 1280 KEHEVKNLLEKGAEQQTADQLLARADAALAEAAKKGSTLQEAANDILNNLKDQFDRR 1339
Db 1323 SVADARNELQSSQDQORVSDQLMLELEKSRERIVDSVSTADTKLDAEAALQVLEEFQAK 1382
QY 1340 VNDNKTAAEEALRRIPAINR---TIAEANEKTR-----EAQLALGNAAAD 1381
Db 1383 IEKSRNDAAVEAFAGVEGINQRLDDIIDAQDKRRNSLPIDKQFVIDYRKSADVLNETHAL 1442
QY 1382 ATEAKNKAHEABRIASAAQKNAT-STKADAERTFGEVTDLDNEVNGMLRQLEEAENELKR 1440
Db 1443 ADRYKDIH-----SDVTRDSTEAQVQDIEQLMEELTDSNENL-----QYK 1485
QY 1441 QODDADQDMMAGMASQ-----AAQEAELNARKAKNSVSLLSQLNNLLDQLGLDVT 1493
Db 1486 QOAEDDKQWATEAVRKQLLPRILPSKQMLPFSLRKMKSILWLV----- 1532
QY 1494 DLNKLNEIEGSLNKAKDEMKAASDLDRKVSLESEARKQEAALMDYNRDIAETIKDIHNLE 1553
Db 1533 -----NLE 1535

QY 1554 DIKTLPTGCFNTPSIEK 1571
Db 1536 EIRDNLPTKCFNVINLEQ 1553

RESULT 13

US-10-392-113-14
; Sequence 14, Application US/10392113
; Publication No. US20030224993A1
; GENERAL INFORMATION:
; APPLICANT: Land, Hartmut
; APPLICANT: Deleu, Laurent
; TITLE OF INVENTION: COMPOSITIONS THAT INHIBIT PROLIFERATION
; TITLE OF INVENTION: OF CANCER CELLS
; FILE REFERENCE: 21108.0005U3
; CURRENT APPLICATION NUMBER: US/10/392,113
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: 60/365,078
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: PCT/US01/32127
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/239,705
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1193
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
; OTHER INFORMATION: Synthetic Construct
US-10-392-113-14

Query Match 30.4%; Score 2592; DB 12; Length 1193;
Best Local Similarity 39.1%; Pred. No. 2.2e-142;
Matches 510; Conservative 235; Mismatches 422; Indels 138; Gaps 13;

QY 284 CLPFFNDRPWRRTAESAECCLPCDCNRSQBCYFDPPELYRSTGHGHCNCRDNTDGA 343
Db 9 CLCFSLLLPAARATSRRE---VCDGNGKSRQCFIDRELHRTQGTGNGFRCLNCNDNTDGIH 64
QY 344 CERENFRRLNGTEACSPVGSLSSTOCDYGRCSCKPGVMGDKDCRCQPGFHS 403
Db 65 CERKNGFYHRERDRCLPCNCSKGSLSARCDNSGRCSCKPGVTGARCDCLPGFHM 124
QY 404 EAGC-----RPSGCDPSGSTDECNVETGRCVCKDNVEGNCERCKPGFFNLESSNPK 455
Db 125 DAGTQDQRLDLSKCDPAGIAGPC--DAGRCVCKPAVTGERCDRCRSGYNNLDGNGPE 182
QY 456 GCTPCFCFGHSSVCTNAVGYSYDIDISSTFOIDEDGWRVEQORDGSSEASLEWSSDRQYIAVI 515
Db 183 GCTQCFYGHSAASCRSSAEYSVHKITSTFHQDVGDKAVQNRNGSPAKLQWSQRHQDVFS 242
QY 516 SDSYFPRIYFIAPVKFLGNQVLSYQNLFSFRVDRDRRLSAEDLVLEGAGLRVSVPLIA 575
Db 243 AQRDPVYFVAPAKFLGNQVLSYQNLFSFRVDRDRRLSAEDLVLEGAGLRITAPLMP 302
QY 576 QGNSYPSSETTVKIFRLHEATDYPWRPALSPFEFQKLNNLTSIKIRGYTSERSAGYLD 635
Db 303 LGKTLPCGLTKTYTFRNLNEHPNNSPQSYFEYRRLRLNLALRIRATYGEYSTGYDN 362
QY 636 VTLQSRAPGPGVPATWVESCTCPVGYGGQFCETCLPGYRRETSPSLGYPSPCVLCTCNH 695
Db 363 VTLISARVSGAPAPWVEQICPVGYKQGCQDCASGYKRDARSARLGPFGTICPCNQCG-G 421
QY 696 ETCDPETGVCDRCNTAGPHCEKCSGDSYGGDSTLGTSSDCQPCPCPGSSCAIVPKTKEV 755
Db 422 GACDPTGDCYSGDENPDIEACDPIGFYNDP--HDPRSCKPCCHNGFSCSVMPETEVEV 479
QY 756 VCTHCPTGTAGKCELCDDGYFGDPLGNGPVRCLRPCQCNNDNIDPNAVGNCRNLGTGEC 815

Db 480 VCNNCPGVTGARGELCADGYFGDPFGEHGPVRPCQPCQNNVDPSPASGNCNDRLTGRCL 539
QY 816 KCIYNTAGFYCDRCCKEFGFNPLAPNPADCKKACACNYGTVOQSSCNPTGQCQCLPHV 875
Db 540 KCIHNTAGIYCDQCKAGYFGDPLAPNPADKCRACNCN----- 576
QY 876 SGRDCGTCDPGYNNLQSGQCERCDCCHALGSTNGQCDIRTGQCECQPGITGQHCHCETN 935
Db 577 ----- 576
QY 936 HFGFGPEGCKPCDCHHEGSLSLQCKDDGRCCEGFGVGNRCDCQCEENYFYNRSWPGCQEC 995
Db 577 -----PMGSEP-----VGRSDGTCTVCKPGFGGPNCEH-----GAFSC 609
QY 996 PACYRLVKDKAAEHRVKLQELSLIANLGTGDDMTDQAFEDRLKEAREVTDLLREAOE 1055
Db 610 PACYNQVKIQMDQFMQQLQRMALISKAQGGDGVVPTDELEGRMQAEQALQDLRDAQI 669
QY 1056 VKDQVQNLMDRLQVRNSSLHSQISRLQNRNTIETGILAEARRARSRVSTEQLEIASRE 1115
Db 670 SEGASRLGLQAKVRSQENSYSQSRLLDKMTVERVRLGSGYQNRVDRDTHRLITQMLSL 729
QY 1116 LEKAKMA-ANVSITQPESTGEPNMTLLAEARRLAERHKEADDDIVRVAKTANETSAAE 1174
Db 730 LAESEASLGNTNIPASDHYVGPNGPKSLAQEAETRLAESHVESASNMEQLTRETEDYSKQA 789
QY 1175 YNLLRLTL-----AGENQTALEIEELNRKYEQAKNISQLEKQAAARVHEEAKRAGDKA 1227
Db 790 LSLVRKALHEGVSGSGSPDGAV-VQGLVEKLEKTKSLAQQLTREATQAEIEADRSYQHS 848
QY 1228 VEIYASVAQLTPVDSEALE-NEANKIKKEAADLRLIDQKLKDYEDLREDMRGKEHEVKN 1285
Db 849 LRLDLSVSRLOQVSDQSFQVEEAKRIKQKADSLSTLVTRHMDFEKRTQKNLGNWKEEAQQ 908
QY 1287 LLEKGAEQQTADOLLARADAALAEAAKGRSTLQEAANDILNNLKDFDRVNDNKA 1346
Db 909 LLQNGKSGREKSDQLSRANLAKSRACEALSMGNATFYEVSILKNLREFDLQVDNRKAE 968
QY 1347 ABEALRRIPAINRTIAEANEKTRAEQALGNAADAAATEAKNKAHEAERIAASAKNATST 1406
Db 969 ABEAMKRLSYISKVSDASDKTQQAERFALGSAADAQRAKNGAGEALEISSIEIEQIGSL 1028
QY 1407 KADAERTFGEVTDLDNEVNGMLRQLEEAENELKRKQDDADQDMMAGMASQAQAEALNA 1466
Db 1029 NLEANTADGALAMEKGLASLXSENRVEGELEKELEFDNTMDAVQMVITEAQKVDTRA 1088
QY 1467 RKAKNSVSSLISQLNNLLDQLGQDLDVNLKNEIEGSLINKAKDEMKASDIDRKVSDLES 1526
Db 1089 KNAGVTIQDTLNTLDGLLHMDQLSVDEGLVLEQLSRAKTQIN-SQLRPMMSLEE 1147
QY 1527 EARKQEAAMDYNRDIAEIIKDHNLEDIKKTLPCTGCFNTPSIEK 1571
Db 1148 RARQQRGHLHLETSIDGILADVKNLENIRDNLPFGCYNTQALEQ 1192

RESULT 14
US-10-171-311-115
; Sequence 115, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoersh, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF CERVICAL CANCER
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311

; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 115
; LENGTH: 1193
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-311-115

Query Match 30.4%; Score 2592; DB 14; Length 1193;
Best Local Similarity 39.1%; Pred. No. 2.2e-142;
Matches 510; Conservative 235; Mismatches 422; Indels 138; Gaps 13;
QY 284 CLPFFNDPRWRATASASECLPCDCNGRSQECYFDPYRSTGHGCHCTNCRDNTDGA 343
Db 9 CLCFSLLLPAARATSRRE---VDCNCKSRQCIFDRELHRTGTNGFRCLNCDNTDGIH 64

QY 344 CERCENFFRLGNTACSPCHCSPVGSLSLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHS 403
Db 65 CEKCKNGFYRHRERDRCLPCNCNSKGSLSARCDNSGRCSCKPGVTGARCDCLPGFHM 124
QY 404 EAGC-----RPCSDPSGSTDECNVETGRVCCKNVEGFNCERCKPGFFNLESSNPK 455
Db 125 DAGCTDQDRLDSCDCDPAGIAGPC--DAGRCVCKPAVTGERCDRCRSGYNNLDGNGPE 182
QY 456 GCTPCFCFGHSSVCTNAVGSYVDISTFQIDEDGWRVEORDGSEASLEWSSDRQYIAVI 515
Db 183 GCTQCFCYGHSSASCRSSAEYSVHKITSTFHQDVGWKAQVRNGSPAKLQWSQRHQDV 242
QY 516 SDSYFPRYFIAPVKFLGNQVLSYQNLFSFRRVDRDRDRLSAEDLVLEGAGLRVSVPLIA 575
Db 243 AQRLDPVYFVAPAKFLGNQVSYGQSLSFYRVDGRGRHPSAHDVILEGAGLRITAPLMP 302
QY 576 QGNSYPSSETTVKIFRLHEATDYPWRPALSPFEFQKLNLTSLIKIRGTYSERAGYLD 635
Db 303 LGKTLPCGLTKTYTFRLLNEHPSNNWSPQLSYFEYRRLNLTALIRATYGEYSTGYIDN 362
QY 636 VTLQSRAPGPGVPATWVESCTCPVGYGGQFCETCLPGRRETTPSLGYPSPCVLCTCNHGS 695
Db 363 VTLISARVSGAPAPWVEQCICPVGYKGQFCQDCASGYKRDARSARLPGFTCIPCNCGG-G 421
QY 696 ETCDPETGVCDRCNTAGPHCEKSDGYGSDTLGTSSDCQPCPCPGSSCAIYPKTKEV 755
Db 422 GACDPTDGCYSGDENPDIEACDCPIGFYNDP--HDPKRCPCPCCHNGFSCSVMPETE 479
QY 756 VCTHCPGTAGKRCCLCDDGYFGDPLGSGNPGVRLCRPCQCNNDNIDPNVAGNCRNLTGE 815
Db 480 VCNNCPGVTGARGELCADGYFGDPFGEHGPVRPCQPCQNNVDPSPASGNCNDRLTGRCL 539
QY 816 KCIYNTAGFYCDRCCKEFGFNPLAPNPADCKKACACNYGTVOQSSCNPTGQCQCLPHV 875
Db 540 KCIHNTAGIYCDQCKAGYFGDPLAPNPADKCRACNCN----- 576
QY 876 SGRDCGTCDPGYNNLQSGQCERCDCCHALGSTNGQCDIRTGQCECQPGITGQHCHCETN 935
Db 577 ----- 576
QY 936 HFGFGPEGCKPCDCHHEGSLSLQCKDDGRCCEGFGVGNRCDCQCEENYFYNRSWPGCQEC 995
Db 577 -----PMGSEP-----VGRSDGTCTVCKPGFGGPNCEH-----GAFSC 609
QY 996 PACYRLVKDKAAEHRVKLQELSLIANLGTGDDMTDQAFEDRLKEAREVTDLLREAOE 1055
Db 610 PACYNQVKIQMDQFMQQLQRMALISKAQGGDGVVPTDELEGRMQAEQALQDLRDAQI 669
QY 1056 VKDQVQNLMDRLQVRNSSLHSQISRLQNRNTIETGILAEARRARSRVSTEQLEIASRE 1115


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Db 670 SEGASRLGLQAKVRSQENSYSQSRLLDLDLKMVTRVRLGSGYQNRVRDTHRLITOMQLS 729
QY 1116 LEKAKMA-ANVSITQPESTGEPPNMTLLAEAEARRLAERHKEADDDIVRVAKTANETSAAE 1174
Db 730 LAESASLGNTNIPASDHYVGPNGFKSLAQEAETRLAESHVESASNMEQLTRETEDYSKQA 789
QY 1175 YNLLRLTL-----AGENOQTALEIEELNRKYEAKNISQDLEKQAAARVHEEAKRAGDKA 1227
Db 790 LSLVRKALHEGVGSGSPDGAV-VQGLVEKLEKTKSLAQQLTREATQAEIADRSYQHS 848
QY 1228 VEIYASVAQLTPVDSEALE-NEANKIKKEAADLRLIDQKLKYEDLREDMRGKEHEVKN 1286
Db 849 LRLDSVSRLOQVSDQSFOVEEAKRIKQKADSLSTLVTRHMDLQVDFKRTQKNGLNWKEEAQ 908
QY 1287 LLEKGAEOQTADQLLARADAALAEAEAAKKGSTLQEAANDILNKLDPDRRVNDNKTA 1346
Db 909 LLQNGKSGREKSDQLLSRANLAKSRAQEAALSMGNATFYEVESILKNLREFDLQVDNRKAE 968
QY 1347 ABEALRRIPAINRTIAEANEKTRQAALAEAEAAKKGSTLQEAANDILNKLDPDRRVNDNKTA 1406
Db 969 ABEAMKRLSYISQVSDASDKTQQAERALGSAADAQRAKAGAGEALEISSEIEQEIGSL 1028
QY 1407 KADAERTFGEVTDLDNEVNGMLRQLEEAENELKRRQDDADQDMMAGASQAAQAEALNA 1466
Db 1029 NLEAVNTADGALAMEKGLASLKSEMREVEGELEKLEFDTNMDAVQMVITEAQKVDTRA 1088
QY 1467 RKAKNSVSSLLSQNLNLDQGLQDQTLVNLKLEIEGSLNKADEMKAASDLDRKVSULES 1526
Db 1089 KNAGVTIQDNTLTDGLHLMQDPLSVDEEGLVLEQKLSRAKTQIN-SQLRPMMSLEEE 1147
QY 1527 EARKQEAAMDYNRDIAEIIKDIHNLEDIKTLPTGCFNTPSIEK 1571
Db 1148 RARQQRGHLHLLSTSIDGILADVKNLENIRDNLPPLPGCYNTQALEQ 1192

RESULT 15
US-10-053-662A-31
; Sequence 31, Application US/10053662A
; Publication No. US20030143545A1
; GENERAL INFORMATION:
; APPLICANT: Alexandra Charlesworth
; APPLICANT: Palvia Spirito
; APPLICANT: Guerrino Meneguzzi
; APPLICANT: John Baird
; APPLICANT: Keith Linder
; TITLE OF INVENTION: ISOLATION OF THE LAMININ Y2 GENE IN
; TITLE OF INVENTION: HORSES AND ITS USE IN DIAGNOSING JUNCTIONAL EPIDERMOLYSIS
; TITLE OF INVENTION: BULLOSA
; FILE REFERENCE: p84us4
; CURRENT APPLICATION NUMBER: US/10/053,662A
; CURRENT FILING DATE: 2002-01-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 1193
; TYPE: PRT
; ORGANISM: human
; FEATURE:
; OTHER INFORMATION:
US-10-053-662A-31

Query Match 30.4%; Score 2592; DB 14; Length 1193;
Best Local Similarity 39.1%; Pred. No. 2.2e-142;
Matches 510; Conservative 235; Mismatches 422; Indels 138; Gaps 13;

QY 284 CLPFFNDPWRRTAESAECPLPCDNGRSQECYFDPPELYRSTGHGHCNCRDNTDGAK 343
Db 9 CLCFSLLLPAARATSRRE---VCDNGKSRQCIFDRELHRTGTNGFRCLNCNNDTDGIH 64
QY 344 CERCRENFFRLGNTAEACSPCHCSPVGSLSLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSIT 403
Db 65 CEKCKNGFYRHRDRCLPCNCNSKGSLSARCDNSGRCSCKPGVTGARCDRCPLPGFHMILT 124
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QY 404 EAGC-----RPCSCDPSGSTDECNVETGRCVCKDNVEGENCECKPGFFNLESSNPK 455
Db 125 DAGCTQDQRLDLSKDCDPAIAGPC--DAGRCVCKPAVTCGERCDRCRSGYINLDGNGPE 182
QY 456 GCTPCFCFGHSSVCTNAVGYSVYDISTSFTQIDEDGWRVEQDGGSEASLEWSSDRQYIAVI 515
Db 183 GCTQCFCYCHSASCRSSAEYSVHKITSTFHQDVGWKAQVRNGSPAKLQWSQRHQDVFS 242
QY 516 SDSYFPRYFIAPVKFLGNQVLSYGNLSPFSFRVDRDRTRLSAEDLVLEGAGLRVSVPLIA 575
Db 243 AQRLLDPVYFVAPAKFLGNQVSYGQSLSFYRVDGRGRHPSAHDVILEGAGLRITAPLMP 302
QY 576 QGNSYSPSETIVKYIFRLHEATDYPWRPALSPFEFFQKLLNLTISKIRGTYSERSAGYLD 635
Db 303 LGKTLPCGLTKTYTFRLNEHPSNNWSPQLSYFYRRLRLNLTALRIRATYGEYSTGYIDN 362
QY 636 VTLQARPGPGVPATWVESCTCPVGGGQFCETCLPGYRRETPLSLGYPSPCVLCTCNHGS 695
Db 363 VTLISARPVSGAPAPWVEQCICPVYKGQFCQDQDCAAGYKRD SARLPGFTGTCIPCNQCG-G 421
QY 696 ETCDPETGVCDNRDNTAGPHCEKSDGYGDSLTGTSDDCQPCPCPGSSCAIVPKTKEV 755
Db 422 GACDPTGTCYSGDENPDIECADCPIGFYNDP--HDPKCKPCCHNGFSVMPETEVEV 479
QY 756 VCTHCTGTAGKRCCELDDGYFGDPLGSGNGPVRVLCRCQCNNDIDPNVAVGNCNRLTGECL 815
Db 480 VCNNCPGVTGARCELCAADGYFGDPFGEHGPVRPCQPCQCNVNDPSASGNCNDRLTGRCL 539
QY 816 KCIYNTAGFYCDRCKEGFFGNPLAPNPADKCKACAGNYGTVQQSSCNPNVTGQCQCLPHV 875
Db 540 KCIHNTAGIYCDQCKAGYFGDPLAPNPADKCRACN- 576
QY 876 SGRDCGTDPGYYNLQSGQGCRCDCCHALGSTNGQCDIRTGQCECQPGITGQHCECETN 935
Db 577 ----- 576
QY 936 HFGFGECKPCDCHHEGSLSLQCKDDGRCECREGFGVGNRCQDCEENFYFNRSWPGCQEC 995
Db 577 -----PMGSEP-----VGRSDGTCTVCKPFGGPNCEH-----GAFSC 609
QY 996 PACYRLVKDKAAEHRVKLOELESILANLGTGDDMVTDQAFEDRLKEAREVTDLLREAQ 1055
Db 610 PACYNQVKIQMDQFMQLOLMEALISKAQGGDGVVPTDELEGRMQQAEOALQDILRDAQI 669
QY 1056 VKVDONLMDRLQVRNSSLHSQISRLQNRNTTETGILAEARARSVESTESQLEIASRE 1115
Db 670 SEGASRLGLQAKVRSQENSYSQSRLLDLDLKMVTRVRLGSGYQNRVRDTHRLITOMQLS 729
QY 1116 LEKAKMA-ANVSITQPESTGEPPNMTLLAEAEARRLAERHKEADDDIVRVAKTANETSAAE 1174
Db 730 LAESASLGNTNIPASDHYVGPNGFKSLAQEAETRLAESHVESASNMEQLTRETEDYSKQA 789
QY 1175 YNLLRLTL-----AGENOQTALEIEELNRKYEAKNISQDLEKQAAARVHEEAKRAGDKA 1227
Db 790 LSLVRKALHEGVGSGSPDGAV-VQGLVEKLEKTKSLAQQLTREATQAEIADRSYQHS 848
QY 1228 VEIYASVAQLTPVDSEALE-NEANKIKKEAADLRLIDQKLKYEDLREDMRGKEHEVKN 1286
Db 849 LRLDSVSRLOQVSDQSFOVEEAKRIKQKADSLSTLVTRHMDLQVDFKRTQKNGLNWKEEAQ 908
QY 1287 LLEKGAEOQTADQLLARADAALAEAEAAKKGSTLQEAANDILNKLDPDRRVNDNKTA 1346
Db 909 LLQNGKSGREKSDQLLSRANLAKSRAQEAALSMGNATFYEVESILKNLREFDLQVDNRKAE 968
QY 1347 ABEALRRIPAINRTIAEANEKTRQAALAEAEAAKKGSTLQEAANDILNKLDPDRRVNDNKTA 1406
Db 969 ABEAMKRLSYISQVSDASDKTQQAERALGSAADAQRAKAGAGEALEISSEIEQEIGSL 1028
QY 1407 KADAERTFGEVTDLDNEVNGMLRQLEEAENELKRRQDDADQDMMAGASQAAQAEALNA 1466
Db 1029 NLEAVNTADGALAMEKGLASLKSEMREVEGELEKLEFDTNMDAVQMVITEAQKVDTRA 1088
QY 1467 RKAKNSVSSLLSQNLNLDQGLQDQTLVNLKLEIEGSLNKADEMKAASDLDRKVSULES 1526
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Db 1089 KNAGVTIQDTLNTLDGLLHMDQPLSVDEEGLVLEQKLSRAKTQIN-SQLRPMSELEE 1147
Qy 1527 EARKQEAAMDYNRDIAEIIKDIHNLEDIKKTLP TGCENTPSIEK 1571
Db 1148 RARQQRGHLHLETSIDGILADVKNLENIRDNLPPGCVNTQALEQ 1192

Search completed: May 18, 2004, 15:43:13
Job time : 46.9931 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:30:58 ; Search time 11.8919 Seconds
(without alignments)
6824.493 Million cell updates/sec

Title: US-10-037-182-20
Perfect score: 8527
Sequence: 1 AMDECADEGGRPQRCMPFV.....EDIKTLPTGCFNTPSIEKP 1572

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8527	100.0	1572	4	US-09-562-702A-32
2	8527	100.0	1572	4	US-09-561-818A-28
3	8527	100.0	1605	4	US-09-562-702A-30
4	8527	100.0	1605	4	US-09-561-818A-26
5	8038	94.3	1576	4	US-09-562-702A-24
6	8038	94.3	1576	4	US-09-561-818A-24
7	8038	94.3	1584	4	US-09-562-702A-28
8	8038	94.3	1609	4	US-09-562-702A-22
9	8038	94.3	1609	4	US-09-561-818A-22
10	8038	94.3	1617	4	US-09-562-702A-26
11	3586	42.1	1587	4	US-09-845-583A-10
12	3586	42.1	1587	4	US-09-561-709B-3
13	2591	30.4	1193	1	US-08-317-450B-13
14	2591	30.4	1193	3	US-08-800-593-13
15	2476.5	29.0	1111	1	US-08-317-450B-15
16	2476.5	29.0	1111	3	US-08-445-135-1
17	2306.5	27.0	1171	1	US-08-800-593-15
18	1812.5	21.3	3106	4	US-09-562-702A-10
19	1807.5	21.2	3084	4	US-09-562-702A-12
20	1790	21.0	3088	4	US-09-562-702A-8
21	1790	21.0	3089	4	US-09-562-702A-4
22	1790	21.0	3110	4	US-09-562-702A-2
23	1790	21.0	3110	4	US-09-562-702A-6
24	1790	21.0	3110	4	US-09-561-709B-7
25	1789.5	21.0	3111	2	US-08-460-309-4
26	1789.5	21.0	3111	2	US-08-125-077-4
27	1704	20.0	3075	2	US-08-460-309-5

28	1704	20.0	3075	2	US-08-125-077-5	Sequence 5, Appli
29	1677	19.7	1765	4	US-09-562-702A-16	Sequence 16, Appl
30	1677	19.7	1765	4	US-09-561-818A-16	Sequence 16, Appl
31	1677	19.7	1786	4	US-09-562-702A-14	Sequence 14, Appl
32	1677	19.7	1786	4	US-09-561-818A-14	Sequence 14, Appl
33	1677	19.7	1786	4	US-09-561-709B-9	Sequence 9, Appli
34	1661.5	19.5	1786	4	US-09-562-702A-18	Sequence 18, Appl
35	1661.5	19.5	1786	4	US-09-561-818A-18	Sequence 18, Appl
36	1637.5	19.2	1725	4	US-09-562-702A-20	Sequence 20, Appl
37	1637.5	19.2	1725	4	US-09-561-818A-20	Sequence 20, Appl
38	1630	19.1	1761	4	US-09-561-709B-1	Sequence 1, Appli
39	1526	17.9	1799	4	US-09-845-583A-6	Sequence 6, Appli
40	1477.5	17.3	1798	4	US-09-561-709B-11	Sequence 11, Appl
41	1472.5	17.3	1798	4	US-09-845-583A-8	Sequence 8, Appli
42	1357	15.9	251	1	US-08-152-019A-37	Sequence 37, Appl
43	1347.5	15.8	3635	4	US-09-845-583A-2	Sequence 2, Appli
44	1346	15.8	252	2	US-08-460-309-12	Sequence 12, Appl
45	1346	15.8	252	2	US-08-125-077-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-562-702A-32
; Sequence 32, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 1572
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-562-702A-32

Query Match 100.0%; Score 8527; DB 4; Length 1572;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AMDECADEGGRPQRCMPFVNAAFNVTVVATNTCGTPPEEYCVQGTGVTGVTKSchLCDAG	60
Db	1	AMDECADEGGRPQRCMPFVNAAFNVTVVATNTCGTPPEEYCVQGTGVTGVTKSchLCDAG	60
QY	61	QOHLQHGAFLTDYNNQADTTWQSQITMLAGVQYPNSINLTLLHKGAFDITYVRLKFHTS	120
Db	61	QOHLQHGAFLTDYNNQADTTWQSQITMLAGVQYPNSINLTLLHKGAFDITYVRLKFHTS	120
QY	121	RPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQAALCTDEFSDISPL	180
Db	121	RPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQAALCTDEFSDISPL	180
QY	191	TGGNVAFTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVNDPKVLKSYYY	240
Db	191	TGGNVAFTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVNDPKVLKSYYY	240
QY	241	AISDFAVGGRCCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPFFNDPWRRTAES	300
Db	241	AISDFAVGGRCCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPFFNDPWRRTAES	300

Db 481 SSTFQIDEDGWRVEQRDGSEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYGQ 540

Qy 541 NLSFSFRVDRDRDTRLAEDLVLEGAGLRVSVPLIAQNSYPSSETTVKYIFRLHEATDYPW 600

Db 541 NLSFSFRVDRDRDTRLAEDLVLEGAGLRVSVPLIAQNSYPSSETTVKYIFRLHEATDYPW 600

Qy 601 RPALSPFEFQKLLNNLTSIKIRGTYSERSAGYLDVTLQSAKPGVGPATWVESCTCPVG 660

Db 601 RPALSPFEFQKLLNNLTSIKIRGTYSERSAGYLDVTLQSAKPGVGPATWVESCTCPVG 660

Qy 661 YGGQFCETCLPGYRRETSLGYPSPCVLCTCNHGHSETCDPETGVCDNRDNTAGPHCEKCS 720

Db 661 YGGQFCETCLPGYRRETSLGYPSPCVLCTCNHGHSETCDPETGVCDNRDNTAGPHCEKCS 720

Qy 721 DGYGDSLTGTSDDCQPCPCPGSSCAIVPKTKEVVCVTHCPTGTAGKRCCELCDGFGDP 780

Db 721 DGYGDSLTGTSDDCQPCPCPGSSCAIVPKTKEVVCVTHCPTGTAGKRCCELCDGFGDP 780

Qy 781 LGSNGPVRLCRPCQCNNDNIDPNAVGNCRNLTGECCLKCIYNTAGFYCDRCKEGFFGNPLAP 840

Db 781 LGSNGPVRLCRPCQCNNDNIDPNAVGNCRNLTGECCLKCIYNTAGFYCDRCKEGFFGNPLAP 840

Qy 841 NPADKCKACACNYGTVOQSSCNPTVQCCQCLPHVSGRDCGTCDPGYNNLQSGQGGERCD 900

Db 841 NPADKCKACACNYGTVOQSSCNPTVQCCQCLPHVSGRDCGTCDPGYNNLQSGQGGERCD 900

Qy 901 CHALGSTNGQCDIRTGQCECQPGITGQHCERCETNHFHFGFEGEGCKPCDCHHEGSLQCK 960

Db 901 CHALGSTNGQCDIRTGQCECQPGITGQHCERCETNHFHFGFEGEGCKPCDCHHEGSLQCK 960

Qy 961 DDGRCEGREGFVGNRCDQCEENYFNRSWPGQCECPACVRLVKDKAAEHRVKLQLESLL 1020

Db 961 DDGRCEGREGFVGNRCDQCEENYFNRSWPGQCECPACVRLVKDKAAEHRVKLQLESLL 1020

Qy 1021 ANLGTGDDMVTDOAFEDRLKEAREVTDLLREAQEVKVDQNLMDRLQRVNSSLHSQISR 1080

Db 1021 ANLGTGDDMVTDOAFEDRLKEAREVTDLLREAQEVKVDQNLMDRLQRVNSSLHSQISR 1080

Qy 1081 LQNIIRNTIETGILAEARSRVESTEQLIEIASRELEKAKMAANVSITQPESTGEPNMT 1140

Db 1081 LQNIIRNTIETGILAEARSRVESTEQLIEIASRELEKAKMAANVSITQPESTGEPNMT 1140

Qy 1141 LLAEEARLAEHKEADDIIVRAKTANETSAEAYNLLRTLAGENQTALEIEELNRKYE 1200

Db 1141 LLAEEARLAEHKEADDIIVRAKTANETSAEAYNLLRTLAGENQTALEIEELNRKYE 1200

Qy 1201 QAKNISDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLD 1260

Db 1201 QAKNISDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLD 1260

Qy 1261 RLIDQKLKDYEDLREDMRGKEHEVKNLLEKGAEQQTADOLLARADAAKALAEAAKGR 1320

Db 1261 RLIDQKLKDYEDLREDMRGKEHEVKNLLEKGAEQQTADOLLARADAAKALAEAAKGR 1320

Qy 1321 STLQEAANDILNLLKDFDRRVNDNKTAABEALRRI PAINTRTIAEANEKTRTREAQLALGNAAA 1380

Db 1321 STLQEAANDILNLLKDFDRRVNDNKTAABEALRRI PAINTRTIAEANEKTRTREAQLALGNAAA 1380

Qy 1381 DATEAKNKAHEAERIAASAAQKNATSTKADAERTTGEVTDLDNEVNGMLRQLEEAENELKR 1440

Db 1381 DATEAKNKAHEAERIAASAAQKNATSTKADAERTTGEVTDLDNEVNGMLRQLEEAENELKR 1440

Qy 1441 KQDDADQDMMWAGMASQAAQAEALNARKAKNSVSSLISQLNLLDQLGOLDTVDLKNLNE 1500

Db 1441 KQDDADQDMMWAGMASQAAQAEALNARKAKNSVSSLISQLNLLDQLGOLDTVDLKNLNE 1500

Qy 1501 IEGSLNKAKDEMKAASDLDRKVSLESEARKQEAAMIDVNRDIAEIIKDIHNLEDIKKTLP 1560

Db 1501 IEGSLNKAKDEMKAASDLDRKVSLESEARKQEAAMIDVNRDIAEIIKDIHNLEDIKKTLP 1560

Qy 1561 TGCFTNPSIEKP 1572

Db 1561 TGCFTNPSIEKP 1572

RESULT 3

US-09-562-702A-30
; Sequence 30, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 1605
; TYPE: PRT
; ORGANISM: Mus musculus

US-09-562-702A-30

Query Match 100.0%; Score 8527; DB 4; Length 1605;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMDECADEGGRPQRCMPEFVNAFNVTVATNTCGTPPEEYCVQGTGVTGKSKHLCDAG 60

Db 34 AMDECADEGGRPQRCMPEFVNAFNVTVATNTCGTPPEEYCVQGTGVTGKSKHLCDAG 93

Qy 61 QQLHGHGAFLTDYNNQADTTWQOTMLAGVQYPSINLTLHLGKAFDITYVRLKFHTS 120

Db 94 QQLHGHGAFLTDYNNQADTTWQOTMLAGVQYPSINLTLHLGKAFDITYVRLKFHTS 153

Qy 121 RPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTGDEQQAALCTDEFSDISPL 180

Db 154 RPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTGDEQQAALCTDEFSDISPL 213

Qy 181 TGGNVAFTLEGRRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSYYY 240

Db 214 TGGNVAFTLEGRRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSYYY 273

Qy 241 AISDFAVGGRCCKNGHASECVKNEFDKLMCNCKHNTYGVDCBKCLPFFNDRPWRATAES 300

Db 274 AISDFAVGGRCCKNGHASECVKNEFDKLMCNCKHNTYGVDCBKCLPFFNDRPWRATAES 333

Qy 301 ASECLPCDCNGRSQECYFDPPELYRSTGHGCHCTNCRDNTDGAKCERCENFFRLGNTEAC 360

Db 334 ASECLPCDCNGRSQECYFDPPELYRSTGHGCHCTNCRDNTDGAKCERCENFFRLGNTEAC 393

Qy 361 SPCHCSPVGSLSLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLSLTAAGCRPCSCDPSGSTDE 420

Db 394 SPCHCSPVGSLSLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLSLTAAGCRPCSCDPSGSTDE 453

Qy 421 CNVETGRCVCKDNVEGFNCERCCKPGFNLESNNPKGCTPCFCFGHSSVCTNAVGYSVYDI 480

Db 454 CNVETGRCVCKDNVEGFNCERCCKPGFNLESNNPKGCTPCFCFGHSSVCTNAVGYSVYDI 513

Qy 481 SSTFQIDEDGWRVEQRDGSEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYGQ 540

Db 514 SSTFQIDEDGWRVEQRDGSEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYGQ 573

Qy 541 NLSFSFRVDRDRDTRLAEDLVLEGAGLRVSVPLIAQNSYPSSETTVKYIFRLHEATDYPW 600

Db 574 NLSFSFRVDRDRDTRLAEDLVLEGAGLRVSVPLIAQNSYPSSETTVKYIFRLHEATDYPW 633

Qy 601 RPALSPFEFQKLLNNLTSIKIRGTYSERSAGYLDVTLQSAKPGVGPATWVESCTCPVG 660

Db	634	RPALSPFEFQKLLNNLTSIKIRGTYSERSAGYLLDDVTLQ SARPGVPATWVESCTCPVG	693
QY	661	YGGQFCETCLPGYRRETPSLGPYSPCVLCTCNHSETCDP ETGVCD CRDNTAGPHCEKCS	720
Db	694	YGGQFCETCLPGYRRETPSLGPYSPCVLCTCNHSETCDP ETGVCD CRDNTAGPHCEKCS	753
QY	721	DGYYGDS TLGTSSDCQPCPCPGSSCAI VPKTKEVVCTHCPTGTAGKRCEL CDDGYFGDP	780
Db	754	DGYYGDS TLGTSSDCQPCPCPGSSCAI VPKTKEVVCTHCPTGTAGKRCEL CDDGYFGDP	813
QY	781	LGSNGPVRLCRPCQCNNDIDPNAVGN CNRLTGECLKCIYNTAGFYCDRCKEGFFGNPLAP	840
Db	814	LGSNGPVRLCRPCQCNNDIDPNAVGN CNRLTGECLKCIYNTAGFYCDRCKEGFFGNPLAP	873
QY	841	NPADKCKACACNYGTVOQQSSCNPV TGQCCLPHVSGRDCGTCDPGYYNLQSGGCERC D	900
Db	874	NPADKCKACACNYGTVOQQSSCNPV TGQCCLPHVSGRDCGTCDPGYYNLQSGGCERC D	933
QY	901	CHALGSTNGQC DIRTGQCECQPGI TGQH CERCETNHFGFGECKPCDC HEGSLSLQCK	960
Db	934	CHALGSTNGQC DIRTGQCECQPGI TGQH CERCETNHFGFGECKPCDC HEGSLSLQCK	993
QY	961	DDGRCECREGFVGNRCDOCEENYFYNR SWPGCQEC PACYRLVKDKAAEHRVKLQELSLI	1020
Db	994	DDGRCECREGFVGNRCDOCEENYFYNR SWPGCQEC PACYRLVKDKAAEHRVKLQELSLI	1053
QY	1021	ANLGTGDDMVTDQAFEDRLKEAREVTDLLRE AQEVKDV DQNLMDRLQ RVNSSLSHSQISR	1080
Db	1054	ANLGTGDDMVTDQAFEDRLKEAREVTDLLRE AQEVKDV DQNLMDRLQ RVNSSLSHSQISR	1113
QY	1081	LQNI RNTIETGILAEARSRVESTEQLIEIASRELEKAKMAANVSITQPESTGEPNMNT	1140
Db	1114	LQNI RNTIETGILAEARSRVESTEQLIEIASRELEKAKMAANVSITQPESTGEPNMNT	1173
QY	1141	LLAEARRLAE RHKQEA DDIVRVAKTANETSAAEYNLLRLTLAGENQTALEIEELNRKYE	1200
Db	1174	LLAEARRLAE RHKQEA DDIVRVAKTANETSAAEYNLLRLTLAGENQTALEIEELNRKYE	1233
QY	1201	QAKNISQDLEKQAA RVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKI KKEAADLD	1260
Db	1234	QAKNISQDLEKQAA RVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKI KKEAADLD	1293
QY	1261	RLIDQKLKDYEDLRDMRGKEHEVKNLLEKGAEQQTADQLLARADA AKA LAEEAAKKGR	1320
Db	1294	RLIDQKLKDYEDLRDMRGKEHEVKNLLEKGAEQQTADQLLARADA AKA LAEEAAKKGR	1353
QY	1321	STLQEA NDILNLKDFRRVNDNKTAEEALRRIPAINRTIAEANEKTR EAQLALGNAAA	1380
Db	1354	STLQEA NDILNLKDFRRVNDNKTAEEALRRIPAINRTIAEANEKTR EAQLALGNAAA	1413
QY	1381	DATEAKNKAHEAERIA SAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAENELKR	1440
Db	1414	DATEAKNKAHEAERIA SAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAENELKR	1473
QY	1441	KQDDADQDMMAGMASQAQAEALNARKAKNSVSSLLSOLNNLLDQLGOLDTV DLNKLINE	1500
Db	1474	KQDDADQDMMAGMASQAQAEALNARKAKNSVSSLLSOLNNLLDQLGOLDTV DLNKLINE	1533
QY	1501	IEGSLNKAKDEMKA SLD RKVSDLESEARKQEA A IMDYNRDIAEIIKD IHNLEDIKKTLP	1560
Db	1534	IEGSLNKAKDEMKA SLD RKVSDLESEARKQEA A IMDYNRDIAEIIKD IHNLEDIKKTLP	1593
QY	1561	TGCFNTPSIEKP	1572
Db	1594	TGCFNTPSIEKP	1605

RESULT 4

REPORT #
US-09-561-818A-26

US-09-361-818A-28
; Sequence 26, Application US/09561818A

; Sequence no. 6638907
; Patent No. 6638907

; PACELL NO. 663830/
; GENERAL INFORMATION:

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; APPLICANT: Kortessmaa, Jarrko
; APPLICANT: Tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 1605
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-561-818A-26

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Query Match      : 100.0%; Score 8527; DB 4; Length 1605;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1572; Conservative 0; Mismatches 0; Indels 0;
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QY	1	AMDECADEGGRPQRCMPEFVNAAFNVTVVATNTCGTTPPEEYCVQGTGVTGVTKSCHLCDAG	60
DB			
QY	61	QOHLQHGAAFLTDYNNQADTTWQSQTMLAGVOXPNSINLTLLHLGKAFDITYVRLKFHTS	120
DB			
QY	94	QOHLQHGAAFLTDYNNQADTTWQSQTMLAGVOXPNSINLTLLHLGKAFDITYVRLKFHTS	153
DB			
QY	121	RPESFAIYKRTREDGPWIPYQYYSGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDISPL	180
DB			
QY	154	RPESFAIYKRTREDGPWIPYQYYSGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDISPL	213
DB			
QY	181	TGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSYYY	240
DB			
QY	214	TGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSYYY	273
DB			
QY	241	AISDFAVGGRCKCNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPFFNDRPWRRATAES	300
DB			
QY	274	AISDFAVGGRCKCNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPFFNDRPWRRATAES	333
DB			
QY	301	ASECLPCDCNGRSEQECYFDPPELYRSTGHGGHCTNCRDNTDGAKCERCENFFRLGNTEAC	360
DB			
QY	334	ASECLPCDCNGRSEQECYFDPPELYRSTGHGGHCTNCRDNTDGAKCERCENFFRLGNTEAC	393
DB			
QY	361	SPCHCSPVGSLSLTCQDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGRCPCSDPSGSTDE	420
DB			
QY	394	SPCHCSPVGSLSLTCQDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGRCPCSDPSGSTDE	453
DB			
QY	421	CNVETGRVCVKDNDVEGFNCERCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGYSVYDI	480
DB			
QY	454	CNVETGRVCVKDNDVEGFNCERCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGYSVYDI	513
DB			
QY	481	SSTFQIDEDGHRVEQRDGEASLEWSSDRQYIAVTSDSYFPRYFIAPVKFLGNQVLSYGQ	540
DB			
QY	514	SSTFQIDEDGHRVEQRDGEASLEWSSDRQYIAVTSDSYFPRYFIAPVKFLGNQVLSYGQ	573
DB			
QY	541	NLSFSFRVRRDRTRLASAEDLVLEGAGLRVSVPLIAQNSYPSETTVKYIFRLHEATDYPW	600
DB			
QY	574	NLSFSFRVRRDRTRLASAEDLVLEGAGLRVSVPLIAQNSYPSETTVKYIFRLHEATDYPW	633
DB			
QY	601	RPALSPFEFQKLLNNLTSIKIRGTYSERSAGYLDVTLQ SARPGVPATWVESCTCPVG	660
DB			
QY	634	RPALSPFEFQKLLNNLTSIKIRGTYSERSAGYLDVTLQ SARPGVPATWVESCTCPVG	693
DB			
QY	661	YGGQFCETCLPGYRRETPSLGPYSPCVLCTCNGHSETCDPETGVCDNRDNTAGPHECKCS	720
DB			
QY	694	YGGQFCETCLPGYRRETPSLGPYSPCVLCTCNGHSETCDPETGVCDNRDNTAGPHECKCS	753
DB			
QY	721	DGYYGDSLGTSSDCQPCPCPGSSCAI VPKTKEVVCTHCPGTGTAGKRCCELCDDDGYFGDP	780
DB			
QY	754	DGYYGDSLGTSSDCQPCPCPGSSCAI VPKTKEVVCTHCPGTGTAGKRCCELCDDDGYFGDP	813
DB			
QY	781	LGSNGPVRLCRPCQCNNDNIDPNAVGNCRNLTGECCLKCIYNTAGFYCDRCKEGFFGNPLAP	840
DB			
QY	814	LGSNGPVRLCRPCQCNNDNIDPNAVGNCRNLTGECCLKCIYNTAGFYCDRCKEGFFGNPLAP	873
DB			

QY	841	NPADKCKACACNYGTIVQQSSCNPVTGQCQCCLPHVSGRDCGTCDPGYYNLQSGQCERCD	900
Db	874	NPADKCKACACNYGTIVQQSSCNPVTGQCQCCLPHVSGRDCGTCDPGYYNLQSGQCERCD	933
QY	901	CHALGSTNGQCDIRTGQCECQPGITGQHCHERCETNHFSGPEGCKPCDCHHESLSLQCK	960
Db	934	CHALGSTNGQCDIRTGQCECQPGITGQHCHERCETNHFSGPEGCKPCDCHHESLSLQCK	993
QY	961	DDGRCECREGVGNRCDQCEENYFYNRSWPGCQCEPCYRLVKDKAAEHRVKLQELSLI	1020
Db	994	DDGRCECREGVGNRCDQCEENYFYNRSWPGCQCEPCYRLVKDKAAEHRVKLQELSLI	1053
QY	1021	ANLGTGDDMVTDQAFEDRLKEAEREVTDLLREAQEVKDQVQNLMDRLQRVNSSLHQSISR	1080
Db	1054	ANLGTGDDMVTDQAFEDRLKEAEREVTDLLREAQEVKDQVQNLMDRLQRVNSSLHQSISR	1113
QY	1081	LQNIIRNTIETGILAEARARSVESTEQLEIETASRELEKAKMAANVSITQPESTCEPNMNT	1140
Db	1114	LQNIIRNTIETGILAEARARSVESTEQLEIETASRELEKAKMAANVSITQPESTCEPNMNT	1173
QY	1141	LLAEEARLAEERHKQEADDIVRVAKTANETSAEAYNLLRLTLAGENQTALEIEEELNRKYE	1200
Db	1174	LLAEEARLAEERHKQEADDIVRVAKTANETSAEAYNLLRLTLAGENQTALEIEEELNRKYE	1233
QY	1201	QAKNISQDLEKQAAARVHBEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKEAADLD	1260
Db	1234	QAKNISQDLEKQAAARVHBEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKEAADLD	1293
QY	1261	RLIDQKLKDYEDLRDMRGKEHEVKNLLEKGAEEQQTADQLLARADAAKALAEERAAKGR	1320
Db	1294	RLIDQKLKDYEDLRDMRGKEHEVKNLLEKGAEEQQTADQLLARADAAKALAEERAAKGR	1353
QY	1321	STLQEANDIILNNLKDFDRVNDNKTAAEEALRRIPAINRTIAEANEKTRAEQALGNAAA	1380
Db	1354	STLQEANDIILNNLKDFDRVNDNKTAAEEALRRIPAINRTIAEANEKTRAEQALGNAAA	1413
QY	1381	DATEAKNKAHEAERIAASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAENELKR	1440
Db	1414	DATEAKNKAHEAERIAASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAENELKR	1473
QY	1441	KQDDADQDMMAGMASQAAQEAELNARKAKNSVSSLSQLNNLLDQLGQDQVTLNKLNE	1500
Db	1474	KQDDADQDMMAGMASQAAQEAELNARKAKNSVSSLSQLNNLLDQLGQDQVTLNKLNE	1533
QY	1501	IEGSLNKADEMKAESDLDRKVSDLESEARKQEAAMDYNRDIAEIIKDIHNLEDIKKTLP	1560
Db	1534	IEGSLNKADEMKAESDLDRKVSDLESEARKQEAAMDYNRDIAEIIKDIHNLEDIKKTLP	1593
QY	1561	TGCFNTPSIEKP	1572
Db	1594	TGCFNTPSIEKP	1605

RESULT 5
US-09-562-702A-24
; Sequence 24, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 1576
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-24

Query Match      94.3%; Score 8038; DB 4; Length 1576;
Best local Similarity 93.3%; Pred. No. 0;
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;

QY 1 AMDECADEGGRPQRCMPFEFVNAAFNVTVAATNTCGTPPEEYCVQGTGVTGVTKSCHLCDAG 60
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Db 3 AMDECTDEGGRPQRCMPFEFVNAAFNVTVAATNTCGTPPEEYCVQGTGVTGVTKSCHLCDAG 62
   |||||
QY 61 QOHLQHGAFLTDYNNQADTTWQSQTMLAGVQVPSINLTLHLGKAFDITYVRLKFHTS 120
   |||||
Db 63 QPHLQHGAFLTDYNNQADTTWQSQTMLAGVQVPSINLTLHLGKAFDITYVRLKFHTS 122
   |||||
QY 121 RPESFAIYKRTREDGPWIPYQYYSGSCENTYSKANRGFIRTTGGDEQQAALCTDEFSDISPL 180
   |||||
Db 123 RPESFAIYKRTREDGPWIPYQYYSGSCENTYSKANRGFIRTTGGDEQQAALCTDEFSDISPL 182
   |||||
QY 181 TGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTLNRLNTFGDEVNDPKVLKSYYY 240
   |||||
Db 183 TGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTLNRLNTFGDEVNDPKVLKSYYY 242
   |||||
QY 241 AISDFAVGGRCCKNGHASECVKNEFDKLMCNKHNTYGVDCCKLPFFNDRPWRRATAES 300
   |||||
Db 243 AISDFAVGGRCCKNGHASECMKNEFDKLVCNKHNTYGVDCCKLPFFNDRPWRRATAES 302
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QY 301 ASECLPCDCNGRSQECYFDPPELYRSTGHGGHCTNCRDNTDGAKCERCENFFRLGNTEAC 360
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Db 303 ASECLPCDCNGRSQECYFDPPELYRSTGHGGHCTNCRDNTDGAHCERCENFFRLGNNEAC 362
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QY 361 SPCHCSPVGSLSLTCDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSDPSSGSTE 420
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Db 363 SSCHCSPVGSLSLTCDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSDPSSGSTE 422
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QY 421 CNVETGRCVCKDNVEGFNCERCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGSVYDI 480
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Db 423 CNVETGRCVCKDNVEGFNCERCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGSVYSI 482
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QY 481 SSTFQIDEDGWRVEQRDGEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYGQ 540
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Db 483 SSTFQIDEDGWRVEQRDGEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSYGQ 542
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QY 541 NLSFSFRVDRDRTRLSAEDLVLEGAGLRVSVPLLAQNSYPSETTVKYIFRLHEATDYPW 600
   |||||
Db 543 NLSFSFRVDRDRTRLSAEDLVLEGAGLRVSVPLLAQNSYPSETTVKYVFRLHEATDYPW 602
   |||||
QY 601 RPALSPFEFQKLLNNLTISKIRGTYSERSAGYLLDVTLQSRPGRPVPATWVESCTCPVG 660
   |||||
Db 603 RPALTPEFQKLLNNLTISKIRGTYSERSAGYLLDVTLASARPGVPATWVESCTCPVG 662
   |||||
QY 661 YGGQFCETCLPGYRRETPSLGYPSPCVLCTCNHSETCDPETGVCDRCRDNTAGPHCEKCS 720
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Db 663 YGGQFCMCLSGYRRETPNLGYPSPCVLCAACNHSETCDPETGVCNCRDNTAGPHCEKCS 722
   |||||
QY 721 DGYYGDSLTGTSDDCQPCPCPGGSSCAIVPKTKEVVVCTHCPTGTAGKRCCLCDDGYFGDP 780
   |||||
Db 723 DGYYGDSLTGTSDDCQPCPCPGGSSCAVVPKTKEVVVCTNCPTGTTGKRCCLCDDGYFGDP 782
   |||||
QY 781 LGSNGPVLRCPCQCNNDIDPNAVGNCRNLTGECCLKCIYNTAGFYCDRCCKEGFFGNPLAP 840
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Db 783 LGRNGPVLRCQLCCSDNIDPNAVGNCRNLTGECCLKCIYNTAGFYCDRCCKDGGFFGNPLAP 842
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QY 841 NPADKCKACACN-YGTVQQQSSCNPNVTGQCQCLPHVSGRDCGTCDPGYINLQSGQCERC 899
   |||||
Db 843 NPADKCKACACNPNYGMKQQSSCNPNVTGQCECLPHVTGQDCGACDPGFYNLQSGQCERC 902
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QY 900 DCHALGSTNGQCDIRTGQCECQPGITGQHCERCETNHPFGPEGCKPCDCHHEGSLSLQC 959
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Db 903 DCHALGSTNGQCDIRTGQCECQPGITGQHCEVNHFGFEGCKPCDCHPEGSLSLQC 962
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Db 963 KDDGRCECREGFGVGNRCDCQCEENYFYNRSWPGCECPACRYLVKDKAAEHRVKLQELSL 1022
QY 1020 IANLGTGDDMTVDQAFEDRLKEAREVTDLLREAEQVVDONLMDRLQVRNSSLHSQIS 1079
Db 1023 IANLGTGDEMVTVDQAFEDRLKEAREVMDLLREAEQVVDONLMDRLQVRNSSLHSQIS 1082
QY 1080 RLQNIIRNTIETGILAEARARSRVESTEQLIEIASRELEKAKM-AANVSITQPESTGEPNN 1138
Db 1083 RLQNIIRNTIETGILAEARAHVENTERLIEIASRELEKAKAAVAAVSVTQPESTGDPNN 1142
QY 1139 MTLAEEARLAEERHKEADDIRVAKTANETSAAEYNLLRTLAGENQTALEIHELNRK 1198
Db 1143 MTLAEEARLAEERHKEADDIRVAKTANDTSTEAYNLLRTLAGENQTALEIHELNRK 1202
QY 1199 YEAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAAD 1258
Db 1203 YEAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDSETLENEANNIKWEAEN 1262
QY 1259 LDRLIDQKLDYEDLREDMRGKEHEVKMLLEKGAEQQTADQLLARADAALAEAEAAK 1318
Db 1263 LEQLIDQKLDYEDLREDMRGKEHEVKMLLEKGAEQQTADQLLARADAALAEAEAAK 1322
QY 1319 GRSTLOEANDILNNLKDFDRRVNDNKTAAEALRRIPAINRTIAEANEKTRAEQALGNA 1378
Db 1323 GRDTLOEANDILNNLKDFDRRVNDNKTAAEALRRIPAINQITTEANEKTRAEQALGSA 1382
QY 1379 AADATEAKNKAHEAERIAASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAENEL 1438
Db 1383 AADATEAKNKAHEAERIAASAVQKNATSTKAEARTFAEVTDLNEVNNMLKQLEAEKEL 1442
QY 1439 KRKQDDADQDMMWAGMASQAAQAEALNARKAKNSVSSLLSQNNLLDQLGQDITVDLNL 1498
Db 1443 KRKQDDADQDMMWAGMASQAAQAEALNARKAKNSVTSLSIINDLLEQLGQDITVDLNL 1502
QY 1499 NEIEGSLNKADEMKASDLDRKVSLESEARKQEAAMDNRDIAEIIKDTHNLEDIKKT 1558
Db 1503 NEIEGTLNKADEMKVSDLRKVSLENEAKQEAAMDNRDIEEIMKDIRNLEDIRKT 1562
QY 1559 LPTGCFNTPSIEKP 1572
Db 1563 LPSGCFNTPSIEKP 1576
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RESULT 6

US-09-561-818A-24

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; Sequence 24, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortessmaa, Jarrko
; TITLE OF INVENTION: Tryggvason, Karl
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 1576
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-818A-24
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Query Match 94.3%; Score 8038; DB 4; Length 1576;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;
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QY 1 AMDECADEGGRPQRCMPEFVNAAFNVTVATNTCGTPPEEYCVQGTGVTKSKCHLCDAG 60
Db 3 AMDECTDEGGRPQRCMPEFVNAAFNVTVATNTCGTPPEEYCVQGTGVTGVTKSKCHLCDAG 62
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Db 63 QPHLQHGAFLTDYNNQADTTWQSQTMLAGVOYVPSINLTLHLGKAFDITYVRLKFHTS 122
QY 121 RPESFAIYKRTREDGWPWIPYQYYSGSCENTYSKANRGFIRTTGGDEQOALCTDEFSDISPL 180
Db 123 RPESFAIYKRTREDGWPWIPYQYYSGSCENTYSKANRGFIRTTGGDEQOALCTDEFSDISPL 182
QY 181 TGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSYYY 240
Db 183 TGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSYYY 242
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QY 301 ASECLPCDCNGRSQECYFDPPELYRSTGHGCHTNCRDNTDGAHCHRCRENFRLGNTEAC 360
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QY 361 SPCHCSPVGLSTQCDYSYGRCSCKPGVMGDKDCRCQPGFHSLSLTAECRCPSCDPSGSTDE 420
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QY 421 CNVETGRCVCKDNVEGFNCERCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGSYVDI 480
Db 423 CNVETGRCVCKDNVEGFNCERCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGSYVSI 482
QY 481 SSTFQIDEDGWRVQORDGSEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYGQ 540
Db 483 SSTFQIDEDGWRABQORDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSYGQ 542
QY 541 NLSFSFRVDRDRRLSAEDLVLEGAGLVSVPLIAQNSYSPSETTVKYIFRLHEATDYPW 600
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Db 603 RPALTPEEFQKLLNLTISKIRGTYSERSAGYLDVTLQSAAPGPGVPATWVESCTCPVG 662
QY 661 YGGQFCETCLPGYRRETPSLGPYSPCVLCTCNHSETCDPBTGVCDNRDNTAGPHCEKCS 720
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QY 721 DGYYGDSLTGTSSDCQPCPCPGGSSCAIVPKTKEVVTCHPTGTAGKRCCELDDGYFGDP 780
Db 723 DGYYGDSLTGTSSDCQPCPCPGGSSCAVVPKTEVVCTNCPTGTTGKRCCELDDGYFGDP 782
QY 781 LGSNGPVLRCPCQNDNIDPNAVGNCRNLTGECCLKIYNTAGFYCDRCCKEGFFGNPLAP 840
Db 783 LGRNGPVLRCRLCQCSNIDPNAVGNCRNLTGECCLKIYNTAGFYCDRCCKDGGFFGNPLAP 842
QY 841 NPADKCKACACN-YGTVQQSSCNPTVTGQCCLPHVSGRDCGTCDPGYNNLQSGQCERC 899
Db 843 NPADKCKACACNPGYGTMTKQSSCNPTVTGQCCECLPHVTGQDCGACDPPGYNNLQSGQCERC 902
QY 900 DCHALGSTNGQCDIRTGQCECQPGITGQHCEVNHFGFEGCKPCDCHPEGSLSLQC 959
Db 903 DCHALGSTNGQCDIRTGQCECQPGITGQHCEVNHFGFEGCKPCDCHPEGSLSLQC 962
QY 960 KDDGRCECREGFGVGNRCDCQCEENYFYNRSWPGCECPACRYLVKDKAAEHRVKLQELSL 1019
Db 963 KDDGRCECREGFGVGNRCDCQCEENYFYNRSWPGCECPACRYLVKDKAAEHRVKLQELSL 1022
QY 1020 IANLGTGDDMTVDQAFEDRLKEAREVTDLLREAEQVVDONLMDRLQVRNSSLHSQIS 1079
Db 1023 IANLGTGDEMVTVDQAFEDRLKEAREVMDLLREAEQVVDONLMDRLQVRNSSLHSQIS 1082
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Db 1083 RLQNIIRNTIETGILAEARAHVENTERLIEIASRELEKAKAAVAAVSVTQPESTGDPNN 1142
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QY	1259	LDRLIDQKLXDYEDLRDMRGKEHEVNKLLLEKGAEQQTADQLLARADAAKALAEAAKK	1318
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Db	1323	GRDTLQEAANDILNLLKDFRRVNDNKTAEEAALRKIPAINQTIITEANEKTPRAQQALGSA	1382
QY	1379	AADATEAKNKAHEAERIAASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAENEL	1438
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QY	1439	KRKQDDADQDMMAGMASQAAQEAELNARKAKNSVSSLSQLNNLLDQLGQDFTVDLNL	1498
Db	1443	KRKQDDADQDMMAGMASQAAQEAELNARKAKNSVTLSIINDLLEQLGQDFTVDLNL	1502
QY	1499	NEIEGSLNKADEMKASDLDRKVSDDLESEARKQEAAIMDYNRDIAEIIKDHNLEDIKKT	1558
Db	1503	NEIEGTLNKADEMKVSDLDLRKVSDDLENEAKQEAAIMDYNRDIEEIMKDIRNLEDIRKT	1562
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Db	1563	LPSGCFNTPSIEKP	1576

RESULT 8

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US-09-562-702A-22
; Sequence 22, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 1609
; TYPE: prt
; ORGANISM: Homo sapiens
; US-09-562-702A-22

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		Query Match	94.3%;	Score 8038;	DB 4;	Length 1609;	
		Best Local Similarity	93.3%;	Pred. No. 0;			
		Matches 1469;	Conservative	56;	Mismatches	47;	Gaps 2;
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Dd	36	AMDECTDEGGRPQR	CMPCEFNAAFNVT	VWATNTCGTPPEEYCVQT	GVGTGVTKSCHLCDAG	95	
QY	61	QQHLQHGAFLTDYNNQADTTWWQSQTMLAGVQYPNSINLTILHLGKAFDITYVRLKFHTS	120				
Dd	96	QPHLQHGAFLTDYNNQADTTWWQSQTMLAGVQYPSSINLTILHLGKAFDITYVRLKFHTS	155				
QY	121	RPESFAIYKRTREDGPWIPIQYYSGSSENTYSKANRGFIRTGDEQQALCTDEFSDISPL	180				
Dd	156	RPESFAIYKRTREDGPWIPIQYYSGSSENTYSKANRGFIRTGDEQQALCTDEFSDISPL	215				
QY	181	TGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNLTFGDEVNDPKVLKSYYY	240				
Dd	216	TGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNLTFGDEVNDPKVLKSYYY	275				
QY	241	AISDPAVGGRCKNGHASECIVXNEFDKLMCNCCKHNTYGVDCCKCLPFENDRPPWRRATAES	300				

Db	276	AI	SFAVGRCKCN	GHASECMKNEFDKLV	CNCKHNTYGV	DCEKCLFF	FNDRPWRR	ATAES	335					
QY	301	ASECLPC	DCNGRSQECY	FDPELYRSTGH	GGHCTNCRD	NTDGA	KCERCEREN	FFRLGNTEAC	360					
Db	336	ASECLPC	DCNGRSQECY	FDPELYRSTGH	GGHCTNQD	NTDGA	KCERCEREN	FFRLGNNEAC	395					
QY	361	SPCHCSP	VGSLSTQ	DSYGRCSCKP	GVMDKCDR	CQPGF	HSLSLTEAG	CRPCSDPSGSTDE	420					
Db	396	SSCHCSP	VGSLSTQ	DSYGRCSCKP	GVMDKCDR	CQPGF	HSLSLTEAG	CRPCSDPSGSIDE	455					
QY	421	CNVETGR	CVCKDN	VEGFCERC	KPGFFN	LESSNPKG	CTPCFCF	GHSSVCTNAVGYSYDI	480					
Db	456	CNVETGR	CVCKDN	VEGFCERC	KPGFFN	LESSNPRG	CTPCFCF	GHSSVCTNAVGYSYSI	515					
QY	481	SSTFQI	DEDEGW	RDRLSAED	LVLEGAG	LRVSQDIA	IVISDSY	FPFYFIAPAKFLGKQVLSYGQ	540					
Db	516	SSTFQI	DEDEGW	RDRLSAED	LVLEGAG	LRVSQDIA	IVISDSY	FPFYFIAPAKFLGKQVLSYGQ	575					
QY	541	NLSFSFR	VRDRD	TRL	SAEDLV	LEGAGLRVS	VPLIAQ	NSYSPSETTVKYIFRLHEATDYPW	600					
Db	576	NLSFSFR	VRDRD	TRL	SAEDLV	LEGAGLRVS	VPLIAQ	NSYSPSETTVKYIFRLHEATDYPW	635					
QY	601	REALSP	FEFQKLL	NNL	TSIKIR	GTYSERS	AGYLD	DDVTLOS	ARPGVPATWVESCTCPVG	660				
Db	636	RPALT	PFQKLL	NNL	TSIKIR	GTYSERS	AGYLD	DDVTLAS	ARPGVPATWVESCTCPVG	695				
QY	661	YGGQFC	ETCLPGY	RET	PSLGPY	SPCVLCT	CNGHSET	CDPETG	VCDCRDNTAGPHCEKCS	720				
Db	696	YGGQFC	EMCLSGY	RET	PNLGPY	SPCVLCA	CNGHSET	CDPETG	VCNCRDNTAGPHCEKCS	755				
QY	721	DGYYG	DS	TGLTSS	DCQPC	PCPGG	SSCAIV	PKTKVWVTHC	PTGTAGKRC	ELCDDGYFGDP	780			
Db	756	DGYYG	DS	TGLTSS	DCQPC	PCPGG	SSCAIV	PKTKVWVTHC	PTGTGTG	KRC	ELCDDGYFGDP	815		
QY	781	LGSNGP	VR	LCR	PCQ	CNDNID	PN	AVGNCNRLTG	ECLKCIY	NTAGFYCDRC	KEGFFGNPLAP	840		
Db	816	LGRNGP	VR	LCR	LCQ	CSDNID	PN	AVGNCNRLTG	ECLKCIY	NTAGFYCDRC	KDGF	FGNPLAP	875	
QY	841	NPADK	CKACACN	-YGT	VQQOSS	CNPVTG	QCQCLPHV	SGRDCGT	CDPGY	YNLQSGGC	CERC	899		
Db	876	NPADK	CKACACN	CNPYGT	MKQOSS	CNPVTG	QCQCLPHV	TGQD	CGACDPGF	YNLQSGGC	CERC	935		
QY	900	DCHALG	STNG	QC	DINTG	QC	ECQPGITG	QHCERC	ETNHFG	FGPEG	CKPCDCH	HEGSLQ	959	
Db	936	DCHALG	STNG	QC	DINTG	QC	ECQPGITG	QHCERC	EVNHFG	FGPEG	CKPCDCH	HEGSLQ	995	
QY	960	KDDGR	CE	REGFV	GNRCDQ	CEENYF	YNRSWP	GQCECPAC	YRLVKD	KAAEH	VRKLQ	ELESL	1019	
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QY	1080	RLQNIR	NTI	ETGILAE	RARS	RVEST	EQLIEI	ASRELEKAKM	-AAN	VSI	TQPE	STCEPNN	1138	
Db	1116	RLQNIR	NTI	ETGILAE	RARS	RVENTER	LIEI	ASRELEKAKV	AAAN	VSVTQ	PE	STGDPNN	1175	
QY	1139	MTLLAE	EARR	LAERH	KQ	EADDIV	RVAKTAN	ETSABAY	NLLRLT	LAGE	NTALEI	EELNRK	1198	
Db	1176	MTLLAE	EARKLAERH	KQ	EADDIV	RVAKTAND	TSTAY	NLLRLT	LAGE	NTALEI	EELNRK	1235		
QY	1199	YEQA	KNISQD	LEKQ	AARV	HEEAKR	AGDKAVEI	YAS	VAQ	LTPV	DSEAL	ENEANKIKKEAD	1258	
Db	1236	YEQA	KNISQD	LEKQ	AARV	HEEAKR	AGDKAVEI	YAS	VAQ	LSP	LDSET	LENEANNIKMEAE	1295	
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Db	1296	LEQLI	DQKL	KDYED	LR	EDMRG	KEHEV	KNLLEK	GKTEQ	QQTADQ	LLARADA	AKALAEAAK	1355	
QY	1319	GRST	LOEAND	ILNNL	KD	FRRVND	NKTA	AAEEAL	RRIPAIN	RTIA	EANEK	TREAO	LALGNA	1378

Db 1356 GRDTLQEAANDILNNLKDFDRRVNDNKTAAEEALRKIPAINQITITEANEKTRQAQALGSA 1415
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Db 1416 AADATEAKNKAHEAERIAASAVQKNATSTKAEABERTFAEVTDLNNEVNNMLKQLQEAKEKEL 1475
QY 1439 KRKQDDADQDMMAGMASQAQAEALNARKAKNSVSSILLSQLNNLLDQLGQDLDVTLNKL 1498
Db 1476 KRKQDDADQDMMAGMASQAQAEALNARKAKNSVSSILLSIINDLLEQLGQDLDVTLNKL 1535
QY 1499 NEIEGSLNKAKDEMKASDLDRKVSYLESEARKQEAALMDYNRDIAEIIKDIHNLEDIKKT 1558
Db 1536 NEIEGTLNKAKDEMKVSDLDKVSYLESEARKQEAALMDYNRDIEEIMKDIRNLEDIRKT 1595
QY 1559 LPTGCFNTPSIEKP 1572
Db 1596 LPSGCFNTPSIEKP 1609

RESULT 9

US-09-561-818A-22
; Sequence 22, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortessmaa, Jarrko
; APPLICANT: Tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 1609
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-818A-22

Query Match 94.3%; Score 8038; DB 4; Length 1609;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;

QY 1 AMDECADEGRPQRCMPEFVNAFNVVATNTCGTPPEEYCVQGTGVTKSCHLCDAG 60
Db 36 AMDECTDEGRPQRCMPEFVNAFNVVATNTCGTPPEEYCVQGTGVTKSCHLCDAG 95
QY 61 QHQLHGAAFLTDYNNQADTTWQSQTMLAGVQYVNSINLTJHLGKAFDITYVRLKFHTS 120
Db 96 QHQLHGAAFLTDYNNQADTTWQSQTMLAGVQYVNSINLTJHLGKAFDITYVRLKFHTS 155
QY 121 RPESFAIYKTRREDGPWIPYQYSGSCENTYSKANRGFIRTGDEQALCTDEFSDISPL 180
Db 156 RPESFAIYKTRREDGPWIPYQYSGSCENTYSKANRGFIRTGDEQALCTDEFSDISPL 215
QY 181 TGGNVAFTLEGRPSAYNFDNSPVLQEWVWVATDIRVTNLRLNTFGDEVFNDPKVLKSYYY 240
Db 216 TGGNVAFTLEGRPSAYNFDNSPVLQEWVWVATDIRVTNLRLNTFGDEVFNDPKVLKSYYY 275
QY 241 AISDFAVGGRCCKNGHASECVKNEFDKIMCNCKHNTYGVDCBKCLPFFNDRPWRRATAES 300
Db 276 AISDFAVGGRCCKNGHASECMNEFDKLVNCCKHNTYGVDCBKCLPFFNDRPWRRATAES 335
QY 301 ASECLPCDCNGRSQECYFDPELYRSTGHGCHTCNRDNTDGAKCRCRNFRLGNTEAC 360
Db 336 ASECLPCDCNGRSQECYFDPELYRSTGHGCHTCNQDNTDGAHCRCRNFRLGNNEAC 395
QY 361 SPCHCSPVGSLSLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLSLTEAGCRPCSCDPSGSTDE 420
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QY 421 CNVETGRVCVKDNVEGFNCERCCKPGFFNLESSNPKGCTPCFCFHHSSVCTNAVGYSVYDI 480
Db 456 CNVETGRVCVKDNVEGFNCERCCKPGFFNLESSNPRGCTPCFCFHHSSVCTNAVGYSVYSI 515

QY 481 SSTFOIDEDGMRVEQORDGSEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYQ 540
Db 516 SSTFOIDEDGMRVEQORDGSEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYQ 575
QY 541 NLSFSFRVDRRDLRLSAEDLVLEGAGLRVSPLIAQNSVPSETTVKYIERLHEATDYPW 600
Db 576 NLSFSFRVDRRDLRLSAEDLVLEGAGLRVSPLIAQNSVPSETTVKYIERLHEATDYPW 635
QY 601 RPALSPREFQKLLNNLTSIKIRGYTSERSAGYLDVTLQSRPGRPVPATWVESCTCPVG 660
Db 636 RPALTPFEFQKLLNNLTSIKIRGYTSERSAGYLDVTLQSRPGRPVPATWVESCTCPVG 695
QY 661 YGGQFCETCLPGYRRETPLSLGYPSPCVLCTCNHGHSETCDPETGVCDNRDNTAGPHCEKCS 720
Db 696 YGGQFCETCLPGYRRETPLSLGYPSPCVLCTCNHGHSETCDPETGVCDNRDNTAGPHCEKCS 755
QY 721 DGYGDSITLGTSSDCQPCPCPGSSCAIVPKTKEVVCTHCTGTAGKRCCELDDGYFGDP 780
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QY 900 DCHALGSTNGQCDIRTGQCECQPGITGQHCHERCETNHFGEFGCKPCDCHHEGSLSLQC 959
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Db 996 KDDGRCEBEGFVGNRCDQCEENFYNSWPGCQECPCYRLVKDKAAEHRVKLOELES 1055
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Db 1056 IANLGTGDDMVTDOAFEDRLKEAREVTDLLREAEVQVVDQNDLMDRLQVNSSLHSQIS 1115
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Db 1116 RLQNIIRNTIETGILAEARSRVSETEQLIEIASRELEKAKM-AANVSITQPESTGEPNN 1175
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QY 1199 YEAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAD 1258
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QY 1259 LDRLIDQKLKDYEDLREDMRGKEHEVKNLLEKGAEQQTADQLLARADAALAEAAK 1318
Db 1296 LEQLIDQKLKDYEDLREDMRGKEHEVKNLLEKGAEQQTADQLLARADAALAEAAK 1355
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Db 1356 GRSTLQEAANDILNNLKDFDRRVNDNKTAAEEALRRIPAINRTIAEANEKTRQAQALGNA 1415
QY 1379 AADATEAKNKAHEAERIAASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAENEL 1438
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QY 1439 KRKQDDADQDMMAGMASQAQAEALNARKAKNSVSSILLSQLNNLLDQLGQDLDVTLNKL 1498
Db 1476 KRKQDDADQDMMAGMASQAQAEALNARKAKNSVSSILLSIINDLLEQLGQDLDVTLNKL 1535
QY 1499 NEIEGSLNKAKDEMKASDLDRKVSYLESEARKQEAALMDYNRDIAEIIKDIHNLEDIKKT 1558
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QY 1559 LPTGCFNTPSIEKP 1572
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Db 1596 LPSCGCFNTPSIEKP 1609
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RESULT 10
US-09-562-702A-26
; Sequence 26, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 1617
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-26
Query Match 94.3%; Score 8038; DB 4; Length 1617;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;
QY 1 AMDECADEGGRPQRCMPEFVNAAFNTVATNTCGTPPEEYCVQGTGVTKSKCHLCDAG 60
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Db 36 AMDECTDEGGRPQRCMPEFVNAAFNTVATNTCGTPPEEYCVQGTGVTKSKCHLCDAG 95
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QY 61 QOHLQHGAFLTDYNNQADTTWQSQTMLAGVQYVNSINLTLLHLGKAFDITYVRLKFHTS 120
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QY 121 RPESFAIYKRTREDGPWIPYQYYSGSCENTYSKANRGFI RTGGDEQQALCTDEFSDISPL 180
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QY 181 TGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVNDPKVLKSYYY 240
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QY 241 AISDPFVGGRCCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPFFNDPWRRTAAES 300
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QY 361 SPCHSPVGSLSLSTQCDSYGRCSCKPGVMGDKDRCPQGFHSLTEAGCRPCSDPSPGSTDE 420
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Db 696 YGGQFCMCLSGYRRETPLNLPYSPCVLCA GNGHSETCDPETGVCNCRDNTAGPHCEKCS 755
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QY 721 DGYGDSLTGSSDCQPCPCPGGSSCAIVPKTKWVWTHCPTGTAGKCELCDDGYFGDP 780
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Db 1536 NEIEGTLNKAKDEMKA SLDLRKVS DLENEAKQEAAIMDYNRDI EEMKDIRNLEDIRKT 1595
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QY 1559 LPTGCFNTPSIEKP 1572
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Db 1596 LPSCGCFNTPSIEKP 1609
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; Sequence 10, Application US/09845583A
; Patent No. 6635616
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Brunken, William Joseph
; APPLICANT: Champliand, Marie-France
; APPLICANT: Hunter, Dale
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
; FILE REFERENCE: 10287-056001
; CURRENT APPLICATION NUMBER: US/09/845,583A
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/200,863
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1587
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-845-583A-10

Query Match      42.1%; Score 3586; DB 4; Length 1587;
Best Local Similarity 43.8%; Pred. No. 4.3e-206;
Matches 700; Conservative 258; Mismatches 568; Indels 72; Gaps 23;

QY 2 MDECADEGGRPQRCMPFVNAENVVATNTCGTPPEEYCVQTVGTGVTKSKCHLCDAGQ 61
DQ 22 MGACYDGAGRQRCPLPVFENAAFGRLAQASHTCGSPPEDECFPHVGAAGAGAHQRCDAAD 81

QY 62 QHLOHGAFLTDYNNQADTTWQSQTMLAGVQYVNSINLTILHKGAFDITYVRLKFTSR 121
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QY 182 GGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVDNDPKVLKSYYYA 241
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QY 242 ISDFAVGGRCKNGHASECVKNEFDKLMCNCKHNTYGVDCXKCLPFFNDRPWRRAATAESA 301
DQ 262 VSDFSVGRCKNGHASECGPDVAGQLACRCQHNTTGTDCERCLPFFQDRPWRARGTAEAA 321

QY 302 SECLPCDCNGRSQECYFDPYELYSRSTGHGGHCTNCRDNTDGAKCERCRENFFRLGNTEACS 361
DQ 322 HECLPCNGSRSEECTFDRELFRSTGHGGRCHHCRDHTAGHCERCQENFYHWDPRMPCQ 381

QY 362 PCHCSPVGSLSQDCSYGRCSCKPGYMGDKCDRCQPGFHSLSHTEAGCRPCSCDPSGSTDEC 421
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QY 422 NVETGRCVCKDNVEGFNCERCCKPGFFNLESSNPKGCTPCFCPGHSSVCTNAVGSVYDIS 481
DQ 442 DPRSGRCPCKENVEGNLDCRCPGTENLQPHNPAGCSCSCFCYGHSKVCASTAQFQVHHIL 501

QY 482 STFQIDEDGWRVEQORDGSEASLEWSSDRQYIAVISDSYFPRYPIAPVKFLGNQVLSYQN 541
DQ 502 SDFHQGAEGWARSVGGSEHSPQWSPN---GVLLSPEDEEBELTAPGKFLGDQRFSYQGP 557

QY 542 LSFSFRVDRDRLSAEDLVLEGAGLRVSVPLIAQGNYSYPSETTVKYIFRLH---EATDY 598
DQ 558 LILTFRVPPGDSPLPVQ-LRLEGTGLALS--LRHSSLGPDQARASQGGRAQVPLQETSE 614

QY 599 PWRPALSPFEQKLLNNLTLSIKIRGTYRSERSAG--YLDVDTLOSARPPGVPATWVESCT 656
DQ 615 DVAPPLPPFHFQRLANLTLRLRVSPGSPAGVPVFLTEVRLTSARPGLSPPASWVEICS 674

QY 657 CPVYGGQFCETCLPGYRRRETPSLGYPSPCVLCTCNHSETCDPETGVCDNRDNTAGPHC 716
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QY 896 CERCDCHALGSTNGQCDIRTCQCECOPGITQHCERCETNHFQFGECKPCDCCHHEGSL 955
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QY 1071 NSSLHSQISRLQNIIRNTIETGILAEARARSVESTEQLEIASRE-LEKAKMAANVSITQ 1129
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DQ 1201 LETQRDLEDRYQEVQAAQKALRTAVAEVLPEAE-----SVLATVQOVGADTAPYLALL 1253

QY 1238 -----TPVDSEA--LENEANKIKKEAADLRLIDQLKDYEDLRE-DMRGKEHEVKNLLE 1289
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QY 1469 AKNSVSSLLSOLNNLLDQLQLDGT--VDLNKLINEIEGSLNKADEM-KASDLDRKVSdle 1525
DQ 1486 SRISLEKDIETLSSELLARLGSLDTHQAPALNETQWALERLRLQLGSPGSLQRLKSLLE 1545

QY 1526 SEARKQEAAMNDYNRDIAEIIKDIHNLEDIKKTLPTGC 1563
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RESULT 12
US-09-561-709B-3
; Sequence 3, Application US/09561709B
; Patent No. 6682911
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Champliand, Marie-France
; APPLICANT: Olson, Pamela
; APPLICANT: Koch, Manuel
; APPLICANT: Brunken, William
; TITLE OF INVENTION: LAMININS AND USES THEREOF
; FILE REFERENCE: 10287-060001
```

; CURRENT APPLICATION NUMBER: US/09/561,709B									
; CURRENT FILING DATE: 2000-05-01									
; PRIOR APPLICATION NUMBER: US 09/168,949									
; PRIOR FILING DATE: 1998-10-09									
; PRIOR APPLICATION NUMBER: US 60/061,609									
; PRIOR FILING DATE: 1997-10-10									
; NUMBER OF SEQ ID NOS: 13									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 3									
; LENGTH: 1587									
; TYPE: PR1									
; ORGANISM: Homo sapiens									
US-09-561-709B-3									
Query Match									
Best Local Similarity 42.1%; Score 3586; DB 4; Length 1587;									
Matches 700; Conservative 258; Mismatches 568; Indels 72; Gaps 23;									
QY	2	MDECADEGGRPQRCMPEFVNAFNVTVVATNTCGTPPEEYCVQIGVTGVTKSCHLCDAGQ	61						
Db	22	MGACYDGAGRPQRCLEVFENAAFRLAQASHTCGSPPEDFCPHVGAAGAGAHQCQRCDAAAD	81						
QY	62	QHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYVNSINLTLLHLGKAFDITYVRLKFHTSR	121						
Db	82	QORHNASYLTDFHSQDESTWQSPSMAFGVQYVTSVNTLRGKAYEITYVRLKFHTSR	141						
QY	122	PESFAIYKRTREDGPNIPYQYYSGCENTYSKANRGFIKRTGGDEQQALCTDEFSDISPLT	181						
Db	142	PESFAIYKRSRADGPWEFYQFYSASCQTYGRPEGQYLRPGEDERVAFTSEFSDISPLS	201						
QY	182	GGNVAFSTLEGPRPSAYNFDNSPVLQEWVTATDIRVTLNRLNTFGDEVNDPKVLKSYYYA	241						
Db	202	GGNVAFSTLEGPRPSAYNFEESPLQEWVTSTELLISLDRLNTFGDDIFKDPKVLQSYYYA	261						
QY	242	ISDPAVGGRCCKNGHASECVKNEFDKLMCNCKNHTYGVDCCKLPFFNDRPWRRTAESA	301						
Db	262	VSDFSVGGRCCKNGHASECGPDVAGQLACRCQHNHTGTDCERCCLPFFQDRPWARGTAEA	321						
QY	302	SECLPCDCNGRSQECYFDPDELRYRSTGHGGHCTNCRDNTDGAKCERCENPFRLNGTEACS	361						
Db	322	HECLPCNCSGRSEECTFDRELFRSTGHGGRCHHCRDHTAGPHCERCQENFYHWDPRMPCQ	381						
QY	362	PCHCSPVGSLSQDSYGRCSCKPGVMGDKDCRCQPGFHSLSLTAAGCRPCSDPSGSTDEC	421						
Db	382	PCDCQSAGSLHLQCDDTGTCAKPTVTGWKCDRCPLGFGHLSLSEGGCRPCTCNPAGSLDTC	441						
QY	422	NVETGRVCVKONVEGFNCERCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGVSYVDIS	481						
Db	442	DPRSGRCPCKENVEGNLDCRCRPGTFLNLPHPNAPAGSSCFYGHSKVCASTAQFQVHHIL	501						
QY	482	STFQIDEDGWRVEQRDGEASLEWSSDRQYIAVTSYFPRYFIAPVKFLGNQVLSYQGN	541						
Db	502	SDFHQAEGWARSVGGSEHSPQWSPN---GVLLSPDEEBELTAPGKFLGDQRFSGYQGP	557						
QY	542	LSFSFRVDRRDLRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYIFRLH---EATDY	598						
Db	558	LILTRVPPGDSPLPVQ-LRLEGTGLALS--LRHSSLGSPQDARASQGGRAQVPLQETSE	614						
QY	599	PWRPALSPPFEFQKLLNLTSLKIRGTYSERSAG--YLDVVTLQSRPQPGVPATWVESCT	656						
Db	615	DVAPPLPPFHFQRLLANLTSURLRVSPGSPAGPVLTEVRLTSARPPGLSPASWVEICS	674						
QY	657	CPVGGQFCETCLPGYRRRTPSLGYPSPCVLCTCNHSETCDPETGVCDNRDNTAGPHC	716						
Db	675	CPTGYTGQFCESCAPGYKREMPQGGPYASCVPCTCNHG-TCDPNTGICVCSHHTGPPSC	733						
QY	717	EKCSDBGYDSTLGTSSDCQPCPCPGSSCAIVPKTKBVVVTHCPTGTAGKRCCLCDDGY	776						
Db	734	ERCLPGFYGNPFAGQADDCQPCPCQSACTTIPESGEVVVTHCPCPPQGRGRCEVDDGF	793						
QY	777	FGDPLGNGPVLRCRQCQNDNTDPNAVGNLRTGECCLKIYNTAGFYCDRCCKEGFFGN	836						
Db	794	FGDPLGLFHPQPCQCQCSGNVDPNAVGNCDPLSGHCLRLHNTTGDHCEHCQEGFYGS	853						

RESULT 13
US-08-317-450B-13
; Sequence 13, Application US/08317450B
; Patent No. 5660982
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Kallunki, Pekka
; APPLICANT: Pyke, Charles
; TITLE OF INVENTION: Laminin Chains: Diagnostic and
; TITLE OF INVENTION: Therapeutic Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & ALLEGRETTI, LTD.
; STREET: Ten South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:25:32 ; Search time 42.6441 Seconds
(without alignments)
10415.614 Million cell updates/sec

Title: US-10-037-182-20
Perfect score: 8527
Sequence: 1 AMDECADEGGRPQRCMPFV.....EDIKKTLPCTGCFNTPSIEKP 1572

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8527	100.0	1572	3 AAB19806	Aab19806 Mouse lam
2	8527	100.0	1572	3 AAB48455	Aab48455 Mouse lam
3	8527	100.0	1572	5 ABB81597	Abb81597 Mouse lam
4	8527	100.0	1605	3 AAB19805	Aab19805 Mouse lam
5	8527	100.0	1605	3 AAB48454	Aab48454 Mouse lam
6	8527	100.0	1605	5 ABB81596	Abb81596 Mouse lam
7	8446	99.1	1607	2 AAW50897	Aaw50897 Mouse lam
8	8038	94.3	1576	3 AAB19802	Aab19802 Human lam
9	8038	94.3	1576	3 AAB48453	Aab48453 Human lam
10	8038	94.3	1576	5 ABB81595	Abb81595 Human lam
11	8038	94.3	1584	3 AAB19804	Aab19804 Human lam
12	8038	94.3	1609	3 AAB19801	Aab19801 Human lam
13	8038	94.3	1609	3 AAB48452	Aab48452 Human lam
14	8038	94.3	1609	5 ABB81594	Abb81594 Human lam
15	8038	94.3	1609	7 ADC01887	Adc01887 Human lam
16	8038	94.3	1617	3 AAB19803	Aab19803 Human lam
17	8034	94.2	1609	2 AAW50898	Aaw50898 Human lam
18	3588	42.1	1587	3 AAB40917	Aab40917 Human ORF
19	3586	42.1	1587	5 AAM50361	Aam50361 Mouse lam
20	3586	42.1	1587	6 ABR58467	Abr58467 Human NOV
21	3583	42.0	1575	6 ABR58468	Abr58468 Human NOV
22	3476	40.8	1639	4 ABB59807	Abb59807 Drosophil
23	3445.5	40.4	1524	2 AAY15458	Aay15458 Human lam
24	2592	30.4	1193	5 AAE14712	Aae14712 Human lam
25	2592	30.4	1193	6 ABR48214	Abr48214 Human bla

26	2592	30.4	1193	6 ABUS6513	Abu56513 Lung canc
27	2592	30.4	1193	6 ABUS6696	Abu56696 Lung canc
28	2592	30.4	1193	6 ABR92103	AbR92103 Human cer
29	2592	30.4	1193	6 ADA74120	Ada74120 Human lam
30	2591	30.4	1193	2 AAR91427	Aar91427 Kalinin/1
31	2591	30.4	1193	3 AAB48468	Aab48468 Human lam
32	2591	30.4	1193	5 AAO14992	Aao14992 Laminin g
33	2584	30.3	1172	3 AAB48469	Aab48469 Human lam
34	2583	30.3	1193	3 AAB48470	Aab48470 Human lam
35	2577.5	30.2	1190	6 ADA74091	Ada74091 Equine la
36	2576	30.2	1172	3 AAB48471	Aab48471 Human lam
37	2477.5	29.1	1111	5 AAE14713	Aae14713 Human lam
38	2476.5	29.0	1111	2 AAR91428	Aar91428 Kalinin/1
39	2476.5	29.0	1111	5 AAO14993	Aao14993 Laminin g
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41	2400.5	28.2	1192	3 AAB48472	Aab48472 Mouse lam
42	2400.5	28.2	1192	5 AAE14711	Aae14711 Mouse lam
43	2400.5	28.2	1192	6 ADA74121	Ada74121 Murine la
44	2306.5	27.0	1171	2 AAW26583	Aaw26583 Rat hemid
45	1812.5	21.3	3106	3 AAB19795	Aab19795 Mouse lam

ALIGNMENTS

RESULT 1
AAB19806
ID AAB19806 standard; protein; 1572 AA.
XX
AC AAB19806;
XX
DT 05-MAR-2001 (first entry)
XX
DE Mouse laminin 2 mature gamma-1 chain.
XX
KW Laminin 2; mouse; nerve regeneration; angiogenic; cell adhesion;
KW degenerative muscle disorder; muscular dystrophy; cell therapy.
XX
OS Mus musculus.
XX
PN WO200066730-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US011378.
XX
PR 30-APR-1999; 99US-0131720P.
PR 15-JUN-1999; 99US-0139198P.
PR 12-JUL-1999; 99US-0143289P.
PR 24-SEP-1999; 99US-0155945P.
XX
(UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
Yurchenco P;
XX
WPI; 2000-687537/67.
DR N-PSDB; AAA88906.
XX
PT Purified laminin 2 protein, useful for research and therapeutic purposes
PT including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.
XX
PS Claim 5; Page 302-306; 305pp; English.
XX
CC The present sequence is that of mouse laminin 2 gamma-1 chain mature
CC protein. Laminin-2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and
CC gamma-1 (100 kDa) chains. It is thought to be specifically required for
CC stabilizing myotubes during skeletal muscle development, and for
CC preventing apoptosis. Genetic defects in human laminin 2 structure or
CC expression are associated with a major type of congenital muscular
CC dystrophy. Laminin 2 is also thought to be important in Schwann
CC cell/basal lamina interactions. The invention provides laminin 2 alpha-2,
CC beta-1 and gamma-1 chain polypeptides (see AAB19791-806) and the

CC polynucleotides encoding them (see AAA88891-906), methods for making
CC recombinant laminin 2, cells that express recombinant laminin 2, and
CC methods for using purified laminin 2 for research and therapeutic
CC purposes including peripheral nerve regeneration, treatment of
CC degenerative muscle disorders, angiogenesis regulation, promoting cell
CC attachment and migration, ex vivo cell therapy, improving the take of
CC grafts, improving the biocompatibility of medical devices and preparing
CC improved culture devices and media
XX
SQ Sequence 1572 AA;
Query Match 100.0%; Score 8527; DB 3; Length 1572;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AMDECADEGGRPQRCMPEFVNAAFNVTVVATNTCTPPEEYCVQGTGVTGKSKHLCADAG 60
DB 1 AMDECADEGGRPQRCMPEFVNAAFNVTVVATNTCTPPEEYCVQGTGVTGKSKHLCADAG 60
QY 61 QQHLQHGAFLTDYNNQADTTWQSQTMLAGVQVFNINLTLLHKGAFDITYVRLKFHTS 120
DB 61 QQHLQHGAFLTDYNNQADTTWQSQTMLAGVQVFNINLTLLHKGAFDITYVRLKFHTS 120
QY 121 RPESFAIYKRTREDGPIYQYSGSCENTYSKANRGFI RTGGDEQQALCTDEFSDISPL 180
DB 121 RPESFAIYKRTREDGPIYQYSGSCENTYSKANRGFI RTGGDEQQALCTDEFSDISPL 180
QY 181 TGGNVAFTLEGRPSAYNFNDSVPLQEWVTATDIRVTNRLNTFGDEVNDPKVLKSYYY 240
DB 181 TGGNVAFTLEGRPSAYNFNDSVPLQEWVTATDIRVTNRLNTFGDEVNDPKVLKSYYY 240
QY 241 ATSDFAVGGRCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPFFNDRPWRRTAES 300
DB 241 ATSDFAVGGRCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPFFNDRPWRRTAES 300
QY 301 ASECLPCDCNGRSQECYFDPBELYRSTGHGCHCTNCRDNTDGA KCRCRENFRLGNTEAC 360
DB 301 ASECLPCDCNGRSQECYFDPBELYRSTGHGCHCTNCRDNTDGA KCRCRENFRLGNTEAC 360
QY 361 SPCHCSPVGLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSDPSGSTDE 420
DB 361 SPCHCSPVGLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSDPSGSTDE 420
QY 421 CNVETGRCVKDNGVEGFNCERCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGSYVDI 480
DB 421 CNVETGRCVKDNGVEGFNCERCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGSYVDI 480
QY 481 SSTFQIDEDGWRVEQDGEASLEWSSDRQYIAVTSYFPRYFIAPVKFLGNQVLSYGQ 540
DB 481 SSTFQIDEDGWRVEQDGEASLEWSSDRQYIAVTSYFPRYFIAPVKFLGNQVLSYGQ 540
QY 541 NLSFSFRVDRRDLRLSAEDLVLEGAGLRVSVPLIAQNSYPSSETTVKYIFRLHEATDYPW 600
DB 541 NLSFSFRVDRRDLRLSAEDLVLEGAGLRVSVPLIAQNSYPSSETTVKYIFRLHEATDYPW 600
QY 601 RPALSPFEFQKLLNLTSLKIRGTYSERSAGYLDVTLQ SARPGVPATWVESCTCPVG 660
DB 601 RPALSPFEFQKLLNLTSLKIRGTYSERSAGYLDVTLQ SARPGVPATWVESCTCPVG 660
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QY 721 DGYGDBSTLGTSSDCQPCPGSSCAIVPKTKEVVCTHCPTGTAGKRCCLCDDGYFGDP 780
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QY 781 LGSNGPVRLCRPCQCNNDNIDPNAVGNCRNLTGECCLKIYNTAGFYCDRCKEGFGNPLAP 840
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DB 841 NPADKCKACACNYGTVOQQSSCNVPTGQCCLPHVSGRDCGTCDPGYYNLQSGQCERCD 900

DB 841 NPADKCKACACNYGTVOQQSSCNVPTGQCCLPHVSGRDCGTCDPGYYNLQSGQCERCD 900
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DB 901 CHALGSTNGQCDIRTGQCECQPGITGQHCHERCETNHFHFGPEGCKPCDCHHBSLSLQCK 960
QY 961 DDGRCECREGFGVGNRCQCEENYFYNRSWPGCQCPACRYLVKDKAAAEHRVKLQLES LI 1020
DB 961 DDGRCECREGFGVGNRCQCEENYFYNRSWPGCQCPACRYLVKDKAAAEHRVKLQLES LI 1020
QY 1021 ANLGTGDDMTDQAFEDRLKEAREVTDLLREAEVKDQVNDQNLMDRLQVNSSLSHSQISR 1080
DB 1021 ANLGTGDDMTDQAFEDRLKEAREVTDLLREAEVKDQVNDQNLMDRLQVNSSLSHSQISR 1080
QY 1081 LQNRNTIETGILAEARARSVESTEQLEIEIASRELEKAKMAANVSITQPESTCEPNNMT 1140
DB 1081 LQNRNTIETGILAEARARSVESTEQLEIEIASRELEKAKMAANVSITQPESTCEPNNMT 1140
QY 1141 LLAEARRLAERHKQEAADDIVRVAKTANETSAEAYNLLRLTLAGENQTALEIEELNRKYE 1200
DB 1141 LLAEARRLAERHKQEAADDIVRVAKTANETSAEAYNLLRLTLAGENQTALEIEELNRKYE 1200
QY 1201 QAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLD 1260
DB 1201 QAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLD 1260
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QY 1501 IEGSLNKADEMKA SLDLRKVS DLESEARKQEAAIMDYNRDIAEIIKDIHNLEDIKKTL P 1560
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QY 1561 TGCENTPSIEKP 1572
DB 1561 TGCENTPSIEKP 1572
RESULT 2
AAB48455
ID AAB48455 standard; protein; 1572 AA.
XX
AC AAB48455;
XX
DT 02-MAR-2001 (first entry)
XX
DE Mouse laminin 8 polypeptide, SEQ ID NO: 28.
XX
KW Mouse; laminin 8; neuroprotective; angiogenic; osteopathic;
KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;
KW vascular tissue injury; neural injury; angiogenesis regulation.
XX
OS Mus musculus.
XX
PN WC200066732-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US011543.
XX

PR 30-APR-1999; 99US-0131720P.
PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.
PR 11-FEB-2000; 2000US-0182012P.
XX
PA (BIOS-) BIOSTRATUM INC.
XX
XX Kortessmaa J, Tryggvason K;
PI
XX
XX WPI; 2000-687539/67.
DR N-PSDB; AAC83716.
XX
PT Purified laminin 8 protein, useful for research and therapeutic purposes
PT including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.
XX
PS Claim 5; Page 240-245; 245pp; English.
XX
CC The present sequence is a laminin 8 polypeptide chain. Laminins are a
CC family of heterotrimeric glycoproteins that function via binding
CC interactions with neighbouring cell receptors and by forming laminin
CC networks. They are signalling molecules which influence cellular
CC function. Laminin 8 is useful for treating injuries to tissue of
CC mesenchymal origin, such as bone, cartilage, tendon, and ligament,
CC treating injuries to vascular tissue, promoting cell attachment and
CC migration, ex vivo cell therapy, improving the biocompatibility of
CC medical devices, and preparing improved cell culture devices and media.
CC Laminin 8 is also useful for promoting re-endothelialisation at the site
CC of vascular injuries, improving the take of grafts, improving the
CC biocompatibility of medical devices, treating neural injuries (neural
CC regeneration), regulating angiogenesis, and promoting cell attachment and
CC migration
XX
SQ Sequence 1572 AA;
Query Match 100.0%; Score 8527; DB 3; Length 1572;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AMDECADEGGRPQRCMPEFVNAAFNVTVVATNTCGTPPEYCVQGTGVTKSKCHLCDAG 60
DB 1 AMDECADEGGRPQRCMPEFVNAAFNVTVVATNTCGTPPEYCVQGTGVTKSKCHLCDAG 60
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DB 61 QQHLOHGAFLTDYNNQADITWQSQTMLAGVQYPNSINLTLHLGKAFDITYVRLKFHTS 120
QY 121 RPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQALCTDFSDISPL 180
DB 121 RPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQALCTDFSDISPL 180
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DB 241 AISDFAVGGRCKCNHGHASECVKNEFDKLMCNCKHNTYGVDCCKLPFFNDRPWRRTAES 300
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DB 301 ASECLPCDCNGRSQECYFDPPELYRSTGHGGHCTNCRDNTDGAKCERCENFFRLGNTEAC 360
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QY 421 CNVETGRVCVKDNVEGFNCERCCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGSVYDI 480
DB 421 CNVETGRVCVKDNVEGFNCERCCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGSVYDI 480
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DB 481 SSTFQIDEDGWRVEQRDGSEASLEWSSDRQYIAVISDSYPPRYFIAPVKFLGNQVLSYGQ 540
QY 541 NLSFSFRVDRDTRLAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYIFRLHEATDYPW 600
DB 541 NLSFSFRVDRDTRLAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYIFRLHEATDYPW 600
QY 601 RPALSPFEFQKLLNLTISIIRGYTSERSAGYLDVTLQARPGPGVPATWVESCTCPVG 660
DB 601 RPALSPFEFQKLLNLTISIIRGYTSERSAGYLDVTLQARPGPGVPATWVESCTCPVG 660
QY 661 YGQFCETCLPGYRRETPSLGPYSPCVLCTCNHSETCDPETGVCDCRDNTAGPHCEKCS 720
DB 661 YGQFCETCLPGYRRETPSLGPYSPCVLCTCNHSETCDPETGVCDCRDNTAGPHCEKCS 720
QY 721 DGYGDSLTGTSDDCQPCPCPGSSCAIVPKTKEVVCTHCTGTAGKRCCELDDGYFGDP 780
DB 721 DGYGDSLTGTSDDCQPCPCPGSSCAIVPKTKEVVCTHCTGTAGKRCCELDDGYFGDP 780
QY 781 LGSNGPVRLCRPCQCNNDNIDPNAVGNCRNLTGECLKCIYNTAGFYCDRCKEGFFGNPLAP 840
DB 781 LGSNGPVRLCRPCQCNNDNIDPNAVGNCRNLTGECLKCIYNTAGFYCDRCKEGFFGNPLAP 840
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DB 841 NPADKCKACACNYGTVQQSSCNPTVGTQCQCLPHVSGRDCGTCDPGYYNLQSGQCERCDC 900
QY 901 CHALGSTNGQCDIRTGQCECQPGITGQHCCERCETNHFSGEGCKPCDCHHEGSLSLCK 960
DB 901 CHALGSTNGQCDIRTGQCECQPGITGQHCCERCETNHFSGEGCKPCDCHHEGSLSLCK 960
QY 961 DDGRCECEGFGVGNRCDCQCEENFYNRSWPGCQCECPACVRLVKDKAAEHRVKLQELSLI 1020
DB 961 DDGRCECEGFGVGNRCDCQCEENFYNRSWPGCQCECPACVRLVKDKAAEHRVKLQELSLI 1020
QY 1021 ANLGTGDDMVTDOAFEDRLKEAREVTDLLREAOEVKVDQNDLMDRLQVNSSLSHSQISR 1080
DB 1021 ANLGTGDDMVTDOAFEDRLKEAREVTDLLREAOEVKVDQNDLMDRLQVNSSLSHSQISR 1080
QY 1081 LQINRTIETGILAEARARSRVESTEOQLIEIASRELEKAKVAANVSITQPESTGEPNNMT 1140
DB 1081 LQINRTIETGILAEARARSRVESTEOQLIEIASRELEKAKVAANVSITQPESTGEPNNMT 1140
QY 1141 LLAEEARRLAERHKQEAADDIVRAKTANETSAAEYNLLRTLRTLAGENQTALEIEELNRKYE 1200
DB 1141 LLAEEARRLAERHKQEAADDIVRAKTANETSAAEYNLLRTLRTLAGENQTALEIEELNRKYE 1200
QY 1201 QAKNISQDLEKQAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLD 1260
DB 1201 QAKNISQDLEKQAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLD 1260
QY 1261 RLIDQKLKDYEDLREDMRGKEHEVKNLLEKGAEOQTADQLLARADAALAEAAKGR 1320
DB 1261 RLIDQKLKDYEDLREDMRGKEHEVKNLLEKGAEOQTADQLLARADAALAEAAKGR 1320
QY 1321 STLQEANDILNNLKDFDRRVNDNKTAEEALRRIPAINRTIAEANEKTRQAQLALGNAAA 1380
DB 1321 STLQEANDILNNLKDFDRRVNDNKTAEEALRRIPAINRTIAEANEKTRQAQLALGNAAA 1380
QY 1381 DATEAKNKAHEAERIAASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAENELKR 1440
DB 1381 DATEAKNKAHEAERIAASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAENELKR 1440
QY 1441 KQDDADQDMMWAGMASQAAQAEALNARKAKNSVSSLSQLNNLLDQLGQDLDVTLNKLNE 1500
DB 1441 KQDDADQDMMWAGMASQAAQAEALNARKAKNSVSSLSQLNNLLDQLGQDLDVTLNKLNE 1500
QY 1501 IEGSLNKADEMKAASDLDRKVSLESEARKQEAAMIDVNRDIAEIIKDIHNLEDIKKTLIP 1560
DB 1501 IEGSLNKADEMKAASDLDRKVSLESEARKQEAAMIDVNRDIAEIIKDIHNLEDIKKTLIP 1560
QY 1561 TGCFTNTPSIEKP 1572
DB 1561 TGCFTNTPSIEKP 1572

Db 1261 RLIDQKLXDVEDLRMRGKEHEVKNLLEKGAEQQTADQLLARADAAKALAEAAKKGR 1320
QY 1321 STLQEAANDILNNLKDFDRRVNDNKTAAEEALRRIPAINRTIAEANEKTRQAQLALGNAAA 1380
Db 1321 STLQEAANDILNNLKDFDRRVNDNKTAAEEALRRIPAINRTIAEANEKTRQAQLALGNAAA 1380
QY 1381 DATEAKNKAHEAERIAASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAENELXR 1440
Db 1381 DATEAKNKAHEAERIAASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAENELXR 1440
QY 1441 KQDDADQDMMAGMASQAAQAEALNARKAKNSVSSLLSQLNNLLDQLGQLDVTVDLNKLE 1500
Db 1441 KQDDADQDMMAGMASQAAQAEALNARKAKNSVSSLLSQLNNLLDQLGQLDVTVDLNKLE 1500
QY 1501 IEGSLNKADEMKAASDLDRKVSDESEARKQEAAIMDYNRDIABIIKDIHNLEDIKKTLP 1560
Db 1501 IEGSLNKADEMKAASDLDRKVSDESEARKQEAAIMDYNRDIABIIKDIHNLEDIKKTLP 1560
QY 1561 TGCFTNTPSIEKP 1572
Db 1561 TGCFTNTPSIEKP 1572

RESULT 4
AAB19805
ID AAB19805 standard; protein; 1605 AA.

XX AAB19805;

XX 05-MAR-2001 (first entry)

XX Mouse laminin 2 gamma-1 chain.

DE Laminin 2; mouse; nerve regeneration; angiogenic; cell adhesion;
XX degenerative muscle disorder; muscular dystrophy; cell therapy.

KW Mus musculus.

OS Key Location/Qualifiers
FH Peptide 1. .33
FT /label= Signal_peptide
FT Protein 34. .1605
FT /label= Mature_protein

XX W0200066730-A2.

PN 09-NOV-2000.

XX 28-APR-2000; 2000WO-US011378.

XX 30-APR-1999; 99US-0131720P.

PR 15-JUN-1999; 99US-0139198P.

PR 12-JUL-1999; 99US-0143289P.

PR 24-SEP-1999; 99US-0155945P.

XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.

PA Yurchenco P;

XX WPI; 2000-687537/67.

DR N-PSDB; AAA88905.

XX Purified laminin 2 protein, useful for research and therapeutic purposes

PT including peripheral nerve regeneration, treatment of degenerative muscle

PT disorders, angiogenesis regulation, and ex vivo cell therapy.

XX Claim 5; Page 288-294; 305pp; English.

XX The present sequence is that of the gamma-1 chain of mouse laminin 2.
CC Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1

CC (100 kDa) chains. It is thought to be specifically required for

CC stabilizing myotubes during skeletal muscle development, and for

CC preventing apoptosis. Genetic defects in human laminin 2 structure or

CC expression are associated with a major type of congenital muscular
CC dystrophy. Laminin 2 is also thought to be important in Schwann
CC cell/basal lamina interactions. The invention provides laminin 2 alpha-2,
CC beta-1 and gamma-1 chain polypeptides (see AAB19791-806) and the
CC polynucleotides encoding them (see AAA8891-906), methods for making
CC recombinant laminin 2, cells that express recombinant laminin 2, and
CC methods for using purified laminin 2 for research and therapeutic
CC purposes including peripheral nerve regeneration, treatment of
CC degenerative muscle disorders, angiogenesis regulation, promoting cell
CC attachment and migration, ex vivo cell therapy, improving the take of
CC grafts, improving the biocompatibility of medical devices and preparing
CC improved culture devices and media
XX
SQ Sequence 1605 AA;

Query Match 100.0%; Score 8527; DB 3; Length 1605;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMDECADEGGRPQRCMPEFVNAAFNVTVVATNTCGTPPEEYCVQGTGVTGKSKHLCDAG 60
Db 34 AMDECADEGGRPQRCMPEFVNAAFNVTVVATNTCGTPPEEYCVQGTGVTGKSKHLCDAG 93
QY 61 QQHLQHGAFLTDYNNQADTTWQSQTMLAGVQYPNSINLTLLHLGKAEDITYVRLKFHTS 120
Db 94 QQHLQHGAFLTDYNNQADTTWQSQTMLAGVQYPNSINLTLLHLGKAEDITYVRLKFHTS 153
QY 121 RPESFAIYKRTREDGPWIPYQYYSGSCENTYSKANRGFI RTGGDEQALCTDEFSDISPL 180
Db 154 RPESFAIYKRTREDGPWIPYQYYSGSCENTYSKANRGFI RTGGDEQALCTDEFSDISPL 213
QY 181 TGGNVAFTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVNDPKVLKSYYY 240
Db 214 TGGNVAFTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVNDPKVLKSYYY 273
QY 241 AISDFAVGGRCCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPFFENDRPWRRATAES 300
Db 274 AISDFAVGGRCCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPFFENDRPWRRATAES 333
QY 301 ASECLPCDCNGRSQECYFDPPELYRSTGHGCHTNCRDNTDGA KCRCRENFRLGNTEAC 360
Db 334 ASECLPCDCNGRSQECYFDPPELYRSTGHGCHTNCRDNTDGA KCRCRENFRLGNTEAC 393
QY 361 SPCHCSPVGSLSSTQCDSYGRCSCKPGVMGDKDCRCQPGFHSLTEAGRPCSCDPSGSTDE 420
Db 394 SPCHCSPVGSLSSTQCDSYGRCSCKPGVMGDKDCRCQPGFHSLTEAGRPCSCDPSGSTDE 453
QY 421 CNVETGRVCVKDNVEGFNCERCCKPGFFENLESSNPKGCTPCFCFGHSSVCTNAVGSYVDI 480
Db 454 CNVETGRVCVKDNVEGFNCERCCKPGFFENLESSNPKGCTPCFCFGHSSVCTNAVGSYVDI 513
QY 481 SSTFQIDEDGWRVEQORDGSEASLEWSSDRQYIAVISDSYFPRIAPVKFLGNQVLSYGQ 540
Db 514 SSTFQIDEDGWRVEQORDGSEASLEWSSDRQYIAVISDSYFPRIAPVKFLGNQVLSYGQ 573
QY 541 NLSFSFRVDRDRRLSAEDLVLEGAGLRVSVPLIAQGNISYPSSETTVKYIFRLHEATDYPW 600
Db 574 NLSFSFRVDRDRRLSAEDLVLEGAGLRVSVPLIAQGNISYPSSETTVKYIFRLHEATDYPW 633
QY 601 RPALSPFEFQKLLNLTISI KIRGTYSEASAGYLDVTLQ SARPGVPATWVESCTCPVG 660
Db 634 RPALSPFEFQKLLNLTISI KIRGTYSEASAGYLDVTLQ SARPGVPATWVESCTCPVG 693
QY 661 YGGQFCETCLPGYRRETPSLGPYPVLCNCGHSETCDPETGVDCRDNTAGPHCEKCS 720
Db 694 YGGQFCETCLPGYRRETPSLGPYPVLCNCGHSETCDPETGVDCRDNTAGPHCEKCS 753
QY 721 DGYYGDSSTLGTSSDCQPCPCPGGSSCAIVPKTKEVWCTHCPTAGKRCCELDDGYFGDP 780
Db 754 DGYYGDSSTLGTSSDCQPCPCPGGSSCAIVPKTKEVWCTHCPTAGKRCCELDDGYFGDP 813
QY 781 LGSNGPVLRCRQCNDNIDPNAVGNCRNLTGECCLKCIYNTAGFYCDRCCKEGFFGNPLAP 840

Db 454 CNVETGRCVCKDNVEGFNCERCKPGFPFNLESSNPKGCTPCFCFGHSSVCTNAVGSVYDI 513

QY 481 SSTFOIDEDGWRVEQRDGEASLEWSSDRQYIAVISDSYFPRIAPVKFLGNQVLSYGQ 540

Db 514 SSTFOIDEDGWRVEQRDGEASLEWSSDRQYIAVISDSYFPRIAPVKFLGNQVLSYGQ 573

QY 541 NLSFSFRVDRDRTRLAEDLVLEGAGLRVSVPLIAQGNSYSPSETTVKYIFRLHEATDYPW 600

Db 574 NLSFSFRVDRDRTRLAEDLVLEGAGLRVSVPLIAQGNSYSPSETTVKYIFRLHEATDYPW 633

QY 601 RPALSPFEFOKLLNNLTISKIRGTYSERSAGYLDVTLQSRPQPGVPATWVESCTCPVG 660

Db 634 RPALSPFEFOKLLNNLTISKIRGTYSERSAGYLDVTLQSRPQPGVPATWVESCTCPVG 693

QY 661 YGQFCETCLPGYRRETSLGYPSPCVLCTCNGHSETCDPETGVDCDRDNTAGPHCEKCS 720

Db 694 YGQFCETCLPGYRRETSLGYPSPCVLCTCNGHSETCDPETGVDCDRDNTAGPHCEKCS 753

QY 721 DGYYGDSLTGTSDDCQPCPCPGSSCAIVPKTKEVWCTHCPTGTAGKRCELCDDGYFGDP 780

Db 754 DGYYGDSLTGTSDDCQPCPCPGSSCAIVPKTKEVWCTHCPTGTAGKRCELCDDGYFGDP 813

QY 781 LGSNGPVRLCRPCQCNNDIDPNAVGNMRLTGECLKCIYNTAGFYCDRCKEGFFGNPLAP 840

Db 814 LGSNGPVRLCRPCQCNNDIDPNAVGNMRLTGECLKCIYNTAGFYCDRCKEGFFGNPLAP 873

QY 841 NPADKCKACACNYGTVOQSSCNPVGTGQCCLPHVSGRDCGTCDPGYNLSQGGCERCDC 900

Db 874 NPADKCKACACNYGTVOQSSCNPVGTGQCCLPHVSGRDCGTCDPGYNLSQGGCERCDC 933

QY 901 CHALGSTNGQCDIRTGQCECQPGITGQHCCERCETNHFHFGFPEGCKPCDCHHEGSLSLQCK 960

Db 934 CHALGSTNGQCDIRTGQCECQPGITGQHCCERCETNHFHFGFPEGCKPCDCHHEGSLSLQCK 993

QY 961 DDGRCECREGVGNRCDCQCEENYFYNRSPWGCQPCACYRLVKDKAAEHRVKLOELESLLI 1020

Db 994 DDGRCECREGVGNRCDCQCEENYFYNRSPWGCQPCACYRLVKDKAAEHRVKLOELESLLI 1053

QY 1021 ANLGTGDDMVTDOAFEDRLKEAEREVTDLLREAEQEVKDVQDQNLMDRLQRVNSSLHLSQISR 1080

Db 1054 ANLGTGDDMVTDOAFEDRLKEAEREVTDLLREAEQEVKDVQDQNLMDRLQRVNSSLHLSQISR 1113

QY 1081 LQNIIRNTIETGILAEARARSRVESTEQLEIEIASRELEKAKMAANVSITQPESTGEPNNMT 1140

Db 1114 LQNIIRNTIETGILAEARARSRVESTEQLEIEIASRELEKAKMAANVSITQPESTGEPNNMT 1173

QY 1141 LLAEEARRLAEHRKQEAADDIVRVAKTANETSAEAYNLLRLTAGENQTALEIEELNRKYE 1200

Db 1174 LLAEEARRLAEHRKQEAADDIVRVAKTANETSAEAYNLLRLTAGENQTALEIEELNRKYE 1233

QY 1201 QAKNISQDLEKQAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLD 1260

Db 1234 QAKNISQDLEKQAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLD 1293

QY 1261 RLIDQKLKDYEDLREDMRGKEHEVKNLLEKGAEQQTADQLLARADAATAKALAEAAKGR 1320

Db 1294 RLIDQKLKDYEDLREDMRGKEHEVKNLLEKGAEQQTADQLLARADAATAKALAEAAKGR 1353

QY 1321 STLQEAANDILNNLKDQRRVNDNKTAAEEALRRIPAINRTIAEANEKTREQAALGNAAA 1380

Db 1354 STLQEAANDILNNLKDQRRVNDNKTAAEEALRRIPAINRTIAEANEKTREQAALGNAAA 1413

QY 1381 DATEAKNKAHAERIAASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAENELKR 1440

Db 1414 DATEAKNKAHAERIAASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAENELKR 1473

QY 1441 QODDADQDMMWAGMASQAAQEAELNAPKAKNSVSSLLSQNLNLLDQLGQDQDLDVNLKLINE 1500

Db 1474 QODDADQDMMWAGMASQAAQEAELNAPKAKNSVSSLLSQNLNLLDQLGQDQDLDVNLKLINE 1533

QY 1501 IEGLSNKAKDEMKAASDLDRKVSQDLESEARKQEAAMIDYNRDIAEIIKDIHNLEDIKKTLP 1560

Db 1534 IEGLSNKAKDEMKAASDLDRKVSQDLESEARKQEAAMIDYNRDIAEIIKDIHNLEDIKKTLP 1593

QY 1561 TGCFTNTPSIEKP 1572

Db 1594 TGCFTNTPSIEKP 1605

RESULT 6

ABB81596

ID ABB81596 standard; protein; 1605 AA.

XX ABB81596;

DT 19-SEP-2002 (first entry)

Mouse laminin 10 third chain protein sequence SEQ ID NO:18.

Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation; tissue repair development; laminin; healing; vascular tissue; re-endothelialisation; vascular injury; cell attachment; cell stasis; proliferation; migration.

Mus musculus.

Key Location/Qualifiers

Peptide 1..33

Protein 34..1605

FT /label= signal

FT /label= laminin_10_third_chain

XX WO200250111-A2.

XX 27-JUN-2002.

XX 21-DEC-2001; 2001WO-US051035.

XX 21-DEC-2000; 2000US-0257449P.

PR 28-MAR-2001; 2001US-0279282P.

PR 13-NOV-2001; 2001US-00279282.

XX (BIOS-) BIOSTRATUM INC.

XX Tryggvason K, Doi M, Thyboll J;

DR WPI; 2002-557650/59.

DR N-PSDB; ABQ72914.

XX New human laminin-10 proteins, useful for accelerating the healing of vascular tissue, improving the biocompatibility of grafts, or for promoting re-endothelialization at the site of vascular injuries.

Claim 9; Page 191-195; 231pp; English.

The present invention describes human laminin alpha 5. Also described is an isolated laminin 10. Laminin 10 has vulnery activity. Laminins are useful in maintaining cell/tissue phenotype as well as promoting cell growth and differentiation in tissue repair development. Specifically, laminin 10 can be used for accelerating the healing injuries of vascular tissue, improving the biocompatibility of grafts useful for treating such injuries, for promoting re-endothelialisation at the site of vascular injuries, and promote cell attachment and subsequent cell stasis, proliferation, differentiation, and/or migration. The present sequence represents a third chain protein of laminin 10, from the present invention.

XX Sequence 1605 AA;

Query Match 100.0%; Score 8527; DB 5; Length 1605;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMDECADEGGRPQRCMPFVNAAFNVTVATNTCGTPPEEYCVQGTGVTKSchLCDAG 60

Db 34 AMDECADEGGRPQRCMPFVNAAFNVTVATNTCGTPPEEYCVQGTGVTKSchLCDAG 93

QY 61 QOHLQGAFLTDYNNQADTTWQSQTMLAGVQYPSINLTLHLGKAFDITYVRLKFHTS 120
Db 94 QOHLQGAFLTDYNNQADTTWQSQTMLAGVQYPSINLTLHLGKAFDITYVRLKFHTS 153
QY 121 RPESFAIYKRTREDGPWIPQYYSGSCENTYSKANRGFIRTTGGDEQQAALCTDEFSDISPL 180
Db 154 RPESFAIYKRTREDGPWIPQYYSGSCENTYSKANRGFIRTTGGDEQQAALCTDEFSDISPL 213
QY 181 TGGNVAFSTLEGRPSAYNFDPNSPVLQEWVTATDIRVTNLRLNTFGDEVENDPKVLKSYYY 240
Db 214 TGGNVAFSTLEGRPSAYNFDPNSPVLQEWVTATDIRVTNLRLNTFGDEVENDPKVLKSYYY 273
QY 241 AISDFAVGGRCKNCNGHASECVKNEFDKLMCNCKHNTYGVDCCKCLPFFNDPWRATAES 300
Db 274 AISDFAVGGRCKNCNGHASECVKNEFDKLMCNCKHNTYGVDCCKCLPFFNDPWRATAES 333
QY 301 ASECLPCDCNRSQECYFDPELYRSTGHGGHCTNCRDNTDGAKCERCENEFRLGNTAEAC 360
Db 334 ASECLPCDCNRSQECYFDPELYRSTGHGGHCTNCRDNTDGAKCERCENEFRLGNTAEAC 393
QY 361 SPCHCSPVGSLSSTQCDYGRCSCKPGWMDKCDRCQPGFHSLSLTAAGCRPCSDPSGSTDE 420
Db 394 SPCHCSPVGSLSSTQCDYGRCSCKPGWMDKCDRCQPGFHSLSLTAAGCRPCSDPSGSTDE 453
QY 421 CNVETGRVCVKDNVEGFNCERCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGSYVDI 480
Db 454 CNVETGRVCVKDNVEGFNCERCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGSYVDI 513
QY 481 SSTFOJDEDEGWRVEQRDGSEASLEWSSDRQYIAVISDSYPPRYFIAPVKFLGNQVLSYGQ 540
Db 514 SSTFOJDEDEGWRVEQRDGSEASLEWSSDRQYIAVISDSYPPRYFIAPVKFLGNQVLSYGQ 573
QY 541 NLSFSFRVDRRDLRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYIFRLHEATDYPW 600
Db 574 NLSFSFRVDRRDLRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYIFRLHEATDYPW 633
QY 601 RPALSPFEFQKLLNLTISIIRGTYSERSAGYLDVTLQSAARPGPGVPATWVESCTCPVG 660
Db 634 RPALSPFEFQKLLNLTISIIRGTYSERSAGYLDVTLQSAARPGPGVPATWVESCTCPVG 693
QY 661 YGGQFCETCLPGYRRETPSLGYPSPCVLCTCNHSETCDBETGVCDNRDNTAGHCEKCS 720
Db 694 YGGQFCETCLPGYRRETPSLGYPSPCVLCTCNHSETCDBETGVCDNRDNTAGHCEKCS 753
QY 721 DGYIGDSTLGTSSDCQPCPCPGSSCAIVPKTKVVCVCHTPTGTAGKRCCLCDGYYFGDP 780
Db 754 DGYIGDSTLGTSSDCQPCPCPGSSCAIVPKTKVVCVCHTPTGTAGKRCCLCDGYYFGDP 813
QY 781 LGSNGPVLRCRQCQNDNIDPNVAGNCNRLTGECLKCIYNTAGFYCDRCCKEGFGNPLAP 840
Db 814 LGSNGPVLRCRQCQNDNIDPNVAGNCNRLTGECLKCIYNTAGFYCDRCCKEGFGNPLAP 873
QY 841 NPADKCKACACNYGTVQQSSCNPTVGTQCQCLPHVSGRDCGTCDPGYYNLQSGQCRCRD 900
Db 874 NPADKCKACACNYGTVQQSSCNPTVGTQCQCLPHVSGRDCGTCDPGYYNLQSGQCRCRD 933
QY 901 CHALGSTNGQCDIRTGQCECQPGITGQHCHERCETNHFHFGPEGCKPCDCHHESLSLQCK 960
Db 934 CHALGSTNGQCDIRTGQCECQPGITGQHCHERCETNHFHFGPEGCKPCDCHHESLSLQCK 993
QY 961 DDGRCECEGVGNRCDCQCEENYFYNRSWPGCQECPCYRLVKDKAAEHRVKLQELSLI 1020
Db 994 DDGRCECEGVGNRCDCQCEENYFYNRSWPGCQECPCYRLVKDKAAEHRVKLQELSLI 1053
QY 1021 ANLGTGDDMVTDQAFEDRLKEAREVTDLLREAEQVKDQNDLMDRLQVRNSSLHSQISR 1080
Db 1054 ANLGTGDDMVTDQAFEDRLKEAREVTDLLREAEQVKDQNDLMDRLQVRNSSLHSQISR 1113
QY 1081 LQNIIRNTIETGILAEARSRVESTEQIIEIASRELEKAKMAANVSITQPESTGEFNMT 1140
Db 1114 LQNIIRNTIETGILAEARSRVESTEQIIEIASRELEKAKMAANVSITQPESTGEFNMT 1173

QY 1141 LLAEEARRLAERHKQEAADDIVRVAKTANETSAAEYNNLLRLTLAGENQTALEIEELNRKYE 1200
Db 1174 LLAEEARRLAERHKQEAADDIVRVAKTANETSAAEYNNLLRLTLAGENQTALEIEELNRKYE 1233
QY 1201 QAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLD 1260
Db 1234 QAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLD 1293
QY 1261 RLIDQKLKDYEDLREDMRGKEHEVKNLLEKGAEQQTADQLLARADAALAEAAKKGR 1320
Db 1294 RLIDQKLKDYEDLREDMRGKEHEVKNLLEKGAEQQTADQLLARADAALAEAAKKGR 1353
QY 1321 STLOEANDILNNLKDFRRVNDNKTAEEALRRIPAINRTIAEANEKTRTREAQLALGNAAA 1380
Db 1354 STLOEANDILNNLKDFRRVNDNKTAEEALRRIPAINRTIAEANEKTRTREAQLALGNAAA 1413
QY 1381 DATEAKNKAHEAERIAASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAENELKR 1440
Db 1414 DATEAKNKAHEAERIAASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAENELKR 1473
QY 1441 KQDDADQDMMAGMASQAQAQAEELNARKAKNSVSSLLSQNNLLDQLGQDLDTVDLNKLNE 1500
Db 1474 KQDDADQDMMAGMASQAQAQAEELNARKAKNSVSSLLSQNNLLDQLGQDLDTVDLNKLNE 1533
QY 1501 IEGLNKAKDEMKAQDLDRKVSVDLESEARKQEAAMNDYNRDIAEIIKDIHNLEDIKKTLF 1560
Db 1534 IEGLNKAKDEMKAQDLDRKVSVDLESEARKQEAAMNDYNRDIAEIIKDIHNLEDIKKTLF 1593
QY 1561 TGCFTNTPSIEKP 1572
Db 1594 TGCFTNTPSIEKP 1605
RESULT 7
AAW50897
ID AAW50897 standard; protein; 1607 AA.
XX
AC AAW50897;
XX 07-DEC-1998 (first entry)
XX Mouse laminin GI chain.
DE Laminin; mouse; beta-amyloid; amyloidosis; Alzheimer's disease;
XX Down's syndrome; hereditary cerebral haemorrhage; inflammation;
KW malignancy; Familial Mediterranean Fever; multiple myeloma;
KW type II diabetes; prion disease; Creutzfeldt-Jacob disease; CJD;
KW Gertsmann-Strausler syndrome; kuru; scrapie; haemodialysis;
KW carpal tunnel syndrome; senile cardiac amyloid polynuropathy;
KW Familial Amyloidotic Polynuropathy; thyroid carcinoma; diagnosis;
XX therapy.
XX Mus sp.
XX WO9815179-A1.
PN 16-APR-1998.
XX 08-OCT-1997; 97WO-US018145.
PF 08-OCT-1996; 96US-0027981P.
XX (UNIW) UNIV WASHINGTON.
PA Castillo G, Snow AD;
PI WPI; 1998-240534/21.
XX Use of laminin and fragments - for developing products for use in the
DR diagnosis and treatment of amyloid disease, e.g. Alzheimer's disease or
XX CJD.
PS Claim 15; Page 102-105; 132pp; English.

XX This is the amino acid sequence of the mouse laminin G1 chain. The primary object of the invention is to use laminin, laminin-derived protein fragments and/or laminin-derived polypeptides as potent inhibitors of amyloid formation, deposition, accumulation and/or persistence in Alzheimer's disease and other amyloidoses. The laminin products (see AAW50888-98) may include mouse or human laminin A or A1 chain, laminin B1 or B2 chain, laminin A2 chain (merosin), laminin G1 chain, the globular repeats of the laminin A1 chain and the beta-amyloid binding domain of the laminin A chain. A claimed method for treating an amyloid disease comprises administering a polypeptide having a conformational similarity to a fragment of a laminin protein. A method for diagnosing an amyloid disease involves determining levels of laminin in a sample. Production of laminin or its fourth globular repeat in vivo provides a method for in vivo inhibition of beta-amyloid amyloidosis. The products and methods can be used for the diagnosis, prognosis, monitoring and treatment of amyloidoses such as Alzheimer's disease, Down's syndrome and hereditary cerebral haemorrhage with amyloidosis of the Dutch type (where the specific amyloid is the beta-amyloid protein), the amyloidosis associated with chronic inflammation, various forms of malignancy and Familial Mediterranean Fever (AA amyloid or inflammation-association amyloidosis), the amyloidosis associated with multiple myeloma and other B-cell abnormalities (AL amyloid), the amyloidosis associated with type II diabetes (amylin or islet amyloid), the amyloidosis associated with prion diseases including Creutzfeldt-Jacob disease, Gertsmann-Straussler syndrome, kuru and animal scrapie (PrP amyloid), the amyloidosis associated with long-term haemodialysis and carpal tunnel syndrome (beta 2-microglobulin amyloid), the amyloidosis associated with senile cardiac amyloid and Familial Amyloidotic Polyneuropathy (prealbumin or transthyretin amyloid), and the amyloidosis associated with endocrine tumours such as medullary carcinoma of the thyroid (variant of procalcitonin)

XX Sequence 1607 AA;

Query Match		99.1%;	Score 8446;	DB 2;	Length 1607;
Best Local Similarity		99.3%;	Pred. No. 0;		
Matches 1563;		Conservative	2;	Mismatches	7;
				Indels	2;
				Gaps	2;
QY	1	AMDECADEGGRPQRCMPFVNAAFNVTVATNTCGTPPEYCVQGTGVTGTRKSHLCDAG	60		
Db	34	AMDECADEGGRPQRCMPFVNAAFNVTVATNTCGTPPEYCVQGTGVTGTRKSHLCDAG	93		
QY	61	QQLHQAFLTDYNNQADTTWQSQTMLAGVQPNISNLTLLHGAFTDITYVRLKFTS	120		
Db	94	QQLHQAFLTDYNNQADTTWQSQTMLAGVQPNISNLTLLHGAFTDITYVRLKFTS	153		
QY	121	RPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTGDEQALCTDEFSDISPL	180		
Db	154	RPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTGDEQALCTDEFSDISPL	213		
QY	181	TGGNVAFTLEGRPSAYNFDNSPVLQEWVATDTRVTLNRLNTPFGDEVNDPKVLKSYVY	240		
Db	214	TGGNVAFTLEGRPSAYNFDNSPVLQEWVATDTRVTLNRLNTPFGDEVNDPKVLKSYVY	273		
QY	241	AISDFAVGGRCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPFFNDRPWRRATAES	300		
Db	274	AISDFAVGGRCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPFFNDRPWRRATAES	333		
QY	301	ASECLPCDCNGRSQECYFDPPELYRSTGCHGCHTNCRDNTDGAKCERCERENFFRLGNTEAC	360		
Db	334	ASESLPCDCNGRSQECYFDPPELYRSTGCHGCHTNCRDNTDGAKCERCERENFFRLGNTEAC	393		
QY	361	SPCHCSPVGLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSITEAGCRPCSCDPSGSTDE	420		
Db	394	SPCHCSPVGLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSITEAGCRPCSCDPSGSTDE	453		
QY	421	CNVETGRVCVCKDNVEGFNCERCKPGFNLESSNPKGCTPCFCFGHSSVCTNAVGSYVDI	480		
Db	454	CNVETGRVCVCKDNVEGFNCERCKPGFNLESSNPKGCTPCFCFGHSSVCTNAVGSYVDI	513		
QY	481	SSTFQIDEDGWRVEQRDGSEASLEWSSDRQYIAVISDSYFPRFYFIAPVKFLGNQVLSYQ	540		

Db	514	SSTFQIDEDGWRVEQRDGSEASLEWSSDRQYIAVISDSYFPRFYFIAPVKFLGNQVLSYQ	573		
QY	541	NLSFSFRVDRRDLRLSAEDLVLEGAGLRVSVPLIAQGNSSYPSETTVKYIFRLHEATDYPW	600		
Db	574	NLSFSFRVDRRDLRLSAEDLVLEGAGLRVSVPLIAQGNSSYPSETTVKYIFRLHEATDYPW	633		
QY	601	RPALSPFEFQKLLNNLTISKIRGTYSERSAGYLDVTLQSAARPGPGVPATWVESCTCPVG	660		
Db	634	RPALSPFEFQKLLNNLTISKIRGTYSERTAGYLDVTLQSAARPGPGVPATWVESCTCPVG	693		
QY	661	YGGQFCETCLPGYRRETPLSLGYPSPCVLCTCNHGHSETCDPVGCDRCRDNTAGPHCEKCS	720		
Db	694	YGGQFCETCLPGYRRETPLSLGYPSPCVLCTCNHGHSETCDPVGCDRCRDNTAGPHCEKCS	753		
QY	721	DGYGDSLTGTSDDCQPCPCPGSSCAIVPKTKEVVCTHCPTGTAGKRCCLCDDGYFGDP	780		
Db	754	DGYGDSLTGTSDDCQPCPCPGSSCAIVPKTKEVVCTHCPTGTAGKRCCLCDDGYFGDP	813		
QY	781	LGSNGPVRCLRPCQCNNDIDPNAVGNCRNLGTGELCKIYNTAGFYCDRCCKEGFFGNPLAP	840		
Db	814	LGSNGPVRCLRPCQCNNDIDPNAVGNCRNLGTGELCKIYNTAGFYCDRCCKEGFFGNPLAP	873		
QY	841	NPADKCKACACN-YGTVQQSSCNFVTGQCQCLPHVSGRDCGTCDPGYNLSQSGGCERC	899		
Db	874	NPADKCKACACNPGYGTVQQSSCNFVTGQCQCLPHVSGRDCGTCDPGYNLSQSGGCERC	933		
QY	900	DCHALGSTNGQCDIRTGCECQPGITGHCERCETNHFHGFEGPEGKPCDCHHGSLSLQC	959		
Db	934	DCHALGSTNGQCDIRTGCECQPGITGHCERCETNHFHGFEGPEGKPCDCHHGSLSLQC	993		
QY	960	KDDGRCECREGFGVGNRCDCQCEENYFYNRSPWPGCECPACRYLVKDKAAEHRVKLQELSL	1019		
Db	994	KDDGRCECREGFGVGNRCDCQCEENYFYNRSPWPGCECPACRYLVKDKAAEHRVKLQELSL	1053		
QY	1020	IANLGTGDDMTDQAFEDRLKEAREVTDLLREAEQVKVDQNLMDRLQRVNSSLSHSQIS	1079		
Db	1054	IANLGTGDDMTDQAFEDRLKEAREVTDLLREAEQVKVDQNLMDRLQRVNSSLSHSQIS	1113		
QY	1080	RLQNIRNTIETGILAEARARSVESTEQILIEIASRELEKAKM-AANVSITQPESTGEPNN	1138		
Db	1114	RLQNIRNTIETGILAEARARSVESTEQILIEIASRELEKAKMAANVSITQPESTGEPNN	1173		
QY	1139	MTLLAEARRLAEHRKQEAADDIVRVAKTANETSAAEYNLLRLTLAGENQTALEIEELNRK	1198		
Db	1174	MTLLAEARRLAEHRKQEAADDIVRVAKTANETSAAEYNLLRLTLAGENQTALEIEELNRK	1233		
QY	1199	YEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSALEANEANKIKKEAAD	1258		
Db	1234	YEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSALEANEANKIKKEAAD	1293		
QY	1259	LDRLIDQKLDYEDLREDMRGKEHEVKNLLEKGAEOQTADQLLARADAAKALAEAAKK	1318		
Db	1294	LDRLIDQKLDYEDLREDMRGKEHEVKNLLEKGAEOQTADQLLARADAAKALAEAAKK	1353		
QY	1319	GRSTLQEAANDILNNLKDFDRRVNDNKTAAEEALRRIPAINRTIAEANEKTRQAOLALGNA	1378		
Db	1354	GRSTLQEAANDILNNLKDFDRRVNDNKTAAEEALRRIPAINRTIAEANEKTRQAOLALGNA	1413		
QY	1379	AADATEAKNKAHEAERIAASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAENEL	1438		
Db	1414	AADATEAKNKAHEAERIAASAVQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAENEL	1473		
QY	1439	KRKQDDADQDNMMAGMASQAAQAEALNARKAKNSVSSLLSQLNNLLDQLGQDLDVTLNKL	1498		
Db	1474	KRKQDDADQDNMMAGMASQAAQAEALNARKAKNSVSSLLSQLNNLLDQLGQDLDVTLNKL	1533		
QY	1499	NEIEGSLNKADEMKAASDLDRKVSDESEARKQAAAIMDYNRDIAEIIKDHNLEDIKKT	1558		
Db	1534	NEIEGSLNKADEMKAASDLDRKVSDESEARKQAAAIMDYNRDIAEIIKDHNLEDIKKT	1593		
QY	1559	LPTGCFNTPSIEKP	1572		
Db	1594	LPTGCFNTPSIEKP	1607		

RESULT 8
AAB19802

ID AAB19802 standard; protein; 1576 AA.

XX AC AAB19802;

XX DT 05-MAR-2001 (first entry)

XX DE Human laminin 2 mature gamma-1 chain.

XX Laminin 2; human; nerve regeneration; angiogenic; cell adhesion;
KW degenerative muscle disorder; muscular dystrophy; cell therapy.

XX OS Homo sapiens.

XX PN WO200066730-A2.

XX PD 09-NOV-2000.

XX PF 28-APR-2000; 2000WO-US011378.

XX PR 30-APR-1999; 99US-0131720P.

XX PR 15-JUN-1999; 99US-0139198P.

XX PR 12-JUL-1999; 99US-0143289P.

XX PR 24-SEP-1999; 99US-0155945P.

XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.

XX Yurchenco P;

XX WPI; 2000-687537/67.

XX N-PSDB; AAA88902.

PT Purified laminin 2 protein, useful for research and therapeutic purposes
PT including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.

PS Claim 5; Page 251-256; 305pp; English.

CC The present sequence is that of human laminin 2 gamma-1 chain mature
CC protein. Laminin-2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and
CC gamma-1 (100 kDa) chains. It is thought to be specifically required for
CC stabilizing myotubes during skeletal muscle development, and for
CC preventing apoptosis. Genetic defects in its structure or expression are
CC associated with a major type of congenital muscular dystrophy. Laminin 2
CC is also thought to be important in Schwann cell/basal lamina
CC interactions. The invention provides laminin 2 alpha-2, beta-1 and gamma-
CC 1 chain polypeptides (see AAB19791-806) and the polynucleotides encoding
CC them (see AAA8891-906), methods for making recombinant laminin 2, cells
CC that express recombinant laminin 2, and methods for using purified
CC laminin 2 for research and therapeutic purposes including peripheral
CC nerve regeneration, treatment of degenerative muscle disorders,
CC angiogenesis regulation, promoting cell attachment and migration, ex vivo
CC cell therapy, improving the take of grafts, improving the
CC biocompatibility of medical devices and preparing improved culture
CC devices and media

XX Sequence 1576 AA;

Query Match 94.3%; Score 8038; DB 3; Length 1576;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;

QY 1 AMDECADEGGRPQRCMPEFVNAAFNVTVVATNTCGTPPEEYCVQGTGVTGKSchLCDAG 60

DB 3 AMDECTDEGGRPQRCMPEFVNAAFNVTVVATNTCGTPPEEYCVQGTGVTGKSchLCDAG 62

QY 61 QOHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYPNSINLT.LHLGKAFDITYVRLKFHTS 120

DB 63 QPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYPSSINLT.LHLGKAFDITYVRLKFHTS 122

QY	121	RPESPAIYKRTREDGPWIPYQYVSGSCENTYSKANRGFIRTTGGDEQQAALCTDFSDISPL	180
DB	123	RPESPAIYKRTREDGPWIPYQYVSGSCENTYSKANRGFIRTTGGDEQQAALCTDFSDISPL	182
QY	181	TGGNVAFSTLEGRPSAYNFNSPVLQEWVTATDIRVTLNRLNTFGDEVFNDPKVLKSYYY	240
DB	183	TGGNVAFSTLEGRPSAYNFNSPVLQEWVTATDIRVTLNRLNTFGDEVFNDPKVLKSYYY	242
QY	241	AISDFAVGGRCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPFFNDRPWRATAES	300
DB	243	AISDFAVGGRCKNGHASECMKNEFDKLVNCKHNTYGVDCCKLPFFNDRPWRATAES	302
QY	301	ASECLPCDCNCRSGRQECYFDPPELYRSTGHGGHCTNCRDNTDGAKCRCRENFFRLGNTEAC	360
DB	303	ASECLPCDCNCRSGRQECYFDPPELYRSTGHGGHCTNCRDNTDGAHCRCRENFFRLGNNEAC	362
QY	361	SPCHCSPVGSLSLSTQCDSYGRCSCKPGVMGDKCDRCOPGFHSLTEAGCRPCSCDPSGSTDE	420
DB	363	SSCHCSPVGSLSLSTQCDSYGRCSCKPGVMGDKCDRCOPGFHSLTEAGCRPCSCDPSGSIDE	422
QY	421	CNVETGRVCVKDNVEGFNCRCCKPGFFNLESSNPKGCTPCFCFHSSVCTNAVGYSVYDI	480
DB	423	CNVETGRVCVKDNVEGFNCRCCKPGFFNLESSNPGRCTPCFCFHSSVCTNAVGYSVSI	482
QY	481	SSTFQIDEDGWRVEQORDGSEASLEWSSDRQYIAVTSDSYFPYFIAPVKFLGNQVLSYGQ	540
DB	483	SSTFQIDEDGWRVEQORDGSEASLEWSSERQDIAVTSDSYFPYFIAPAKFLGKQVLSYGQ	542
QY	541	NLSFSFRVDRRDLRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYIFRLHEATDYPW	600
DB	543	NLSFSFRVDRRDLRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYVFLHEATDYPW	602
QY	601	RPALSPPEFQKLLNLTLSIKIRGTYSERSAGYLDVTLQARPGPGVPATWVESCTCPVG	660
DB	603	RPALTPEFQKLLNLTLSIKIRGTYSERSAGYLDVTLASARPGPGVPATWVESCTCPVG	662
QY	661	YGGQFCETCLPGYRRETSLGYPSPCVLCTCNHSETCDPETGVCDCRDNATAGPHCEKCS	720
DB	663	YGGQFCETCLPGYRRETSLGYPSPCVLCAACNHSETCDPETGVCNCRDNATAGPHCEKCS	722
QY	721	DGYGDSSTLGTSSDCQPCPCFGSSCAIVPKTKEVVCTHCPTGTAGKRCCLCDDGYFGDP	780
DB	723	DGYGDSSTLGTSSDCQPCPCFGSSCAIVPKTKEVVCTNCPTGTTGKRCCLCDDGYFGDP	782
QY	781	LGSGNPVRLCRPCQCNNDNIDPNAVGNCRNLTGECILKCIYNTAGFYCDRCCKGFFGNPLAP	840
DB	783	LGRNGPVRLCRLCQCSNDNIDPNAVGNCRNLTGECILKCIYNTAGFYCDRCCKGFFGNPLAP	842
QY	841	NPADKCKACACN-YGTVOQSSCNPVVTGQCQCLPHVSGRDCGTCDPGYVNLQSGQGCERC	899
DB	843	NPADKCKACACNPNYGTVMQSSCNPVVTGQCCELPHTVGTGDCGACDPGFYVNLQSGQGCERC	902
QY	900	DCHALGSTNGQCDIRTGQCECQPGITGQHCCERCTNHFHFGPEGCKPCDCHHGSLSLQ	959
DB	903	DCHALGSTNGQCDIRTGQCECQPGITGQHCCERCEVNHFGPEGCKPCDCHHGSLSLQ	962
QY	960	KDDGRCCEGREGFVGNRCDCQCEENYFYNRSWPGCQECPCACRYLVKDKAAEHRVKLQELSL	1019
DB	963	KDDGRCCEGREGFVGNRCDCQCEENYFYNRSWPGCQECPCACRYLVKDKVADHRVKLQELSL	1022
QY	1020	IANLGTGDDMTDQAFEDRLKEAREVTDLLREAOEVKDVQDQNLMDRLQRVNSSLHSQIS	1079
DB	1023	IANLGTGDDMTDQAFEDRLKEAREVMDLLREAOEVKDVQDQNLMDRLQRVNSSLHSQIS	1082
QY	1080	RLQNTIRNTIETGILAEARAFSRVSTEQILIEIASRELEKAKM-AANVSITQPESTGEPNN	1138
DB	1083	RLQNTIRNTIETGILAEARAFSRVSTEQILIEIASRELEKAKVAAANVSITQPESTGEPNN	1142
QY	1139	MTLLAEAEARLAEERHKEADDIRVAKTANETSAAEYVLLRTLAGENQTALEIEELNRK	1198
DB	1143	MTLLAEAEARLAEERHKEADDIRVAKTANDTSTEAYNLLRTLAGENQTALEIEELNRK	1202
QY	1199	YEQAKNISQDLEKQAAARVHEERAKRAGDKAVEIYASVAQLTPVDSEALEANEANKIKKEAAD	1258

Db 843 NPADKCKACNCPYGTWKQSSCNPVITGQCECLPHVTGQDCGACDPGFNLSQGQCERC 902
QY 900 DCHALGSTNGQCDIRTGQCECQPGITGQHCERCETHFGFGPEGCKPCDCHHEGSLSLQC 959
Db 903 DCHALGSTNGQCDIRTGQCECQPGITGQHCERCETHFGFGPEGCKPCDCHHEGSLSLQC 962
QY 960 KDDGRCECREGVGNRCDCQCEENYFYNRSWPGCQCEPCACRYLVKDKAAEHRVKLQLESL 1019
Db 963 KDDGRCECREGVGNRCDCQCEENYFYNRSWPGCQCEPCACRYLVKDKVADHRVKLQLESL 1022
QY 1020 IANLGTGDDMTVDQAFEDBLKEAREVTDLLREAEVQKVDQNLMDRLQVNSSLSHSQIS 1079
Db 1023 IANLGTGDEMVTVDQAFEDBLKEAREVMDLLREAEVQKVDQNLMDRLQVNTLSSQIS 1082
QY 1080 RLQNRNTIETGILAEARARSVESTEOQLIEIASPELEKAKM-AANVSITQPESTGEPNN 1138
Db 1083 RLQNRNTIETGNLAEQARAHAVENTERLIEIASPELEKAKVAAANVSITQPESTGDPNN 1142
QY 1139 MTLAEEARLAEERHKEADDDIVRVAKTANETSAAAYNLLRLTLAGENQTALEIEELNRK 1198
Db 1143 MTLAEEARKLAERHKEADDDIVRVAKTANDTSTEAAYNLLRLTLAGENQTALEIEELNRK 1202
QY 1199 YEOAKNISQDLEKQAAARVHBEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAAD 1258
Db 1203 YEOAKNISQDLEKQAAARVHBEAKRAGDKAVEIYASVAQLSPDSETLENEANNIKMEAEEN 1262
QY 1259 LDRLLDKLKOYEDLREDNRGKEHEVKNLLLEKGAEQQTADQLLARADAALAEAAKK 1318
Db 1263 LEQLIDQKLKOYEDLREDNRGKEHEVKNLLLEKGAEQQTADQLLARADAALAEAAKK 1322
QY 1319 GRSTLQEAANDILNNLKDFRRVNDNKTAAEEALRRIPAINRTIAEANEKTRQAALGNA 1378
Db 1323 GRDTLQEAANDILNNLKDFRRVNDNKTAAEEALRXIPAINQTITEANEKTRQAALGSA 1382
QY 1379 AADATEAKNKAHEAERIAAQAQKATSTKADAERTFGEVTDLDNEVNGMLRQLEEAENEL 1438
Db 1383 AADATEAKNKAHEAERIAAQAQKATSTKADAERTFAEVTDLDNEVNNMLKQLQEAKEKEL 1442
QY 1439 KRKODDADQDMMAGMASQAQAQAEALNARKAKNSVSLLSQLNNLLDQLGQDQDVTDLNKL 1498
Db 1443 KRKODDADQDMMAGMASQAQAQAEALNARKAKNSVSLLSIINDLLEQLGQDQDVTDLNKL 1502
QY 1499 NEIEGSLNKADEMKAQSDLDKRVSDLESEARKQEAAIMDYNRDIAEIIKDHNLEDIKKT 1558
Db 1503 NEIEGTLNKADEMKAQSDLDKRVSDLENEAKQEAAIMDYNRDIEEIMKDIRNLEDIRKT 1562
QY 1559 LPTGCFNTPSIEKP 1572
Db 1563 LPSCGCFNTPSIEKP 1576

RESULT 10
ABB81595
ID ABB81595 standard; protein; 1576 AA.
XX AC ABB81595;
XX DT 19-SEP-2002 (first entry)
XX DE Human laminin 10 third chain protein sequence SEQ ID NO:16.
XX KW Laminin alpha 5; laminin 10; vulneryary; cell growth; differentiation;
KW tissue repair development; laminin; healing; vascular tissue;
KW re-endothelialisation; vascular injury; cell attachment; cell stasis;
KW proliferation; migration.
XX OS Homo sapiens.
XX PN WO200250111-A2.
XX PD 27-JUN-2002.
XX

PF 21-DEC-2001; 2001WO-US051035.
XX 21-DEC-2000; 2000US-0257449P.
PR 28-MAR-2001; 2001US-0279282P.
PR 13-NOV-2001; 2001US-00279282.
XX (BIOS-) BIOSTRATUM INC.
PA Tryggvason K, Doi M, Thyboll J;
XX WPI; 2002-557650/59.
PI N-PSDB; ABQ72913.
XX DR
DR N-PSDB; ABQ72913.
XX PT
PT New human laminin-10 proteins, useful for accelerating the healing of
PT vascular tissue, improving the biocompatibility of grafts, or for
PT promoting re-endothelialization at the site of vascular injuries.
XX PS
XX Claim 9; Page 177-182; 231pp; English.
XX CC
CC The present invention describes human laminin alpha 5. Also described is
CC an isolated laminin 10. Laminin 10 has vulneryary activity. Laminins are
CC useful in maintaining cell/tissue phenotype as well as promoting cell
CC growth and differentiation in tissue repair development. Specifically,
CC laminin 10 can be used for accelerating the healing injuries of vascular
CC tissue, improving the biocompatibility of grafts useful for treating such
CC injuries, for promoting re-endothelialisation at the site of vascular
CC injuries, and promote cell attachment and subsequent cell stasis,
CC proliferation, differentiation, and/or migration. The present sequence
CC represents a third chain protein of laminin 10, from the present
CC invention
XX SQ
SQ Sequence 1576 AA;
Query Match 94.3%; Score 8038; DB 5; Length 1576;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;
QY 1 AMDECADEGGRPQRCMPEFVNAAFNVTVAATNTCGTPPEEYCVQGTGVTKSCHLCDAG 60
Db 3 AMDECTDEGGRPQRCMPEFVNAAFNVTVAATNTCGTPPEEYCVQGTGVTKSCHLCDAG 62
QY 61 QHQLQHGAFLTDYNNQADTTWQSQOTMLAGVQVYNSINLTHLGKAFDITYYRLKFHTS 120
Db 63 QHQLQHGAFLTDYNNQADTTWQSQOTMLAGVQVYSSINLTHLGKAFDITYYRLKFHTS 122
QY 121 RPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFI RTGGDEQQAALCTDEFSDISPL 180
Db 123 RPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFI RTGGDEQQAALCTDEFSDISPL 182
QY 181 TGGNVAFASTLEGRPSAYNFNDSFVLQEWVTATDIRVTNRLNTFGDEVFNDPKVLSYYY 240
Db 183 TGGNVAFASTLEGRPSAYNFNDSFVLQEWVTATDIRVTNRLNTFGDEVFNDPKVLSYYY 242
QY 241 AISDFAVGGRCKCNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPFFNDRPWRATAES 300
Db 243 AISDFAVGGRCKCNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPFFNDRPWRATAES 302
QY 301 ASECLPCDCNRSQECYFDPBLYRSTGHGGHCTNCRDNTDGAKCERCENFFRLGNTEAC 360
Db 303 ASECLPCDCNRSQECYFDPBLYRSTGHGGHCTNCRDNTDGAKCERCENFFRLGNNEAC 362
QY 361 SPCHCSPVGSLSLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLSLTAAGCRPCSDPSGSTDE 420
Db 363 SSCHCSPVGSLSLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLSLTAAGCRPCSDPSGSIDE 422
QY 421 CNVETGRVCVKDNVEGFNCBRCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGSYVDI 480
Db 423 CNVETGRVCVKDNVEGFNCBRCKPGFFNLESSNPGRCTPCFCFGHSSVCTNAVGSYVSI 482
QY 481 SSTFQIDEDGWRAEQRDGSEASLEWSSDRQYIAVISDSYFFPRYFIAPVKFLGNQVLSYGQ 540
Db 483 SSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFFPRYFIAPAKFLGKQVLSYGQ 542

Qy 541 NLSFSFRVDRRTRLAEDLVLEGAGLRVSVPLIAQGSYPSETTVKYIFRLHEATDYPW 600
Db |||||
Qy 543 NLSFSFRVDRRTRLAEDLVLEGAGLRVSVPLIAQGSYPSETTVKYVFRLEATDYPW 602
Db |||||
Qy 601 RPALSPFEFQKLLNNLTSIKIRGTYSERSAGYLDVTLQSRPGPGVPATWVESCPCPVG 660
Db |||||
Qy 603 RPALTFFEFQKLLNNLTSIKIRGTYSERSAGYLDVTLASARPGPGVPATWVESCPCPVG 662
Db |||||
Qy 661 YGQFCETCLPGYRRRETPLSGYSPCVLCTCNHSEICDPETGVCDNRDNTAGPHCEKCS 720
Db |||||
Qy 663 YGQFCMCLSGYRRRETPLSGYSPCVLCAHNGHSEICDPETGVCDNRDNTAGPHCEKCS 722
Db |||||
Qy 721 DGYVGDSTLTGSSDCQPCPCGSSCAIVPKTKEVVCHTCTGTAGRCRCELDDGYFGDP 780
Db |||||
Qy 723 DGYVGDSTAGTSSDCQPCPCGSSCAIVPKTKEVVCHTCTGTGTGRCRCELDDGYFGDP 782
Db |||||
Qy 781 LGSNGPVRLCRPCQCNNDNIDPNAVGNCRNLTGECCLKCIYNTAGFYCDRCCKEGFNGPLAP 840
Db |||||
Qy 783 LGRNGPVRLCRLCQCSNDNIDPNAVGNCRNLTGECCLKCIYNTAGFYCDRCCKDGFNGPLAP 842
Db |||||
Qy 841 NPADKCKACACN-YGTVQQSSCNPVGTGQCCLPHVSGRDCGTDPGYNLTQSGQCERC 899
Db |||||
Qy 843 NPADKCKACACNPYGTMKQSSCNPVGTGQCECLPHVTGQCGACDPGFYNLTQSGQCERC 902
Db |||||
Qy 900 DCHALGSTNGQCDIRTGQCECQPGITGQHCHERCETNHFGEPEGCKPCDCHHESLSLQC 959
Db |||||
Qy 903 DCHALGSTNGQCDIRTGQCECQPGITGQHCHERCETNHFGEPEGCKPCDCHHESLSLQC 962
Db |||||
Qy 960 KDGRCCEGREGVGNRCDCQCEENFYNRSWPGCQCPACVRLVKDKAAEHRVKLQELSL 1019
Db |||||
Qy 963 KDDGRCEGREGVGNRCDCQCEENFYNRSWPGCQCPACVRLVKDKVADHRVKLQELSL 1022
Db |||||
Qy 1020 IANLGTGDDMVTDQAFEDRLKEAREVTDLLREAEQVQDVQDQNLMDRLQRVNNTLSSQIS 1079
Db |||||
Qy 1023 IANLGTGDDMVTDQAFEDRLKEAREVMDLLREAEQVQDVQDQNLMDRLQRVNNTLSSQIS 1082
Db |||||
Qy 1080 RLQNRNTIETGILAEARSRVSTEQLEIEIASRELEKAKM-AANVSITQPESTCEPNN 1138
Db |||||
Qy 1083 RLQNRNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSITQPESTGDPNN 1142
Db |||||
Qy 1139 MTLLEAEARLAERHKEADDIRVAKTANETSAAEAYNLLRLTAGENQTALEIEELNRK 1198
Db |||||
Qy 1143 MTLLEAEARKLAERHKEADDIRVAKTANDTSTAYNLLRLTAGENQTALEIEELNRK 1202
Db |||||
Qy 1199 YEQAKNISQDLEKQAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAAD 1258
Db |||||
Qy 1203 YEQAKNISQDLEKQAARVHEEAKRAGDKAVEIYASVAQLSPDLSETLENEANNIKMEAN 1262
Db |||||
Qy 1259 LDRLIDQKLKDYEDLREDMRGKEHEVKNLLEKGAEQQTADQLLARADAAKALAEBAAKK 1318
Db |||||
Qy 1263 LEQLIDQKLKDYEDLREDMRGKEHEVKNLLEKKGTEQQTADQLLARADAAKALAEBAAKK 1322
Db |||||
Qy 1319 GRSTLQEAANDILNNLKFDRRVNDNKTAAEEALRRIPAINRTIAEANEKTRAEQALALGNA 1378
Db |||||
Qy 1323 GRDTLQEAANDILNNLKFDRRVNDNKTAAEEALRKIPAINQTITEANEKTRAEQALGSA 1382
Db |||||
Qy 1379 AADATEAKNKAHEAERIAASAAQKNATSTKADAERTTFGEVTDLDNEVNGMLRQLEBAENEL 1438
Db |||||
Qy 1383 AADATEAKNKAHEAERIAASAVQKNATSTKAEARTFAEVTDLNEVNNMLKQLEBAEKEL 1442
Db |||||
Qy 1439 KRKQDDADQDMWAGMASQAAQAEELNARKAKNSVSSLLSOLNNLLDQLGQDITVDLNLK 1498
Db |||||
Qy 1443 KRKQDDADQDMWAGMASQAAQAEELNARKAKNSVTSLLSINDLLEQLGQDITVDLNLK 1502
Db |||||
Qy 1499 NEIEGSLNKADEMKAASDLDRKVSLESEARKQEAAMIDYNRDIAEIIKDIHNLEDIKKT 1558
Db |||||
Qy 1503 NEIEGTLNKADEMKVSDLDLRKVSLENEAKKQEAAMIDYNRDIEEIMKDIRNLEDIRKT 1562
Db |||||
Qy 1559 LPTGCFNTPSIEKP 1572
Db |||||
Qy 1563 LPSGCFNTPSIEKP 1576
Db |||||

RESULT 11
AAB19804
ID AAB19804 standard; protein; 1584 AA.
XX
AC AAB19804;
XX
DT 05-MAR-2001 (first entry)
XX
DE Human laminin 2 gamma-1 chain with C-terminal FLAG epitope.
XX
KW Laminin 2; human; nerve regeneration; angiogenic; cell adhesion;
KW degenerative muscle disorder; muscular dystrophy; cell therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..33
FT /label= Signal_peptide
FT Protein 34..1609
FT /label= Mature_protein
FT Peptide 1610..1617
FT /label= FLAG
XX
PN WO200066730-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US011378.
XX
PR 30-APR-1999; 99US-0131720P.
PR 15-JUN-1999; 99US-0139198P.
PR 12-JUL-1999; 99US-0143289P.
PR 24-SEP-1999; 99US-0155945P.
XX
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
PI Yurchenco P;
XX
DR WPI; 2000-687537/67.
DR N-PSDB; AAA88904.
XX
PT Purified laminin 2 protein, useful for research and therapeutic purposes
PT including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.
XX
PS Claim 5; Page 275-280; 305pp; English.
XX
CC The present sequence is that of the mature gamma-1 chain of human laminin
CC 2, with an additional C-terminal FLAG epitope, resulting from expression
CC in transfected cells from mammalian expression vectors. Laminin 2 is
CC composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1 (100 kDa)
CC chains. It is thought to be specifically required for stabilizing
CC myotubes during skeletal muscle development, and for preventing
CC apoptosis. Genetic defects in its structure or expression are associated
CC with a major type of congenital muscular dystrophy. Laminin 2 is also
CC thought to be important in Schwann cell/basal lamina interactions. The
CC invention provides laminin 2 alpha-2, beta-1 and gamma-1 chain
CC polypeptides (see AAB19791-806) and the polynucleotides encoding them
CC (see AAA8891-906), methods for making recombinant laminin 2, cells that
CC express recombinant laminin 2, and methods for using purified laminin 2
CC for research and therapeutic purposes including peripheral nerve
CC regeneration, treatment of degenerative muscle disorders, angiogenesis
CC regulation, promoting cell attachment and migration, ex vivo cell
CC therapy, improving the take of grafts, improving the biocompatibility of
CC medical devices and preparing improved culture devices and media
XX
SQ Sequence 1584 AA;

Query Match 94.3%; Score 8038; DB 3; Length 1584;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;
Qy 1 AMDECADEGGRPQRCMPFVNAAFNVTVATNTCGTPPEEYCVQGTGVTKSHCLCDAG 60

Db 3 AMDECTDEGRPORCMPEFVNAAFNVTVATNTCGTPPEYCVQIGVTGKTSCHLCDAG 62
Qy 61 QHLOHGAFLTDYNNQADTTWQSQTMLAGVQYPNSINLTLLHAKAFDITYVRLKFTS 120
Db 63 QPHLOHGAFLTDYNNQADTTWQSQTMLAGVQYPSSINLTLLHAKAFDITYVRLKFTS 122
Qy 121 RPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFI RTGGDEQQALCTDEFSDISPL 180
Db 123 RPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFI RTGGDEQQALCTDEFSDISPL 182
Qy 181 TGGNVAFTSTLEGRPSAYNFDSNPSVLQEWVTATDIRVTLNRLNTFGDEVFNDPKVLKSYIY 240
Db 183 TGGNVAFTSTLEGRPSAYNFDSNPSVLQEWVTATDIRVTLNRLNTFGDEVFNDPKVLKSYIY 242
Qy 241 AISDFAVGGRCKNGHASECVKNEFDKLMCNCKHNTYGVDCCEKCLPEFFNDRPWRRTAES 300
Db 243 AISDFAVGGRCKNGHASECMKNEFDKLVNCCKHNTYGVDCCEKCLPEFFNDRPWRRTAES 302
Qy 301 ASECLPCDCNGRSQECYFDPPELYRSTGHGHCTNCRDNTDGA KCRCRENFFRLGNTEAC 360
Db 303 ASECLPCDCNGRSQECYFDPPELYRSTGHGHCTNCRDNTDGA KCRCRENFFRLGNNEAC 362
Qy 361 SPCHCSPVGLSTQCDSYGRCSCKPGVMGDKDRCPQGFHSLTEAGRPCSCDPSGSTDE 420
Db 363 SSCHCSPVGLSTQCDSYGRCSCKPGVMGDKDRCPQGFHSLTEAGRPCSCDPSGSIDE 422
Qy 421 CNVETGRCVCKDNVEGFNCERCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGYSVYDI 480
Db 423 CNVETGRCVCKDNVEGFNCERCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGYSVYSI 482
Qy 481 SSTFQIDEDGWRVEQRDGSEASLEWSSDRQXIAVISDSYFPRYFIAPVKFLGNQVLSYGQ 540
Db 483 SSTFQIDEDGWRVEQRDGSEASLEWSSERQDIAVISDSYFPRYFIAPVKFLGNQVLSYGQ 542
Qy 541 NLSFSFRVDRDRTRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKVI FRLHEATDYPW 600
Db 543 NLSFSFRVDRDRTRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKVI FRLHEATDYPW 602
Qy 601 RPALSPFEFQKLLNLTISKIRGTYSERSAGYLDVDTLQ SARPGPGVPATWVESCTCPVG 660
Db 603 RPALTPFEFQKLLNLTISKIRGTYSERSAGYLDVDTLQ SARPGPGVPATWVESCTCPVG 662
Qy 661 YGGQFCETCLPGYRRETPSLGYPSPCVLCTCNHSETCDPETGVCD CRDNTAGPHCEKCS 720
Db 663 YGGQFCMCLSGYRRETPNLGYPSPCVLCA CNHSETCDPETGVCD CRDNTAGPHCEKCS 722
Qy 721 DGYGDSSTLGTSSDCQPCPCPGSSCAI VPKTKB VVCTHCPTGTAGKRCELCDDGYFGDP 780
Db 723 DGYGDSSTAGTSSDCQPCPCPGSSCAV VPKTKB VVCTNCPTGTTGKRCELCDDGYFGDP 782
Qy 781 LGSNGPVRLCRPCQCNIDPNAVGNCRNLTG ECLKCIYNTAGFYCDRCKEGFFGNPLAP 840
Db 783 LGRNGPVRLCRLCQCSNIDPNAVGNCRNL TG ECLKCIYNTAGFYCDRCCKDGGFFGNPLAP 842
Qy 841 NPADKCKACACN - YGTVQOQSSCNPV TGGCQCLPHVSGRDCGTCDPGYNLQSGQGCERC 899
Db 843 NPADKCKACNCPYGTMKQOQSSCNPV TGQCECLPHVTGQDCGACDPGFYNLQSGQGCERC 902
Qy 900 DCHALGSTNGQCDIRTGQCECQPGITGQH CERCETNHFGFGEKPCDCHHEGSLSLQC 959
Db 903 DCHALGSTNGQCDIRTGQCECQPGITGQH CERCETVNHFGFGEKPCDCHPEGSLSLQC 962
Qy 960 KDDGRCECREGVGNRCQCEENYFYNRSPW GQCPCACRYLVKDKAABHRVKLQLESL 1019
Db 963 KDDGRCECREGVGNRCQCEENYFYNRSPW GQCPCACRYLVKDKVADHRVKLQLESL 1022
Qy 1020 IANLGTGDDMVTDOAFEDRLKEABREVTDL LREAEVQKVDQNLMDRLQVNSSLHSQIS 1079
Db 1023 IANLGTGDEMVTDOAFEDRLKEABREVM DLLREAEVQKVDQNLMDRLQVNTLSSQIS 1082
Qy 1080 RLQNI RNTIETGILAEARPSRVESTEQ LIIEIASRELEKAKM - AANVSITQPESTGDPNN 1138

1083 RLQNI RNTIETGNLAEQARAHVENTERLIE IASRELEKAKVAAANVSITQPESTGDPNN 1142
Qy 1139 MTL LAEEARRLAERHKQEADDIVRVAKTANETS AEAYNLLRLTAGENQTAL EIEELNRK 1198
Db 1143 MTL LAEEARKLAERHKQEADDIVRVAKTANDT STEAYNLLRLTAGENQTAF EIEELNRK 1202
Qy 1199 YEQAKNISQDLEKQAAARVHEEAKRAGDKA VEIYASVAQLTPVDSEALENEANKIKKEAAD 1258
Db 1203 YEQAKNISQDLEKQAAARVHEEAKRAGDKA VEIYASVAQLSPDSELENEANNIKMEAEEN 1262
Qy 1259 LDRLIDQKLKDYEDLREDMRGKEHEVKNLLE KGAEQQTADQLLARADA AKALAEAAKK 1318
Db 1263 LEQLIDQKLKDYEDLREDMRGKELEVKNLLE KGTQEQQQTADQLLARADA AKALAEAAKK 1322
Qy 1319 GRSTLQEANDILNNLKDFDRRVNDNKTAA BEALRRIPAINRTIAEANEKTR EAAQALGNA 1378
Db 1323 GRDTLQEANDILNNLKDFDRRVNDNKTAA BEALRKIPAINQITITEANEKTR EAAQALGSA 1382
Qy 1379 AADATEAKNKAHEAERIAASAAQKNATSTK ADAERTFGEVTDLDNEVNGMLRQLEEAENEL 1438
Db 1383 AADATEAKNKAHEAERIAASAVQKNATSTK AEAERTFAEVTDL DNEVNNMLKQLQEA EKEL 1442
Qy 1439 KRQDDADQDMMAGMASQAQAEALNARKAK NSVSSLLS QLNLLDQLGQLDTV DNLNKL 1498
Db 1443 KRQDDADQDMMAGMASQAQAEALNARKAK NSVTSLLSI INDLLEQLGQLDTV DNLNKL 1502
Qy 1499 NEIEGSLNKAKDEMKASDLDLRKVS DLESEARKQEAAIMDYNR DIAEIIKDIHNLEDIKKT 1558
Db 1503 NEIEGTLNKAKDEMKVSDLDLRKVS DLENEAKQEAAIMDYNR DIBEEIMKDIRNLEDIRKT 1562
Qy 1559 LPTGCFNTPSIEKP 1572
Db 1563 LPSCGCFNTPSIEKP 1576
RESULT 12
AAB19801
ID AAB19801 standard; protein; 1609 AA.
XX
AC AAB19801;
XX
DT 05-MAR-2001 (first entry)
XX
DE Human laminin 2 gamma-1 chain.
XX
KW Laminin 2; human; nerve regeneration; angiogenic; cell adhesion; degenerative muscle disorder; muscular dystrophy; cell therapy.
XX
OS Homo sapiens.
XX
FH Key
FT Peptide 1..33
FT Protein /label= signal_peptide 34..1609
FT /label= Mature_protein
XX
PN WO200066730-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US011378.
XX
PR 30-APR-1999; 99US-0131720P.
PR 15-JUN-1999; 99US-0139198P.
PR 12-JUL-1999; 99US-0143289P.
PR 24-SEP-1999; 99US-0155945P.
XX
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
PI Yurchenco P;
XX
DR WPI; 2000-687537/67.
DR N-PSDB; AAA88901.

XX Purified laminin 2 protein, useful for research and therapeutic purposes
PT including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.
XX
PS Claim 5; Page 239-244; 305pp; English.
XX
CC The present sequence is that of the gamma-1 chain of human laminin 2.
CC Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1
CC (100 kDa) chains. It is thought to be specifically required for
CC stabilizing myotubes during skeletal muscle development, and for
CC preventing apoptosis. Genetic defects in its structure or expression are
CC associated with a major type of congenital muscular dystrophy. Laminin 2
CC is also thought to be important in Schwann cell/basal lamina
CC interactions. The invention provides laminin 2 alpha-2, beta-1 and gamma-
CC 1 chain polypeptides (see AAB19791-806) and the polynucleotides encoding
CC them (see AAA88891-906), methods for making recombinant laminin 2, cells
CC that express recombinant laminin 2, and methods for using purified
CC laminin 2 for research and therapeutic purposes including peripheral
CC nerve regeneration, treatment of degenerative muscle disorders,
CC angiogenesis regulation, promoting cell attachment and migration, ex vivo
CC cell therapy, improving the take of grafts, improving the
CC biocompatibility of medical devices and preparing improved culture
CC devices and media
XX
SQ Sequence 1609 AA;

Query Match 94.3%; Score 8038; DB 3; Length 1609;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;

QY 1 AMDECADEGGPQRCMPEFVNAAFNVTVATNTCGTPPEEYCVQGTGVTGKSCHLCDAG 60
DB 36 AMDECTDEGGRPQRCMPEFVNAAFNVTVATNTCGTPPEEYCVQGTGVTGKSCHLCDAG 95
QY 61 QHQLQHGAFLTDYNNQADTTWQSQIWLQAGVQYPSINLTLHLGKAFDITYVRLKPHTS 120
DB 96 QHQLQHGAFLTDYNNQADTTWQSQIWLQAGVQYPSINLTLHLGKAFDITYVRLKPHTS 155
QY 121 RPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTCGDEQQALCTDEFSDISPL 180
DB 156 RPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTCGDEQQALCTDEFSDISPL 215
QY 181 TGGNVAFTILEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSYYY 240
DB 216 TGGNVAFTILEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSYYY 275
QY 241 AISDFAVGGRCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKCLPFFNDRPWRRATAES 300
DB 276 AISDFAVGGRCKNGHASECMKNEFDKLVNCKHNTYGVDCCKCLPFFNDRPWRRATAES 335
QY 301 ASECLPCDCNRSQECYFDPPELYRSIGHGCHCTNCRDNTDGAHCRCRENFRLGNTEAC 360
DB 336 ASECLPCDCNRSQECYFDPPELYRSIGHGCHCTNCRDNTDGAHCRCRENFRLGNTEAC 395
QY 361 SPCHCSPVGSISTQCDSYGRCSCKPGVNGDKCDRCQPGFHSLTEAGCRPCSDPSGSTDE 420
DB 396 SSCHCSPVGSISTQCDSYGRCSCKPGVNGDKCDRCQPGFHSLTEAGCRPCSDPSGSTDE 455
QY 421 CNVETGRVCVCKDNVEGFNCERCCKPGFNLESSNPKGCTPCFCFGHSSVCTNAVGSYVDI 480
DB 456 CNVETGRVCVCKDNVEGFNCERCCKPGFNLESSNPRGCTPCFCFGHSSVCTNAVGSYVSI 515
QY 481 SSTFQIDEDGWRVEQRDGEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYQQ 540
DB 516 SSTFQIDEDGWRVEQRDGEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSYQQ 575
QY 541 NLSFSFRVDRDRTRLASAEDLVLEGAGLVSVPVLIQAQNSYSPSETTVKYIFRLHEATDYPW 600
DB 576 NLSFSFRVDRDRTRLASAEDLVLEGAGLVSVPVLIQAQNSYSPSETTVKYIFRLHEATDYPW 635
QY 601 RPALSPFEFQKLLNLTISKIRGTYSERSAGYLDVTLQSRPQPGVPATWVESCTCPVG 660
|||||:|||||

DB 636 RPALTPFEFQKLLNLTISKIRGTYSERSAGYLDVTLASARPGPGVPATWVESCTCPVG 695
QY 661 YGQFCETCLPGYRRETPSLGYPSPCVLCTCNHSETCDPETGVCDNRDNTAGPHCEKCS 720
DB 696 YGQFCCEMCLSGYRRETPNLGYPSPCVLCAHNGHSETCDPETGVCDNRDNTAGPHCEKCS 755
QY 721 DGYGDSLTGTSDDCPCPCPGSSCAIVPKTKEVWCHTCTGTAGKRCCLCDDGYFGDP 780
DB 756 DGYGDSLTGTSDDCPCPCPGSSCAIVPKTKEVWCHTCTGTAGKRCCLCDDGYFGDP 815
QY 781 LGSNGPVRLCRPCQCNNDNIDPNAVGNCRNLGTGECCLKIYNTAGFYCDRCCKEGFFGNPLAP 840
DB 816 LGRNGPVRLCRPCQCNNDNIDPNAVGNCRNLGTGECCLKIYNTAGFYCDRCCKEGFFGNPLAP 875
QY 841 NPADKCKACACN-YGTVQQSSCNPNVTGQCCPLPHVSGRDCGTCDPGYNLQSGQGCERC 899
DB 876 NPADKCKACACNPNVTGQCCPLPHVSGRDCGTCDPGYNLQSGQGCERC 935
QY 900 DCHALGSTNGQCDIRTGQCECQPGITGQHCERCETNHFHFGPEGCKPCDCHHESLSLQ 959
DB 936 DCHALGSTNGQCDIRTGQCECQPGITGQHCERCETNHFHFGPEGCKPCDCHHESLSLQ 995
QY 960 KDDGRCECREGFGVNRCDQCEENYFYNRSWPGCQECPCYRLVKDKAAEHRVKLQLESL 1019
DB 996 KDDGRCECREGFGVNRCDQCEENYFYNRSWPGCQECPCYRLVKDKAAEHRVKLQLESL 1055
QY 1020 IANLGTGDDMTDQAFEDRLKEAEREVTDLLEAQQVQKVDQNLMDRLQVNSSLSHSQIS 1079
DB 1056 IANLGTGDDMTDQAFEDRLKEAEREVTDLLEAQQVQKVDQNLMDRLQVNSSLSHSQIS 1115
QY 1080 RLQNIIRNTIETGILAEARARSRVSTEQIIEIASRELEKAKM-AANVSITQPESTGEPPN 1138
DB 1116 RLQNIIRNTIETGILAEARARSRVSTEQIIEIASRELEKAKM-AANVSITQPESTGEPPN 1175
QY 1139 MTLLEAEARLAEHRHKEADDIRVAKTANETSAAEYNNLLRLTAGENQTALEIEELNRK 1198
DB 1176 MTLLEAEARLAEHRHKEADDIRVAKTANETSAAEYNNLLRLTAGENQTALEIEELNRK 1235
QY 1199 YEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAAD 1258
DB 1236 YEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAAD 1295
QY 1259 LDRLIDQKLDYEDLREDMRGKEHEVKNLLEKGAEQQTADQLLARADAAKALAEAAK 1318
DB 1296 LEQLIDQKLDYEDLREDMRGKEHEVKNLLEKGAEQQTADQLLARADAAKALAEAAK 1355
QY 1319 GRSTLQEAANDILNNLKDFDRRVNDNKTAAEEALRRIPAINRTTAAANEKTRQAQLALGNA 1378
DB 1356 GRSTLQEAANDILNNLKDFDRRVNDNKTAAEEALRRIPAINRTTAAANEKTRQAQLALGNA 1415
QY 1379 AADATEAKNKAHEAERIAASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAENEL 1438
DB 1416 AADATEAKNKAHEAERIAASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAENEL 1475
QY 1439 KRKQDDADQDMMAGMASQAAQAEALNARKAKNSVSSLLSQNLNLLDQLGQDLDVLDLNLK 1498
DB 1476 KRKQDDADQDMMAGMASQAAQAEALNARKAKNSVSSLLSQNLNLLDQLGQDLDVLDLNLK 1535
QY 1499 NEIEGSLNKADEMKAASDLDRKVSDELESEARKQEAAMDMYNRDIAEIIKDIHNLEDIKKT 1558
DB 1536 NEIEGSLNKADEMKAASDLDRKVSDELESEARKQEAAMDMYNRDIAEIIKDIHNLEDIKKT 1595
QY 1559 LPTGCFNTPSIEKP 1572
DB 1596 LPTGCFNTPSIEKP 1609

RESULT 13
AAB48452
ID AAB48452 standard; protein; 1609 AA.
XX
AC AAB48452;
XX

DT 02-MAR-2001 (first entry)
XX Human laminin 8 polypeptide, SEQ ID NO: 22.
DE
XX
XX Human; laminin 8; neuroprotective; angiogenic; osteopathic;
KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;
KW vascular tissue injury; neural injury; angiogenesis regulation.
XX
OS Homo sapiens.
XX
XX WO200066732-A2.
PN
XX
PD 09-NOV-2000.
XX
XX 28-APR-2000; 2000WO-US011543.
PF
XX
PR 30-APR-1999; 99US-0131720P.
PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.
PR 11-FEB-2000; 2000US-0182012P.
XX
PA (BIOS-) BIOSTRATUM INC.
XX
XX Kortessmaa J, Tryggvason K;
PI
XX
DR WPI; 2000-687539/67.
DR N-PSDB; AAC83713.
XX
PT Purified laminin 8 protein, useful for research and therapeutic purposes
PT including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.
XX
XX Claim 5; Page 202-207; 245pp; English.
PS
XX
XX The present sequence is a laminin 8 polypeptide chain. Laminins are a
CC family of heterotrimeric glycoproteins that function via binding
CC interactions with neighbouring cell receptors and by forming laminin
CC networks. They are signalling molecules which influence cellular
CC function. Laminin 8 is useful for treating injuries to tissue of
CC mesenchymal origin, such as bone, cartilage, tendon, and ligament,
CC treating injuries to vascular tissue, promoting cell attachment and
CC migration, ex vivo cell therapy, improving the biocompatibility of
CC medical devices, and preparing improved cell culture devices and media.
CC Laminin 8 is also useful for promoting re-endothelialisation at the site
CC of vascular injuries, improving the take of grafts, improving the
CC biocompatibility of medical devices, treating neural injuries (neural
CC regeneration), regulating angiogenesis, and promoting cell attachment and
CC migration
XX
SQ Sequence 1609 AA;

Query Match 94.3%; Score 8038; DB 3; Length 1609;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;

QY 1 AMDECADEGGRPQRCMPEFVNAAFNVTVVATNTCGTPPEEYCVQGTGVTGKSKHLCDAG 60
DB 36 AMDECTDEGGRPQRCMPEFVNAAFNVTVVATNTCGTPPEEYCVQGTGVTGKSKHLCDAG 95
QY 61 QOHLQHGAFLTDYNNQADTTWQSQOTMLAGVQYPNSINLTLLHLGKAFDITYVRLKFHTS 120
DB 96 QPHLQHGAFLTDYNNQADTTWQSQOTMLAGVQYPSSINLTLLHLGKAFDITYVRLKFHTS 155
QY 121 RPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDISPL 180
DB 156 RPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDISPL 215
QY 181 TGGNVAFSTLEGRPSAYNFNSPVLQEWVTATDIRVTNLRLNTFGDEVNDPKVLKSYYY 240
DB 216 TGGNVAFSTLEGRPSAYNFNSPVLQEWVTATDIRVTNLRLNTFGDEVNDPKVLKSYYY 275
QY 241 AISDFAVGGRCCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPFFNDRPWRATAES 300

Db 276 AISDFAVGGRCCKNGHASECMKNEFDKLVNCKHNTYGVDCCKLPFFNDRPWRATAES 335
QY 301 ASECLPCDCNCRSQECYFDPPELYRSTGHGGHCTNCRDNTDGAHCRCRENFRLGNTEAC 360
Db 336 ASECLPCDCNCRSQECYFDPPELYRSTGHGGHCTNCDNTDGAHCRCRENFRLGNNEAC 395
QY 361 SPCHCSPVGSLSLSTQCDSDSYGRCSCKPGVMGDKCDRCQPGFHSLSLTIAGCRPCSCDPSGSTDE 420
Db 396 SSCHCSPVGSLSLSTQCDSDSYGRCSCKPGVMGDKCDRCQPGFHSLSLTIAGCRPCSCDPSGSIDE 455
QY 421 CNVETGRVCVKDNVEGFNCERCCKPGFNLESSNPKGCTPCFCFGHSSVCTNAVGSVYDI 480
Db 456 CNVETGRVCVKDNVEGFNCERCCKPGFNLESSNPRGCTPCFCFGHSSVCTNAVGSVYSI 515
QY 481 SSTFQIDEDGWRVEQORDGSEASLEWSSDRQYIAVISDSYFPRIYFIAPVKFLGNQVLSYGO 540
Db 516 SSTFQIDEDGWRVEQORDGSEASLEWSSERQDIAVISDSYFPRIYFIAPVKFLGKQVLSYGO 575
QY 541 NLSFSFRVDRDTRLRLSAEDLVLEGAGLRVSVPLIAQGNSSYPSETIVKYIFRLHEATDYPW 600
Db 576 NLSFSFRVDRDTRLRLSAEDLVLEGAGLRVSVPLIAQGNSSYPSETIVKYIFRLHEATDYPW 635
QY 601 RPALSPFEFQKLLNLTISIIRGTYSERSAGYLDVTLQSRPGVGPATWVESCTCPVG 660
Db 636 RPALTPEFQKLLNLTISIIRGTYSERSAGYLDVTLQSRPGVGPATWVESCTCPVG 695
QY 661 YGQFCETCLPGYRRETPSLGYPSPCVLCTCNHGHSETCDPETGVCDCRDNTAGPHCEKCS 720
Db 696 YGQFCETCLPGYRRETPSLGYPSPCVLCTCNHGHSETCDPETGVCDCRDNTAGPHCEKCS 755
QY 721 DGYGDSLTGTSDDCQPCPCPGSSCAIVPKTKVCTHCPGTAGKRCCELDDGYFGDP 780
Db 756 DGYGDSLTGTSDDCQPCPCPGSSCAIVPKTKVCTHCPGTAGKRCCELDDGYFGDP 815
QY 781 LGSNGPVLRCPCQCNIDNPNAVGNCLTGECLKCIYNTAGFYCDRCCKEGFFGNPLAP 840
Db 816 LGRNGPVLRCPCQCNIDNPNAVGNCLTGECLKCIYNTAGFYCDRCCKEGFFGNPLAP 875
QY 841 NPADKCKACACN-YGTVQQSSCNPVITGQCCPLPHVSGRDCGTCDPYNQLQSGQGCERC 899
Db 876 NPADKCKACACN-PYGTWKQSSCNPVITGQCCPLPHVSGRDCGTCDPYNQLQSGQGCERC 935
QY 900 DCHALGSTNGQCDIRTGQCECPGITGQHCERCETNHFHFGPEGKPCDCHHEGSLSLQC 959
Db 936 DCHALGSTNGQCDIRTGQCECPGITGQHCERCETNHFHFGPEGKPCDCHHEGSLSLQC 995
QY 960 KDDGRCECREGFGVGNRCDQCEENYFYNRSWPGQCECPACYRLVKDAAEHVRVKLQLESL 1019
Db 996 KDDGRCECREGFGVGNRCDQCEENYFYNRSWPGQCECPACYRLVKDAAEHVRVKLQLESL 1055
QY 1020 IANLGTGDDMTDQAFEDRLKEAREVTDLLEAQQVQKVDQNLMDRLQVNSLSHSQIS 1079
Db 1056 IANLGTGDDMTDQAFEDRLKEAREVTDLLEAQQVQKVDQNLMDRLQVNSLSHSQIS 1115
QY 1080 RLQNIIRNTIETGILAEARARSRVESTEQILIEIASRELEKAKM-AANVSITQPESTGEPNN 1138
Db 1116 RLQNIIRNTIETGILAEARARSRVESTEQILIEIASRELEKAKM-AANVSITQPESTGEPNN 1175
QY 1139 MTLAEEARRLAERHKEADDIRVAKTANETSABAYNLLRLTAGENOTALEIEELNRK 1198
Db 1176 MTLAEEARRLAERHKEADDIRVAKTANETSABAYNLLRLTAGENOTALEIEELNRK 1235
QY 1199 YEOAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAAD 1258
Db 1236 YEOAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAAD 1295
QY 1259 LDRIDQKLKDYEDLREDMRGKEHEVKNLLEKGAEQQTADQLLARADAALAEAAK 1318
Db 1296 LDRIDQKLKDYEDLREDMRGKEHEVKNLLEKGAEQQTADQLLARADAALAEAAK 1355
QY 1319 GRSTLQEAANDILNLDKDFRRVNDNKTAAEEALRIPAINRTIAEANEKTRQAQALGNA 1378
Db 1356 GRSTLQEAANDILNLDKDFRRVNDNKTAAEEALRIPAINRTIAEANEKTRQAQALGNA 1415

QY	1379	AADATEAKNKAHEAERIASAAQKATSTKADAERTFGEVTDLDNEVNGMLRQLBEEAENEL	1438
Db	1416	AADATEAKNKAHEAERIASAVQKNATSTKAEARTFAEVTDLDDNEVNNMLKQLQEAKEKL	1475
QY	1439	KRKQDDADQDDMMAGMASQAAQEAELNARKAKNSVSSLLSQLNLLDQLGOLDTVDLNKL	1498
Db	1476	KRKQDDADQDDMMAGMASQAAQEAELNARKAKNSVTSLLSIINDLLEQLGOLDTVDLNKL	1535
QY	1499	NEIEGSLNKAQDEMKASDLDRKVSQDLESEARKQEAATMDYNRDAEIIKDINHLEDIKKT	1558
Db	1536	NEIEGTLNKAQDEMKVSDLRKVSQDLENEAKQEAATMDYNRDIIEEIMKDIRNLEDIRKT	1595
QY	1559	LPTGCFNTPSIEKP	1572
Db	1596	LPSGCFNTPSIEKP	1609

RESULT 14

ABB81594
ID ABB81594 standard; protein; 1609 AA.

AC ABB81594;

19-SEP-2002 (first entry)

Human laminin 10 third chain protein sequence SEO ID NO:14.

KW Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;
 KW tissue repair development; laminin; healing; vascular tissue;
 KW re-endothelialisation; vascular injury; cell attachment; cell stasis;
 KW proliferation; migration.

xx
OS
Homo sapiens.

XX	Key	Location/Qualifiers
FH		

Key	Peptide	Score
FT		1.33

```

FT
label= signal

```

FT	Protein	34. .1609
FT		

FT
/label= laminin 10 third chain

PN WO200250111-A2.

27-JUN-2002.

21-DEC-2001: 2001WO-US051035.

21-DEC-2000: 2000US-0257449P.

28--MAR-2001: 2001US-0279282P.

PR 13-NOV-2001; 2001US-00279282.

PA (BIOS-) BIOSTRATUM INC.

PI Trygvasson K, Doi M, Thyboll J;

DR WPI: 2002-557650/59.

DR N-PSDB; ABQ72912.

New human laminin-10 proteins, useful for accelerating the healing of vascular tissue, improving the biocompatibility of grafts, or for promoting re-endothelialization at the site of vascular injuries.

xx Claim 9: Page 165-170: 231pp: English. PS

The present invention describes human laminin alpha 5. Also described is an isolated laminin 10. Laminin 10 has vulnerary activity. Laminins are useful in maintaining cell/tissue phenotype as well as promoting cell growth and differentiation in tissue repair development. Specifically, laminin 10 can be used for accelerating the healing injuries of vascular tissue, improving the biocompatibility of grafts useful for treating such injuries, for promoting re-endothelialisation at the site of vascular injuries, and promote cell attachment and subsequent cell stasis, proliferation, differentiation, and/or migration. The present sequence

QY 960 KDDGRCECEGFGVNRCDQCEENYFYNSWPGQCECPACRYLVKDKAAEHRVKLQLESL 1019
Db 996 KDDGRCECEGFGVNRCDQCEENYFYNSWPGQCECPACRYLVKDKVADHRVKLQLESL 1055
QY 1020 IANLGTGDDMTDQAFEDRLKEAEREVTDLLEAQAQVVDQNLMDRLQVNSSLHSQIS 1079
Db 1056 IANLGTGDDMTDQAFEDRLKEAEREVTDLLEAQAQVVDQNLMDRLQVNSSLHSQIS 1115
QY 1080 RLQNIIRNTIETGILAEARSRVSTEOLEIETASRELEKAKM-AANVSITQPESTGPN 1138
Db 1116 RLQNIIRNTIETGILAEARSRVSTEOLEIETASRELEKAKM-AANVSITQPESTGPN 1175
QY 1139 MTLAEEARRLAERHKEADDIRVAKTANETSAAEYNLLRTLAGENOTALTEBELNRK 1198
Db 1176 MTLAEEARRLAERHKEADDIRVAKTANETSAAEYNLLRTLAGENOTALTEBELNRK 1235
QY 1199 YEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAD 1258
Db 1236 YEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAD 1295
QY 1259 LDRIDQKLKDYEDLREDMRGKEHEVKNLLEKGAEQQTADQOLLARADAALAEAEAKK 1318
Db 1296 LEQIDQKLKDYEDLREDMRGKEHEVKNLLEKGAEQQTADQOLLARADAALAEAEAKK 1355
QY 1319 GRSTLQEAANDILNLLKDFDRRVNDNKTAAEALRRIPAINRTIAEANEKTRAEALGNA 1378
Db 1356 GRSTLQEAANDILNLLKDFDRRVNDNKTAAEALRRIPAINRTIAEANEKTRAEALGNA 1415
QY 1379 AADATEAKNKAHEAERIAAQAQKATSTKADAERTFGEVTDLDNEVNGMLPQLEAEENEL 1438
Db 1416 AADATEAKNKAHEAERIAAQAQKATSTKADAERTFGEVTDLDNEVNGMLPQLEAEENEL 1475
QY 1439 KRKQDDADQDMMAGMASQAQAQEAELNARKAKNSVSSLLSQNLNLLDQLGQDLDVNLKL 1498
Db 1476 KRKQDDADQDMMAGMASQAQAQEAELNARKAKNSVSSLLSQNLNLLDQLGQDLDVNLKL 1535
QY 1499 NEIEGSLNKAHEAEMKASDLDRKVSLESEARKQEAAMIDYNRDIAEIIKDIHNLEDIKT 1558
Db 1536 NEIEGSLNKAHEAEMKASDLDRKVSLESEARKQEAAMIDYNRDIAEIIKDIHNLEDIKT 1595
QY 1559 LPTGCENTPSIEKP 1572
Db 1596 LPTGCENTPSIEKP 1609

RESULT 15

ADC01887
ID ADC01887 standard; protein; 1609 AA.
XX AC ADC01887;
AC AC
DT 18-DEC-2003 (first entry)
XX DE Human laminin gamma 1 subunit.
XX KW Cytostatic; human; ds; gene; laminin; tumour; laminin-x; beta3 subunit;
XX KW gamma1 subunit; alpha4 subunit; angiogenesis.
XX OS Homo sapiens.
XX US2003103975-A1.
XX PD 05-JUN-2003.
XX PF 18-NOV-2002; 2002US-00299058.
XX PR 03-NOV-1999; 99US-0163199P.
XX PR 03-NOV-2000; 2000US-00706235.
XX PA (JONE/) JONES J C R.
XX PA (GONZ/) GONZALES M.
PI Jones JCR, Gonzales M;

XX WPI; 2003-755217/71.
DR N-PSDB; ADC01886.
XX Antigenic fragment of alpha4 laminin, useful for preparing a composition for treating tumor.
PT Disclosure; Page 42-46; 52pp; English.
XX The invention relates to an antigenic fragment of the human alpha4 laminin subunit appearing as ADC01881. Also included are a chimeric and/or fusion protein comprising the antigenic fragment, an antibody to the antigenic fragment, a cell line that produces the antibody, an isolated laminin complex (laminin-x, comprising an alpha4 subunit, a beta3 subunit or gamma1 subunit), modulating angiogenesis and a method of inducing tumours. The antigenic fragment of alpha4 laminin subunit is useful for preparing a composition (e.g. the antibody 2A3) for treating a tumour. The present sequence represents the human gamma 1 laminin subunit.
XX SQ Sequence 1609 AA;

Query Match 94.3%; Score 8038; DB 7; Length 1609;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;

QY 1 AMDECADEGGRPORCMPEFVNAAFNVTVATNTCGTPPEEYCVQGTGVTKSKHLCDAAG 60
Db 36 AMDECTDEGGRPORCMPEFVNAAFNVTVATNTCGTPPEEYCVQGTGVTKSKHLCDAAG 95
QY 61 QOHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYVNSINLTLHLGKAFDITYVRLKPHTS 120
Db 96 QOHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYVNSINLTLHLGKAFDITYVRLKPHTS 155
QY 121 RPESFAIYKRTREDGPWIPYQYISGSCENTYSKANRGFIRTGDEQQAALCTDEFSDISPL 180
Db 156 RPESFAIYKRTREDGPWIPYQYISGSCENTYSKANRGFIRTGDEQQAALCTDEFSDISPL 215
QY 181 TGGNVAFTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSYYY 240
Db 216 TGGNVAFTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSYYY 275
QY 241 AISDFAVGGRCKNGHASECVKNEEDKLMCNCKHNTYGVDCCKLPFFNDRPWRATAES 300
Db 276 AISDFAVGGRCKNGHASECMKNEEDKLMCNCKHNTYGVDCCKLPFFNDRPWRATAES 335
QY 301 ASECLPCDCNCRSQECYFDPPELRYSTGHGCHCTNCRDNDGAKCERCRCRENFRLGNTEAC 360
Db 336 ASECLPCDCNCRSQECYFDPPELRYSTGHGCHCTNCRDNDGAKCERCRCRENFRLGNTEAC 395
QY 361 SPCHCSPVGSLSQDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSTDE 420
Db 396 SPCHCSPVGSLSQDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSTDE 455
QY 421 CNVETGRVCCKDNVEGFNCERCKPFFNLESNPKGCTPCFCFCHSSVCTNAVGYSVYDI 480
Db 456 CNVETGRVCCKDNVEGFNCERCKPFFNLESNPKGCTPCFCFCHSSVCTNAVGYSVYDI 515
QY 481 SSTFQIDEDGWRVEQORDGSEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYQ 540
Db 516 SSTFQIDEDGWRVEQORDGSEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYQ 575
QY 541 NLSFSFRVDRDRTRLSAEDLVLEGAGLRVSVPVLIAGNSYPSSETTVKYIFRLHEATDYPW 600
Db 576 NLSFSFRVDRDRTRLSAEDLVLEGAGLRVSVPVLIAGNSYPSSETTVKYIFRLHEATDYPW 635
QY 601 RPALSPFEFQKLLNLTSLIKIRGTYSERSAGYLDVTLQARPGPGVPATWVESCPCPVG 660
Db 636 RPALSPFEFQKLLNLTSLIKIRGTYSERSAGYLDVTLQARPGPGVPATWVESCPCPVG 695
QY 661 YGGQFCETCLPGYRRRETPLSGPSPCVLCTCNHSETCDPETGVCDNRDNTAGPHCEKCS 720
Db 696 YGGQFCETCLPGYRRRETPLSGPSPCVLCTCNHSETCDPETGVCDNRDNTAGPHCEKCS 755

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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:28 ; Search time 43.5393 Seconds
(without alignments)
11631.021 Million cell updates/sec

Title: US-10-037-182-18
Perfect score: 8694
Sequence: 1.MTGGRAALALQPRGLWPL.....EDIKKTLFTGCFNTPSIEKP 1605

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6159	70.8	1593	13 Q8JHV8	Q8jvh8 brachydanio
2	4704	54.1	1007	13 Q90ZN3	Q90zn3 gallus gall
3	3538.5	40.7	1623	5 Q9U3U7	Q9u3u7 anopheles g
4	2583.5	29.7	1196	6 Q867A2	Q867a2 canis famil
5	2579.5	29.7	1190	6 Q8HZI9	Q8hzi9 equus cabal
6	1719.5	19.8	1785	13 Q8JHV7	Q8jvh7 brachydanio
7	1697.5	19.5	529	4 Q8N2D6	Q8n2d6 homo sapien
8	1669.5	19.2	1792	13 O57484	O57484 gallus gall
9	1638	18.8	351	11 P97552	P97552 rattus norv
10	1632	18.8	3102	5 O45614	O45614 caenorhabdi
11	1630	18.7	1761	4 Q86XN2	Q86xn2 homo sapien
12	1549	17.8	1799	11 Q8ROY0	Q8roy0 mus musculu
13	1502.5	17.3	2731	5 Q9VJT5	Q9vjt5 drosophila
14	1502.5	17.3	3367	5 Q9XZC9	Q9xzc9 drosophila
15	1502.5	17.3	3375	5 Q8IP51	Q8ip51 drosophila
16	1482.5	17.1	1827	13 Q8JHV6	Q8jvh6 brachydanio

17	1464	16.8	1631	4 Q9Y6U6	Q9y6u6 homo sapien
18	1458	16.8	3712	5 Q9VRW0	Q9vrw0 drosophila
19	1415	16.3	319	4 Q96BH6	Q96bh6 homo sapien
20	1384	15.9	3704	5 P91904	P91904 caenorhabdi
21	1355.5	15.6	3695	4 Q8TDF8	Q8tdf8 homo sapien
22	1173	13.5	1168	5 Q967S8	Q967s8 schistocerc
23	1164.5	13.4	604	11 Q924Z9	Q924z9 rattus norv
24	1139.5	13.1	603	13 O42140	O42140 brachydanio
25	1135.5	13.1	569	13 O57339	O57339 xenopus lae
26	1129.5	13.0	602	13 O42203	O42203 brachydanio
27	1127.5	13.0	1026	5 Q8SWY0	Q8swy0 drosophila
28	1116.5	12.8	464	11 Q619A5	Q619a5 mus musculu
29	1107.5	12.7	1069	5 Q9BPS2	Q9bps2 bombyx mori
30	1081.5	12.4	1086	4 Q8TAS6	Q8tas6 homo sapien
31	1078.5	12.4	1067	5 O44565	O44565 caenorhabdi
32	1073.5	12.3	555	5 Q9NFW6	Q9nfw6 branchiosto
33	1041.5	12.0	1546	4 Q9NS27	Q9ns27 homo sapien
34	1037.5	11.9	1546	4 O75445	O75445 homo sapien
35	1029	11.8	610	5 O96659	O96659 hirudo medi
36	1003.5	11.5	1461	11 Q9JLP3	Q9jlp3 mus musculu
37	977.5	11.2	984	11 Q8K271	Q8k271 mus musculu
38	970.5	11.2	1512	11 Q8K3K1	Q8k3k1 rattus norv
39	950.5	10.9	1486	4 O14637	O14637 homo sapien
40	926.5	10.7	695	11 Q8C9J2	Q8c9j2 mus musculu
41	924	10.6	1168	11 Q91V90	Q91v90 mus musculu
42	903	10.4	911	11 Q9CRX6	Q9crx6 mus musculu
43	871	10.0	667	5 Q9VY25	Q9vy25 drosophila
44	858	9.9	580	4 O00634	O00634 homo sapien
45	858	9.9	580	11 Q9RIA3	Q9ria3 mus musculu

ALIGNMENTS

RESULT 1
Q8JHV8
ID Q8JHV8 PRELIMINARY; PRT; 1593 AA.
AC Q8JHV8;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Laminin gamma 1.
GN LAMC1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22065263; PubMed=12070089;
RA Parsons M.J., Pollard S.M., Saude L., Feldman B., Coutinho P.,
RA Hirst E.M., Stemple D.L.;
RT "Zebrafish mutants identify an essential role for laminins in
RT notochord formation."
RL Development 129:3137-3146(2002).
DR EMBL; AF468048; AAM61766.1; -.
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR000034; Laminin B.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR008211; LamNT.
DR InterPro; IPR008212; Lam_N2.
DR Pfam; PF00052; laminin_B; 1.
DR Pfam; PF00053; laminin_EGF; 10.
DR Pfam; PF00055; laminin_Nterm; 1.
DR PRINTS; PR00011; EGFLAMININ.
DR ProDom; PD002082; Lam_N2; 1.
DR SMART; SM00180; EGF_Lam; 11.
DR SMART; SM00281; LamB; 1.
DR SMART; SM00136; LamNT; 1.
DR PROSITE; PS00022; EGF_1; 7.

Query Match		99.2%;	Score 8627;	DB 1;	Length 1607;	
Best Local Similarity		99.4%;	Pred. No. 7.6e-318;			
Matches 1598;		Conservative	2;	Mismatches	5;	
		Indels		2;	Gaps	2;
Qy	1	MTGGRAALALQPRGLWPLLAVALAAGCVRAAMDECADEGGRPQRCMPEFVNAAFNV	60			
Db	1	MTGGRAALALQPRGLWPLLAVALAAGCVRAAMDECADEGGRPQRCMPEFVNAAFNV	60			
Qy	61	VVATNTCGTPPEEYCVQGTGVTGKSCHLCLDAGQQHLQHGAAFLT	120			
Db	61	VVATNTCGTPPEEYCVQGTGVTGKSCHLCLDAGQQHLQHGAAFLT	120			
Qy	121	MLAGVQYPNSINLTLLHKGAFDITYVRLKFHTSRPESFAIYKRTREDGPWIPYQY	180			
Db	121	MLAGVQYPNSINLTLLHKGAFDITYVRLKFHTSRPESFAIYKRTREDGPWIPYQY	180			
Qy	181	ENTYSKANRGFIRTTGGDEQQALCTDEFSDISPLTGGNVAESTLEGRPSAYNF	240			
Db	181	ENTYSKANRGFIRTTGGDEQQALCTDEFSDISPLTGGNVAESTLEGRPSAYNF	240			
Qy	241	WVTATDIRVTNRLNLTGDEVFENDPKVLKSYYYAISDFAVGGRCKCNHGASECV	300			
Db	241	WVTATDIRVTNRLNLTGDEVFENDPKVLKSYYYAISDFAVGGRCKCNHGASECV	300			
Qy	301	LMCNCKNTYGVDCCKLPLFFNDRPWRRTAESAESCLPCDCNGRSQECYFDP	360			
Db	301	LMCNCKNTYGVDCCKLPLFFNDRPWRRTAESAESCLPCDCNGRSQECYFDP	360			
Qy	361	HGGHCTNCRDNTDGAKCERCENFFRLGNTEACSPCHCSPVGSLSLSTQCD	420			
Db	361	HGGHCTNCRDNTDGAKCERCENFFRLGNTEACSPCHCSPVGSLSLSTQCD	420			
Qy	421	MGDKCDRCQPGFHSLSLEAGCRPCSDPSGSTDECNVETGRVCCKDNVEGFNC	480			
Db	421	MGDKCDRCQPGFHSLSLEAGCRPCSDLRGSTDECNVETGRVCCKDNVEGFNC	480			
Qy	481	NLESSNPKGCTPCFCFGHSSVCTNAVGSYVDISSTFQIDEDGWRVEQRDG	540			
Db	481	NLESSNPKGCTPCFCFGHSSVCTNAVGSYVDISSTFQIDEDGWRVEQRDG	540			
Qy	541	DRQYIAVISDSYFPRYFIAPVKFLGNQVLSYQNLSPFRVDRDRTRLSEAED	600			
Db	541	DRQYIAVISDSYFPRYFIAPVKFLGNQVLSYQNLSPFRVDRDRTRLSEAED	600			
Qy	601	RVSVPPLIAQNSYSPSETTVKYIFRLHEATDYPWRPALSPFEFQKLLNLT	660			
Db	601	RVSVPPLIAQNSYSPSETTVKYIFRLHEATDYPWRPALSPFEFQKLLNLT	660			
Qy	661	RSAGYLDVTLQSAARPGVPATWVESCTCPVGYGGQFCETCLPGYRRET	720			
Db	661	RTAGYLDVTLQSAARPGVPATWVESCTCPVGYGGQFCETCLPGYRRET	720			
Qy	721	LCTCNHSETCDPBTGVCDNRNTAGPHCEKCSGSDGYVGDSTLTGTSSDC	780			
Db	721	LCTCNHSETCDPBTGVCDNRNTAGPHCEKCSGSDGYVGDSTLTGTSSDC	780			
Qy	781	IVPKTKVVCTHCTGTAGKRCCLCDDGYFGDPLGSDNGVPVRLCRPCQCN	840			
Db	781	IVPKTKVVCTHCTGTAGKRCCLCDDGYFGDPLGSDNGVPVRLCRPCQCN	840			
Qy	841	NRLTGECLKCIYNTAGFYCDRCKEGFFGNPLAPNPADKCKACACN-YGT	899			
Db	841	NRLTGECLKCIYNTAGFYCDRCKEGFFGNPLAPNPADKCKACACNPGY	900			
Qy	900	GQCQLPHVSGRDCGTCDPGYINLSQGGCERCDCCHALGSTNGQCDIRT	959			
Db	901	GQCQLPHVSGRDCGTCDPGYINLSQGGCERCDCCHALGSTNGQCDIRT	960			
Qy	960	QHCCERCETNHFVFGPEGCKPCDCHHEGSLSLQCKDDGRCECREGVGN	1019			
Db	961	QHCCERCETNHFVFGPEGCKPCDCHHEGSLSLQCKDDGRCECREGVGN	1020			

QY	1020	RSWPGCQCECPACYRLVKDKAAEHRVKLQLESLIANLTGDDMTDQAFEDRLKEAREV	1079
Db	1021	RSWPGCQCECPACYRLVKDKAAEHRVKLQLESLIANLTGDDMTDQAFEDRLKEAREV	1080
QY	1080	TDLLREAQEVKVDQNLMDRLQRVNSSLHSQISRLQINRTIETGILAEARARSERVE	1139
Db	1081	TDLLREAQEVKVDQNLMDRLQRVNSSLHSQISRLQINRTIETGILAEARARSERVE	1140
QY	1140	OLIEIASRELEKAKM-AANVSITQPESTGEPNNMTLLAEARLARAEHKKQAEADDIVRVAK	1198
Db	1141	OLIEIASRELEKAKM-AANVSITQPESTGEPNNMTLLAEARLARAEHKKQAEADDIVRVAK	1200
QY	1199	TANETSAEAYNLLRLTLAGENQTALEIEELNRKYEQAQKNSIQLEKQAARVHEEAKRAGD	1258
Db	1201	TANETSAEAYNLLRLTLAGENQTALEIEELNRKYEQAQKNSIQLEKQAARVHEEAKRAGD	1260
QY	1259	KAVEIYASVAQLTPVDSEALENEANKIKKEAADLRLIDQKLKDYEDLREDMRGKEHEVK	1318
Db	1261	KAVEIYASVAQLTPVDSEALENEANKIKKEAADLRLIDQKLKDYEDLREDMRGKEHEVK	1320
QY	1319	NLLEKGAEOQTADQLLARADAALAEAAKGRSTLQEAANDILNNLKDFDRRVNDNKT	1378
Db	1321	NLLEKGAEOQTADQLLARADAALAEAAKGRSTLQEAANDILNNLKDFDRRVNDNKT	1380
QY	1379	AAEEALRRIPAINRTIAEANETREAOALGNAADAATAEKNAKHAHEAERIAASAAQKNATS	1438
Db	1381	AAEEALRRIPAINRTIAEANETREAOALGNAADAATAEKNAKHAHEAERIAASAVQKNATS	1440
QY	1439	TKADAERTFGEVTDLDNEVNGMLRQLEEAENELKQKQDDADQDMMAGMASQAAQAEELN	1498
Db	1441	TKADAERTFGEVTDLDNEVNGMLRQLEEAENELKQKQDDADQDMMAGMASQAAQAEELN	1500
QY	1499	ARKAKNSVSSLLSQNLNLLDQLGQDLDVNLKNEIEGSLNKADEMKAASDLDRKVSLE	1558
Db	1501	ARKAKNSVSSLLSQNLNLLDQLGQDLDVNLKNEIEGSLNKADEMKAASDLDRKVSLE	1560
QY	1559	SEARKQEAALMDYNRDIAEIIKDIHNLEDIKKTLPFGCFNTPTSEKP	1605
Db	1561	SEARKQEAALMDYNRDIAEIIKDIHNLEDIKKTLPFGCFNTPTSEKP	1607

RESULT 2

LMG1_HUMAN	
ID	LMG1_HUMAN
AC	P11047
DT	01-JUL-1989 (Rel. 11, Created)
DT	01-NOV-1991 (Rel. 20, Last sequence update)
DT	15-MAR-2004 (Rel. 43, Last annotation update)
DE	Laminin gamma-1 chain precursor (laminin B2 chain).
GN	LAMC1 OR LAMB2.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=91093128; PubMed=1985895;
RA	Kallunki T., Ikonen J., Chow L.T., Kallunki P., Tryggvason K.;
RT	"Structure of the human laminin B2 chain gene reveals extensive
RT	divergence from the laminin B1 chain gene.";
RL	J. Biol. Chem. 266:221-228(1991).
RN	[2]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=88198245; PubMed=3360804;
RA	Pikkarainen T., Kallunki T., Tryggvason K.;
RT	"Human laminin B2 chain. Comparison of the complete amino acid
RT	sequence with the B1 chain reveals variability in sequence homology
RT	between different structural domains.";
RL	J. Biol. Chem. 263:6751-6758(1988).
RN	[3]
RP	SEQUENCE OF 1393-1609 FROM N.A.
RX	MEDLINE=89169663; PubMed=3234037;
RA	Fukushima Y., Pikkarainen T., Kallunki T., Eddy R.L., Byers M.G.,

RA Haley L.L., Henry W.M., Tryggvason K., Shows T.B.;
RT "Isolation of a human laminin B2 (LAMB2) cDNA clone and assignment of
RT the gene to chromosome region 1q25-->q31.";
RL Cytogenet. Cell Genet. 48:137-141(1988).
RN [4]
RP SEQUENCE OF 1282-1609 FROM N.A.
RC TISSUE=Endothelial cells;
RX MEDLINE=92216129; PubMed=1806043;
RA Santos C.L.S., Sabaga J., Brentani R.;
RT "Differences in human laminin B2 sequences.";
RL DNA Seq. 1:275-277(1991).
RN [5]
RP CARBOHYDRATE-LINKAGE SITE ASN-650.
RX MEDLINE=22660472; PubMed=12754519;
RA Zhang H., Li X.-J., Martin D.B., Aebersold R.;
RT "Identification and quantification of N-linked glycoproteins using
RT hydrazide chemistry, stable isotope labeling and mass spectrometry.";
RL Nat. Biotechnol. 21:660-666(2003).
CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components.
CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC different polypeptide chains (alpha, beta, gamma), which are bound
CC to each other by disulfide bonds into a cross-shaped molecule
CC comprising one long and three short arms with globules at each
CC end. The gamma-1 chain is a subunit of laminin-1 (BHS laminin),
CC laminin-2 (merosin), laminin-3 (S-laminin), laminin-4 (S-merosin),
CC laminin-6 (K-laminin) and laminin-7 (KS-laminin).
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Found in the basement membranes (major
CC component).
CC -!- DOMAIN: The alpha-helical domains I and II are thought to interact
CC with other laminin chains to form a coiled coil structure.
CC -!- DOMAIN: Domains VI and IV are globular.
CC -!- SIMILARITY: Contains 1 laminin N-terminal domain.
CC -!- SIMILARITY: Contains 11 laminin EGF-like domains.
CC -!- SIMILARITY: Contains 1 laminin IV domain.

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CC or send an email to license@isb-sib.ch).

DR EMBL; M55210; AAA59492.1; JOINED.
DR EMBL; M55217; AAA59492.1; JOINED.
DR EMBL; M55201; AAA59492.1; JOINED.
DR EMBL; M55211; AAA59492.1; JOINED.
DR EMBL; M55212; AAA59492.1; JOINED.
DR EMBL; M55213; AAA59492.1; JOINED.
DR EMBL; M55214; AAA59492.1; JOINED.
DR EMBL; M55215; AAA59492.1; JOINED.
DR EMBL; M55216; AAA59492.1; JOINED.
DR EMBL; M55192; AAA59492.1; JOINED.
DR EMBL; M55193; AAA59492.1; JOINED.
DR EMBL; M55194; AAA59492.1; JOINED.
DR EMBL; M55195; AAA59492.1; JOINED.
DR EMBL; M55196; AAA59492.1; JOINED.
DR EMBL; M55197; AAA59492.1; JOINED.
DR EMBL; M55198; AAA59492.1; JOINED.
DR EMBL; M55199; AAA59492.1; JOINED.
DR EMBL; M55200; AAA59492.1; JOINED.
DR EMBL; M55202; AAA59492.1; JOINED.
DR EMBL; M55203; AAA59492.1; JOINED.
DR EMBL; M55204; AAA59492.1; JOINED.
DR EMBL; M55205; AAA59492.1; JOINED.
DR EMBL; M55206; AAA59492.1; JOINED.
DR EMBL; M55207; AAA59492.1; JOINED.
DR EMBL; M55208; AAA59492.1; JOINED.
DR EMBL; M55209; AAA59492.1; JOINED.

DR EMBL; J03202; AAA59488.1; --
DR EMBL; M27654; AAA59489.1; --
DR EMBL; X13939; CAA32122.1; --
DR PIR; S13548; MMHUB2.
DR HSSP; P02468; 1TLE.
DR Genew; HGNC:6492; LAMC1.
DR MIM; 150290; --
DR GO; GO:0005604; C:basement membrane; TAS.
DR GO; GO:0007492; P:embryonic development; TAS.
DR GO; GO:0006461; P:protein complex assembly; TAS.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR008212; Lam_N2.
DR InterPro; IPR000034; Laminin_B.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR008211; LamNT.
DR Pfam; PF00052; laminin_B; 1.
DR Pfam; PF00053; laminin_EGF; 9.
DR Pfam; PF00055; laminin_Nterm; 1.
DR PRINTS; PR00011; EGF_LAMININ.
DR ProDom; PD002082; Lam_N2; 1.
DR SMART; SM00180; EGF_Lam; 8.
DR SMART; SM00281; LamB; 1.
DR SMART; SM00136; LamNT; 1.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 11.
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal; Polymorphism.
FT SIGNAL 1 33 LAMININ GAMMA-1 CHAIN.
FT CHAIN 34 1609 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 34 285 LAMININ EGF-LIKE 1.
FT DOMAIN 286 341 LAMININ EGF-LIKE 2.
FT DOMAIN 342 397 LAMININ EGF-LIKE 3.
FT DOMAIN 398 444 LAMININ EGF-LIKE 4.
FT DOMAIN 445 494 LAMININ EGF-LIKE 5 (N-TERMINAL).
FT DOMAIN 495 504 LAMININ DOMAIN IV.
FT DOMAIN 505 689 LAMININ EGF-LIKE 5 (C-TERMINAL).
FT DOMAIN 690 723 LAMININ EGF-LIKE 6.
FT DOMAIN 724 772 LAMININ EGF-LIKE 7.
FT DOMAIN 773 827 LAMININ EGF-LIKE 8.
FT DOMAIN 828 883 LAMININ EGF-LIKE 9.
FT DOMAIN 884 934 LAMININ EGF-LIKE 10.
FT DOMAIN 935 982 LAMININ EGF-LIKE 11.
FT DOMAIN 983 1030 LAMININ EGF-LIKE 11.
FT DOMAIN 1030 1609 DOMAIN II AND I.
FT DOMAIN 1038 1609 COILED COIL (POTENTIAL).
FT DISULFID 286 295 BY SIMILARITY.
FT DISULFID 288 305 BY SIMILARITY.
FT DISULFID 307 316 BY SIMILARITY.
FT DISULFID 319 339 BY SIMILARITY.
FT DISULFID 342 351 BY SIMILARITY.
FT DISULFID 344 367 BY SIMILARITY.
FT DISULFID 370 379 BY SIMILARITY.
FT DISULFID 382 395 BY SIMILARITY.
FT DISULFID 398 410 BY SIMILARITY.
FT DISULFID 400 416 BY SIMILARITY.
FT DISULFID 418 427 BY SIMILARITY.
FT DISULFID 430 442 BY SIMILARITY.
FT DISULFID 445 456 BY SIMILARITY.
FT DISULFID 447 463 BY SIMILARITY.
FT DISULFID 465 474 BY SIMILARITY.
FT DISULFID 477 492 BY SIMILARITY.
FT DISULFID 724 733 BY SIMILARITY.
FT DISULFID 726 740 BY SIMILARITY.
FT DISULFID 742 751 BY SIMILARITY.
FT DISULFID 754 770 BY SIMILARITY.
FT DISULFID 773 781 BY SIMILARITY.
FT DISULFID 775 792 BY SIMILARITY.
FT DISULFID 795 804 BY SIMILARITY.
FT DISULFID 807 825 BY SIMILARITY.
FT DISULFID 828 842 BY SIMILARITY.
FT DISULFID 830 849 BY SIMILARITY.
FT DISULFID 852 861 BY SIMILARITY.

FT	DISULFID	864	881	BY SIMILARITY.		
FT	DISULFID	884	898	BY SIMILARITY.		
FT	DISULFID	886	905	BY SIMILARITY.		
FT	DISULFID	907	916	BY SIMILARITY.		
FT	DISULFID	919	932	BY SIMILARITY.		
FT	DISULFID	935	947	BY SIMILARITY.		
FT	DISULFID	937	954	BY SIMILARITY.		
FT	DISULFID	956	965	BY SIMILARITY.		
FT	DISULFID	968	980	BY SIMILARITY.		
FT	DISULFID	983	995	BY SIMILARITY.		
FT	DISULFID	985	1001	BY SIMILARITY.		
FT	DISULFID	1003	1012	BY SIMILARITY.		
FT	DISULFID	1015	1028	BY SIMILARITY.		
FT	DISULFID	1031	1031	INTERCHAIN (PROBABLE).		
FT	DISULFID	1034	1034	INTERCHAIN (PROBABLE).		
FT	DISULFID	1600	1600	INTERCHAIN (PROBABLE).		
FT	CARBOHYD	60	60	N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	CARBOHYD	134	134	N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	CARBOHYD	576	576	N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	CARBOHYD	650	650	N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	CARBOHYD	1022	1022	N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	CARBOHYD	1107	1107	N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	CARBOHYD	1161	1161	N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	CARBOHYD	1175	1175	N-LINKED (GLCNAC. . .) (POTENTIAL).		
Query Match 93.7%; Score 8144; DB 1; Length 1609;						
Best Local Similarity 92.7%; Pred. No. 1.2e-299;						
Matches 1492; Conservative 59; Mismatches 54; Indels 4; Gaps 3						
QY	1	MTGGRAALALQPRGRLWPLLA	VL--AAVAGCVRAAMDECADEGGPQRCMPEFVNA	AFN 58		
Db	1	MRGSHRAAPALRPRGRLWPLA	VLAVLAAAAAGCAQAAMDECTDEGGPQRCMPEFVNA	AFN 60		
QY	59	VTVAATNTCGTPPEEYCVQIG	VTGVTKSHLCDAGQQHLQHGAAFLTDYNNQADTTW	QWS 118		
Db	61	VTVAATNTCGTPPEEYCVQIG	VTGVTKSHLCDAGQPHLQHGAAFLTDYNNQADTTW	QWS 120		
QY	119	QTMLAGVQYPSINLTLHLG	KAFDITYVRLKFHTSRPESFAIYKRTREDGPWIPYQY	YSG 178		
Db	121	QTMLAGVQYPSINLTLHLG	KAFDITYVRLKFHTSRPESFAIYKRTREDGPWIPYQY	YSG 180		
QY	179	SCENTYSKANRGFI	RTGGDEQQALCTDEFSDISPLTGGNVAFSTLEGRPSAYNF	DN	SPVL 238	
Db	181	SCENTYSKANRGFI	RTGGDEQQALCTDEFSDISPLTGGNVAFSTLEGRPSAYNF	DN	SPVL 240	
QY	239	QEWVTATDIRVTNRLNT	FGDEVNDPKVLKSYYYAISDFAVGGRCKNGHASECVK	NEF 298		
Db	241	QEWVTATDIRVTNRLNT	FGDEVNDPKVLKSYYYAISDFAVGGRCKNGHASECVK	NEF 300		
QY	299	DKLMCNCKHNTYGV	DCEKCLPFENDRPWRRATAESASECLPCDCNGRSQECY	FDP	PELYRS 358	
Db	301	DKLVNCNCKHNTYGV	DCEKCLPFENDRPWRRATAESASECLPCDCNGRSQECY	FDP	PELYRS 360	
QY	359	TGHGGHCTNCRDNT	DGAKCERCERNFRLGNTAACPCHCSPVGSLSLSTQCD	S	YGRCSCKP 418	
Db	361	TGHGGHCTNCRDNT	DGAHCERCERNFRLGNNEACSSCHCSPVGSLSLSTQCD	S	YGRCSCKP 420	
QY	419	GVMGDKCQCPGFH	SLTEAGCRPCSDPSGSTDECNVETGRVCVCKDNVEGF	NCER	CKPG 478	
Db	421	GVMGDKCQCPGFH	SLTEAGCRPCSDPSGSIDECNVETGRVCVCKDNVEGF	NCER	CKPG 480	
QY	479	FFNLESSNPKGCT	PCFCFGHSSVCTNAVGSYVDISSTFQIDEDGWRVEQ	RDG	SEASLEW 538	
Db	481	FFNLESSNPKGCT	PCFCFGHSSVCTNAVGSYVISSTFQIDEDGWRVEQ	RDG	SEASLEW 540	
QY	539	SSDRQYIAVISDS	YFPYFIAPVKFLGNQVLSYQONLSFSFRVDRDRTRL	SAED	LVLEGA 598	
Db	541	SSERQDIAVISDS	YFPYFIAPAKFLGKQVLSYQONLSFSFRVDRDRTRL	SAED	LVLEGA 600	
QY	599	GLRVSVP	LIAQGNPSYPSSETTVKYIFRLHEATDYPWRPALSP	FFEFQ	KLLNLT	TSIKIRGTY 658
Db	601	GLRVSVP	LIAQGNPSYPSSETTVKYIFRLHEATDYPWRPALTP	FEFQ	KLLNLT	TSIKIRGTY 660

QY	659	SERSAGY	DDVTLOSARPPGVPATWV	ESCTCPVGYGGQFCETCLPGYRRET	PSLGPYSP 718				
Db	661	SERSAGY	DDVTTLASARPPGVPATWV	ESCTCPVGYGGQFCMLSGYRRET	PNLGPYSP 720				
QY	719	CVLCTCNGHSET	CDPETGVCD	CRDNTAGPHCEKCS	DGYGDSLTGTSSDCQPCPCPGSS 778				
Db	721	CVLCA	CNGHSETCDPETGV	CNCRDNTAGPHCEKCS	DGYGDSLTGTSSDCQPCPCPGSS 780				
QY	779	CAIVPKTKEV	VCTHPTGTAGKRC	CLCDDGYFGDPLG	SNGPVRLCRPCQCNNDIDPNAVG 838				
Db	781	CAVVPKTKEV	VCTNCPTGTTGKRC	CLCDDGYFGDPLGR	NGPVRLCRLCQCSNDIDPNAVG 840				
QY	839	NCNRLTGE	CLKCIYNTAGFYCD	RCKEGFFGNPLAPNP	ADKCKACACN-YGTVQQSSCNP 897				
Db	841	NCNRLTGE	CLKCIYNTAGFYCD	RCKDGFNPLAPNP	ADKCKACACNPNYGTMKQQSSCNP 900				
QY	898	VTGQC	CLPHVSGRDCGTDPGY	NLQSGQGERCD	CHALGSTNGQCDIR	TGQCECQPGI 957			
Db	901	VTGQCE	CLPHVGTQDCGACDP	GFYNLQSGQGERCD	CHALGSTNGQCDIR	TGQCECQPGI 960			
QY	958	TGQH	CERCETNHF	GFPGEGKPCDCH	HEGSLQCKDDGRCE	REGFVGNRCDQCEENYF 1017			
Db	961	TGQH	CERCENVNHF	GFPGEGKPCDCH	PEGSLQCKDDGRCE	REGFVGNRCDQCEENYF 1020			
QY	1018	YNRSWPG	CQCEPACYRLVKD	AAEHRVKLQ	LESJANLGTGDDMTVDQAFEDRLKEAER 1077				
Db	1021	YNRSWPG	CQCEPACYRLVKD	KVADHRVKLQ	LESJANLGTGDEMVTVDQAFEDRLKEAER 1080				
QY	1078	EVTDL	LR	EAQEVKQV	DQNLMDRLQ	RVNSSLHSQISRLQ	NIRNTIETGILAEARARS	RVES 1137	
Db	1081	EVMDL	LR	EAQV	KQV	DQNLMDRLQ	RVNNTLSSQISRLQ	NIRNTIETGNLAEQARA	HVEN 1140
QY	1138	TEQL	IEIASRELEKAKM-AAN	VSITQPESTGE	PNMTLLAE	ARRLAERHKE	ADDIRV 1196		
Db	1141	TERL	IEIASRELEKAKVAA	ANVSITQPESTG	DPNMTLLAE	ARKLAERHKE	ADDIRV 1200		
QY	1197	AKTANETS	AEAYNLLRLTLAGENQ	TAL	EIEELNRKYEQAKNISQDLEKQ	AARVHEEAKRA 1256			
Db	1201	AKTANDT	STEAYNLLRLTLAGENQ	TAF	EIEELNRKYEQAKNISQDLEKQ	AARVHEEAKRA 1260			
QY	1257	GDKAVEI	YASVAQLTPVDSE	ALENEANKIKKEA	ADLRLIDQKLKYED	DLREDMRGKEHE 1316			
Db	1261	GDKAVEI	YASVAQLSP	LSDSETLENEANNIKMEAE	ENLEQLIDQKLKYED	DLREDMRGKELE 1320			
QY	1317	VKNLLEK	GKAEQOOTADQ	LLARADAAKALAE	AAKGRSTLOEANDIL	NNLKDFRRVNDN 1376			
Db	1321	VKNLLEK	GKTEQOOTADQ	LLARADAAKALAE	AAKGRDRTLOEANDIL	NNLKDFRRVNDN 1380			
QY	1377	KTAAEEA	LRRIPAINRTTAE	ANEKTRFAQLALG	NAAAADATEAKNKA	HEAERIA	ASAAQKNA 1436		
Db	1381	KTAAEEA	LRRIPAINQIT	EANEKTRFAQ	QAALGSAADATEAKNKA	HEAERIA	ASAVQKNA 1440		
QY	1437	TSTKADA	ERTFGEVTDL	NEVNGMLRQLEEA	ENELKRDQDADQD	MMAGMASQAAQAE 1496			
Db	1441	TSTKAEA	ERTFAEVTDL	NEVNNMLKQLEA	EKELKRDQDADQD	MMAGMASQAAQAE 1500			
QY	1497	LNARKAK	NSVSSLLSQLNNLLD	QLGOLDTVD	LNKLNEIEGSLNK	AKDEMKA	SDLDKRVSD 1556		
Db	1501	INARKAK	NSVTLSLSIIND	LLEQLGOLDTVD	LNKLNEIEGTLNK	AKDEMKV	SDLDKRVSD 1560		
QY	1557	LESEARK	QBAAIMDYNR	DAIEIHKDHN	LEDIKKTLPTGCFNTPSIEKP 1605				
Db	1561	LENEAK	QBAAIMDYNR	DAIEEIMKDIR	NLEDIRKTLPSGCFNTPSIEKP 1609				

RESULT 3
LMG3_HUMAN
ID_LMG3_HUMAN STANDARD; PRT; 1587 AA.
AC_Q9Y6N6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Laminin gamma-3 chain precursor (Laminin 12 gamma 3).

GN LAMC3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=99242614; PubMed=10225960;
RA Koch M., Olson P.F., Albus A., Jin W., Hunter D.D., Brunken W.J.,
RA Burgeson R.E., Champlaud M.F.;
RT "Characterization and expression of the laminin gamma3 chain: a novel,
RT non-basement membrane-associated, laminin chain.";
RL J. Cell Biol. 145:605-618(1999).
CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components.
CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC different polypeptide chains (alpha, beta, gamma), which are bound
CC to each other by disulfide bonds into a cross-shaped molecule
CC comprising one long and three short arms with globules at each
CC end. The gamma-3 chain is a subunit of laminin-12.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Broadly expressed in: skin, heart, lung, and
CC the reproductive tracts.
CC -!- DOMAIN: The alpha-helical domains I and II are thought to interact
CC with other laminin chains to form a coiled coil structure.
CC -!- DOMAIN: Domain IV is globular.
CC -!- SIMILARITY: Contains 1 laminin N-terminal domain.
CC -!- SIMILARITY: Contains 11 laminin EGF-like domains.
CC -!- SIMILARITY: Contains 1 laminin IV domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF041835; AAD36991.1; --
CC HSSP; P02468; 1TLE.
CC Genes; HGNC:6494; LAMC3.
CC MIM; 604349; --
CC GO; GO:0005578; C:extracellular matrix; TAS.
CC GO; GO:0016020; C:membrane; TAS.
CC GO; GO:0005198; F:structural molecule activity; TAS.
CC InterPro; IPR006209; EGF_like.
CC InterPro; IPR008212; Lam_N2.
CC InterPro; IPR000034; Laminin_B.
CC InterPro; IPR002049; Laminin_EGF.
CC InterPro; IPR008211; LamNT.
CC Pfam; PF00052; laminin_B; 1.
CC Pfam; PF00053; laminin_EGF; 9.
CC Pfam; PF00055; laminin_Nterm; 1.
CC PRINTS; PR00011; EGF_LAMININ.
CC ProDom; PD002082; Lam_N2; 1.
CC SMART; SM00180; EGF_Lam; 9.
CC SMART; SM00136; LamNT; 1.
CC PROSITE; PS00022; EGF_1; 7.
CC PROSITE; PS01186; EGF_2; 2.
CC PROSITE; PS01248; LAMININ_TYPE_EGF; 10.
CC Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
FT SIGNAL 1 19
FT CHAIN 20 1587
FT DOMAIN 20 270 LAMININ GAMMA-3 CHAIN.
FT DOMAIN 271 326 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 327 382 LAMININ EGF-LIKE 1.
FT DOMAIN 383 429 LAMININ EGF-LIKE 2.
FT DOMAIN 430 479 LAMININ EGF-LIKE 3.
FT DOMAIN 480 489 LAMININ EGF-LIKE 4.
FT LAMININ EGF-LIKE 5 (N-TERMINAL).

FT	DOMAIN	490	672	LAMININ DOMAIN IV.
FT	DOMAIN	673	706	LAMININ EGF-LIKE 5 (C-TERMINAL).
FT	DOMAIN	707	754	LAMININ EGF-LIKE 6.
FT	DOMAIN	755	809	LAMININ EGF-LIKE 7.
FT	DOMAIN	810	865	LAMININ EGF-LIKE 8.
FT	DOMAIN	866	916	LAMININ EGF-LIKE 9.
FT	DOMAIN	917	964	LAMININ EGF-LIKE 10.
FT	DOMAIN	965	1013	LAMININ EGF-LIKE 11.
FT	DOMAIN	1014	1587	DOMAIN II AND I.
FT	DOMAIN	1071	1141	COILED COIL (POTENTIAL).
FT	DOMAIN	1200	1229	COILED COIL (POTENTIAL).
FT	DOMAIN	1424	1504	COILED COIL (POTENTIAL).
FT	DOMAIN	1535	1579	COILED COIL (POTENTIAL).
FT	SITE	1059	1061	CELL ATTACHMENT SITE (POTENTIAL).
FT	CARBOHYD	87	87	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	119	119	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	295	295	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	328	328	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	631	631	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	837	837	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	980	980	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1185	1185	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1518	1518	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	1587 AA;	172051 MW;	3CB6E09B5F203319 CRC64;

Query Match 41.4%; Score 3596.5; DB 1; Length 1587;
Best Local Similarity 43.8%; Pred. No. 1.8e-128;
Matches 707; Conservative 258; Mismatches 571; Indels 77; Gaps 24;

QY	20	LLAVLA	AVAG	CVRA	AMDE	CADE	GGRR	QRCR	QCMF	EVNA	FNTV	VA	TNTC	GTTP	PEEY	CVQT	79								
Db	12	LLAPRA	AGAG	-----	MGAC	YD	GAGR	QRCR	CLPV	FENA	AFGR	LAQA	ASHT	CGSP	PEDE	FCPH	VG 66								
QY	80	VTGV	TKSCH	LCDA	GQHL	QHGA	FLTD	YNNQ	ADTT	WQSQ	TMLA	GVQY	NSIN	LT	HLGK	139									
Db	67	AAGA	GAHC	QRCDA	ADPQ	RHHN	ASYL	TDFH	SQDE	STWQ	SPSM	AFGV	QYFS	VN	ITRL	GLK 126									
QY	140	AFDITY	VRLK	FHTSR	PEFA	IYKRT	REDG	PWIP	YQY	SGSC	ENTY	SKAN	RGFI	RTG	GGDE	Q 199									
Db	127	AYEITY	VRLK	FHTSR	PEFA	IYKRS	RADG	PWIP	YQY	SGSC	ENTY	SKAN	RGFI	RTG	GGDE	R 186									
QY	200	QALCTD	EFSD	ISPL	TGNN	VAFST	LEGR	PSAY	NFDN	SPVL	QEWV	TATD	IRVT	LN	RLNT	FGD 259									
Db	187	VAPCT	SEFSD	ISPL	SGNN	VAFST	LEGR	PSAY	NFEES	PGLQ	EWVT	STELL	ISLD	RLNT	FGD 246										
QY	260	EVENDP	KVLK	SYYY	AI	SDFA	VGGRC	KCNH	ASCE	VKNF	EDKLM	CNKH	NTY	GV	DCEK	CLP 319									
Db	247	DIFKDP	KVLQ	SYYY	AV	SDFS	VGGRC	KCNH	ASCE	GP	DVAG	QACR	QHNT	TTG	DCEK	CLP 306									
QY	320	FFNDRP	WRRAT	AEAS	EC	LPDC	NCGR	SOEY	FDPB	LYRST	GHHG	CTNC	RNTD	GA	KCER	379									
Db	307	FFQDRP	WARG	TAEAA	HECL	PCNC	SGRSE	ECTF	DELF	FRST	GHHG	CHCR	HCDHT	AG	PHCER 366										
QY	380	CRENPF	RLGNT	EACSP	CHCS	PVGS	LSLST	QCDS	YGRCS	CKPG	VMGDK	CDRC	QCPG	FHSL	TEAG 439										
Db	367	CQENFY	HWDP	RMPC	QPCD	CQSAG	SLHL	QCDD	TGTG	CACT	PTVT	GWKCD	RC	LP	GFHSL	SEG 426									
QY	440	CRPCSD	PSGS	TDEC	NVET	RCVC	KDNV	EGFC	NKCP	GFN	LESSN	PKG	TCF	CF	FGHS 499										
Db	427	CRPCTC	NPAG	SLD	TCD	PRSG	RCPC	KENV	EGNL	CDRC	PRGT	FNLP	HN	PAGC	SCFC	YGHS 486									
QY	500	SVCTNA	VGYS	VYD	IS	STFQ	IDED	GW	VEQR	DGSE	ASLE	WSSD	RQYI	AVIS	DYF	PRYFIA 559									
Db	487	KVCAST	AQFQ	VHHIL	SDFH	QAGW	WARV	SGS	SEHSP	QWSP	N---	GVL	LSPE	DEE	EELTA 542										
QY	560	PVKFLG	NQVL	SYGN	LS	SPSF	RVDR	RRD	TRL	SAED	LV	EGAG	LRV	SVPL	IAQNS	YPS	ETTV 619								
Db	543	PGKFLG	DQRF	SYGQ	PL	IL	TRFV	PPG	DS	PL	VPQ	-	LR	EGT	GL	ALS--	LRHSSLSG	PQDARA 599							
QY	620	KYIFRL	H---	EATD	YP	WR	PAL	SP	FEFQ	KL	NN	LT	SI	K	IRGT	YS	ERSAG--	YLD	DDVT	LQSA 674					
Db	600	SQGRAQ	VPLQ	ET	SE	DV	AP	PL	PP	FF	FF	QRL	LAN	LT	SL	RL	VS	PG	SP	PAGV	FL	TE	VL	TS	A 659

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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:30:58 ; Search time 12.1415 Seconds
(without alignments)
6824.493 Million cell updates/sec

Title: US-10-037-182-18
Perfect score: 8694
Sequence: 1 MTGGRAALALQPRGLWPL.....EDIKTLPTGCFNTPSIEKP 1605

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	8694	100.0	1605	4	US-09-562-702A-30	Sequence 30, Appl
2	8694	100.0	1605	4	US-09-561-818A-26	Sequence 26, Appl
3	8527	98.1	1572	4	US-09-562-702A-32	Sequence 32, Appl
4	8527	98.1	1572	4	US-09-561-818A-28	Sequence 28, Appl
5	8148	93.7	1609	4	US-09-562-702A-22	Sequence 22, Appl
6	8148	93.7	1609	4	US-09-561-818A-22	Sequence 22, Appl
7	8148	93.7	1617	4	US-09-562-702A-26	Sequence 26, Appl
8	8043	92.5	1576	4	US-09-562-702A-24	Sequence 24, Appl
9	8043	92.5	1576	4	US-09-561-818A-24	Sequence 24, Appl
10	8043	92.5	1584	4	US-09-562-702A-28	Sequence 28, Appl
11	3596.5	41.4	1587	4	US-09-845-583A-10	Sequence 10, Appl
12	3596.5	41.4	1587	4	US-09-561-709B-3	Sequence 3, Appl
13	2591	29.8	1193	1	US-08-317-450B-13	Sequence 13, Appl
14	2591	29.8	1193	3	US-08-800-593-13	Sequence 13, Appl
15	2476.5	28.5	1111	1	US-08-317-450B-15	Sequence 15, Appl
16	2476.5	28.5	1111	3	US-08-800-593-15	Sequence 15, Appl
17	2306.5	26.5	1171	1	US-08-445-135-1	Sequence 1, Appl
18	1812.5	20.8	3106	4	US-09-562-702A-10	Sequence 10, Appl
19	1807.5	20.8	3084	4	US-09-562-702A-12	Sequence 12, Appl
20	1795.5	20.7	3110	4	US-09-562-702A-2	Sequence 2, Appl
21	1795.5	20.7	3110	4	US-09-562-702A-6	Sequence 6, Appl
22	1795.5	20.7	3110	4	US-09-561-709B-7	Sequence 7, Appl
23	1795	20.6	3111	2	US-08-460-309-4	Sequence 4, Appl
24	1795	20.6	3111	2	US-08-125-077-4	Sequence 4, Appl
25	1790	20.6	3088	4	US-09-562-702A-8	Sequence 8, Appl
26	1790	20.6	3089	4	US-09-562-702A-4	Sequence 4, Appl
27	1711	19.7	3075	2	US-08-460-309-5	Sequence 5, Appl

28	1711	19.7	3075	2	US-08-125-077-5	Sequence 5, Appl
29	1682	19.3	1786	4	US-09-562-702A-14	Sequence 14, Appl
30	1682	19.3	1786	4	US-09-561-818A-14	Sequence 14, Appl
31	1682	19.3	1786	4	US-09-561-709B-9	Sequence 9, Appl
32	1677	19.3	1765	4	US-09-562-702A-16	Sequence 16, Appl
33	1677	19.3	1765	4	US-09-561-818A-16	Sequence 16, Appl
34	1661.5	19.1	1786	4	US-09-562-702A-18	Sequence 18, Appl
35	1661.5	19.1	1786	4	US-09-561-818A-18	Sequence 18, Appl
36	1637.5	18.8	1725	4	US-09-562-702A-20	Sequence 20, Appl
37	1637.5	18.8	1725	4	US-09-561-818A-20	Sequence 20, Appl
38	1630	18.7	1761	4	US-09-561-709B-1	Sequence 1, Appl
39	1552	17.9	1799	4	US-09-845-583A-6	Sequence 6, Appl
40	1496	17.2	1798	4	US-09-561-709B-11	Sequence 11, Appl
41	1491	17.1	1798	4	US-09-845-583A-8	Sequence 8, Appl
42	1361	15.7	251	1	US-08-152-019A-37	Sequence 37, Appl
43	1351	15.5	252	2	US-08-460-309-12	Sequence 12, Appl
44	1351	15.5	252	2	US-08-125-077-12	Sequence 12, Appl
45	1347.5	15.5	3635	4	US-09-845-583A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-562-702A-30
; Sequence 30, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 1605
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-562-702A-30

Query Match 100.0%; Score 8694; DB 4; Length 1605;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1605; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MTGGRAALALQPRGLWPLLA	VLA	AAVAGCVRAAMDECADEGGRPQRCMPEFVNAAFNVT	60
Db	1	MTGGRAALALQPRGLWPLLA	VLA	AAVAGCVRAAMDECADEGGRPQRCMPEFVNAAFNVT	60
Qy	61	VVAINTCGTPPEEYCVQ	TGVTG	TKSCHLCDAGQOHLQHGA	120
Db	61	VVAINTCGTPPEEYCVQ	TGVTG	TKSCHLCDAGQOHLQHGA	120
Qy	121	MLAGVQYFNSINLT	HLGKAFDITY	VRLKFHTSRPESFAIYKRTREDGPWIPYQYISGSC	180
Db	121	MLAGVQYFNSINLT	HLGKAFDITY	VRLKFHTSRPESFAIYKRTREDGPWIPYQYISGSC	180
Qy	181	ENTYSKANRGFIR	TGGDEQOALCTDEF	SDISPLTGGNVAFSTLEGRPSAYNFNDSPLVQE	240
Db	181	ENTYSKANRGFIR	TGGDEQOALCTDEF	SDISPLTGGNVAFSTLEGRPSAYNFNDSPLVQE	240
Qy	241	WVTATDIRVT	LNRLNTFGDEVFNDP	KVLKSYYYAISDPFVAGGRCKCNHASECVKNEFDK	300
Db	241	WVTATDIRVT	LNRLNTFGDEVFNDP	KVLKSYYYAISDPFVAGGRCKCNHASECVKNEFDK	300

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Db 301 LMCNCKHNTYGVDCCKLPFFNDRPWRRTAESASECLPCDNCGRSQECYFDPPELYRSTG 360
QY 361 HGGHCTNCRDNTDGAKCERCENFFRLNGTEACSPCHCSPVGSLSSTQCDSSYGRCSCKPGV 420
Db 361 HGGHCTNCRDNTDGAKCERCENFFRLNGTEACSPCHCSPVGSLSSTQCDSSYGRCSCKPGV 420
QY 421 MGDKCDRCQPGFHSLTEAGCPCSDPSGSTDECNVETGRCVCKDNVEGFNCERCKPGFF 480
Db 421 MGDKCDRCQPGFHSLTEAGCPCSDPSGSTDECNVETGRCVCKDNVEGFNCERCKPGFF 480
QY 481 NLESSNPKGCTPCFCFGHSSVCTNAVGYSVYDISSTFQIDEDGWRVEQRDGSEASLEWSS 540
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QY 541 DRQYIAVISDSYFPRYFIAPVKFLGNQVLSYGQNLSPFRVDRDRTRLSEAEDLVLEGAGL 600
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QY 601 RVSVPILAQGNSYPSETTVKYIFRLHEATDYPWRPALSPFFEFQKLLNNLTSIKIRGTYSE 660
Db 601 RVSVPILAQGNSYPSETTVKYIFRLHEATDYPWRPALSPFFEFQKLLNNLTSIKIRGTYSE 660
QY 661 RSAGYLDVTLQSARPGVPATWVESCTCPVGYGGQCECTCLPGYRRETPLSPGYSPCV 720
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QY 721 LCTCNHSETCDPETGVCDNRDNTAGPHCEKCSGYYGDSLTGTSSDCQPCPCGGSSCA 780
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Db 841 NRLTGECLKIYNTAGFYCDRCKEGFFGNPLAPNPADKCKACACNYGTVOQSSCNPVTG 900
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QY 1261 VEIYASVAQLTPVDSEALENEANKIKKEAADLRLIDQKLKYEDLREDMRGKEHEVKNL 1320
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QY 1561 ARKQEAAIMDYNRDIAEIIKDHNLEDIKKTLPTGCFNTPSIEKP 1605
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RESULT 2

US-09-561-818A-26
; Sequence 26, Application US/09561818A
; Patent No. 6638907

; GENERAL INFORMATION:
; APPLICANT: Kortessmaa, Jarrko
; APPLICANT: Tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 26
; LENGTH: 1605
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-561-818A-26

Query Match 100.0%; Score 8694; DB 4; Length 1605;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1605; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MTGGGRAALALQPRGLWPLLAVALAAGCVRAAMDECADEGGRPQRCMPEFVNAAFNVT 60
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Db 121 MLAGVOYPNINLTLLHLGKAFDITVRLKFHTSRPESFAIYKRTREDGPWIPYQYSGSC 180
QY 181 ENTYSKANRGFIRTTGGDEQQALCTDEFSDISPLTGGNVAFTLEGRPSAYNFDNSPVLQE 240
Db 181 ENTYSKANRGFIRTTGGDEQQALCTDEFSDISPLTGGNVAFTLEGRPSAYNFDNSPVLQE 240
QY 241 WVTATDIRVTILNRLNTFGDEVFNDPKVLKSYYYAISDFAVGGRCKCNGHASECVKNEFDK 300
Db 241 WVTATDIRVTILNRLNTFGDEVFNDPKVLKSYYYAISDFAVGGRCKCNGHASECVKNEFDK 300
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Db 301 LMCNCKHNTYGVDCCKLPFFNDRPWRRTAESASECLPCDNCGRSQECYFDPPELYRSTG 360
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Db 361 HGGHCTNCRDNTDGAKCERCENFFRLNGTEACSPCHCSPVGSLSSTQCDSSYGRCSCKPGV 420
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Db 481 NLESSNPKGCTPCFCFGHSSVCTNAVGYSVYDIDISTFTQIDEDGWRVEQRDGESEASLEWSS 540
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Db 781 IVPKTKEVVCTHPTGTAGKRCCELDDGYFGDPLGSGNPVRLCRPCQNDNIDPNAVGN 840
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Db 841 NRLTGECLKCIYNTAGFYCDRCKEGFFGNPLAPNPADKCKACACNYGTVOQSSCNPV 900
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Db 901 QCQLPHVSGRDCGTCDPGYYNLQSGQGCRCDCCHALGSTNGQCDIRTGQCECQPGITG 960
QY 961 HECERCETNHFGFPEGCKPCDCHHEGSLSLQCKDDGRCECREGVGNRCDQCEENYFY 1020
Db 961 HECERCETNHFGFPEGCKPCDCHHEGSLSLQCKDDGRCECREGVGNRCDQCEENYFY 1020
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Db 1021 SWPGCQECPCYRLVKDKAAAEHRVKLQELSLANLGTGDDMTDQAFEDRLKEAERE 1080
QY 1081 DLLREAQEVKVDQNLMDRLQRVNSSLHSQISRLQINRNTIETGILAEARARSRVE 1140
Db 1081 DLLREAQEVKVDQNLMDRLQRVNSSLHSQISRLQINRNTIETGILAEARARSRVE 1140
QY 1141 LIEIASRELEKAKMAANYSITQESTGEPNNMTLLAEAEARRLAERHKQEAADDIVR 1200
Db 1141 LIEIASRELEKAKMAANYSITQESTGEPNNMTLLAEAEARRLAERHKQEAADDIVR 1200
QY 1201 NETSABAYNLLRLTLAGENQTALEIEELNRKYEQAKNISQDLEKQAARVHEEAKRAG 1260
Db 1201 NETSABAYNLLRLTLAGENQTALEIEELNRKYEQAKNISQDLEKQAARVHEEAKRAG 1260
QY 1261 VEIYASVAQLTPVDSEALENEANKIKKEAADLRLIDQKLKDYEDLREDMRGKEHEV 1320
Db 1261 VEIYASVAQLTPVDSEALENEANKIKKEAADLRLIDQKLKDYEDLREDMRGKEHEV 1320
QY 1321 LEKGKAEQQTADQLLAPADAALAEAAKKGSRSTLOEANDILNLLKDFDRRVNDNKTAA 1380
Db 1321 LEKGKAEQQTADQLLAPADAALAEAAKKGSRSTLOEANDILNLLKDFDRRVNDNKTAA 1380
QY 1381 BEALRRIPAINRTIAEANETREAOALALGNAADATEAKNKAHEAERIAAQAOKNATSTK 1440
Db 1381 BEALRRIPAINRTIAEANETREAOALALGNAADATEAKNKAHEAERIAAQAOKNATSTK 1440
QY 1441 ADAERTFGEVTDLDNEVNGMLRQLEEAENELKRQDDADQDMMAGMASQAAQAEELNAR 1500
Db 1441 ADAERTFGEVTDLDNEVNGMLRQLEEAENELKRQDDADQDMMAGMASQAAQAEELNAR 1500
QY 1501 KAKNSVSSLLSQLNNLLDQLGQDQTDVLDNKLNEIEGSLNKADEMKAASDLDRKVS 1560
Db 1501 KAKNSVSSLLSQLNNLLDQLGQDQTDVLDNKLNEIEGSLNKADEMKAASDLDRKVS 1560
QY 1561 ARKQEAAMDYNRDIAEIIKDIHNLEDIKKTLPTGCFNTPSIEKP 1605
Db 1561 ARKQEAAMDYNRDIAEIIKDIHNLEDIKKTLPTGCFNTPSIEKP 1605

RESULT 3
US-09-562-702A-32
; Sequence 32, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 1572
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-562-702A-32

Query Match 98.1%; Score 8527; DB 4; Length 1572;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 AMDECADEGGRPQRCMPEFVNAFNVVATNTCTGTPPEEYCVQGTGVTGTSCHLCLDAG 93
Db 1 AMDECADEGGRPQRCMPEFVNAFNVVATNTCTGTPPEEYCVQGTGVTGTSCHLCLDAG 60
QY 94 QOHLQHGAFLTDYNNQADTTWQSQTMLAGVQVPSINLTLHLGKAFDITYVRLKFHTS 153
Db 61 QOHLQHGAFLTDYNNQADTTWQSQTMLAGVQVPSINLTLHLGKAFDITYVRLKFHTS 120
QY 154 RPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTGDEQQALCTDEFSDISPL 213
Db 121 RPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTGDEQQALCTDEFSDISPL 180
QY 214 TGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTLNRLNTFGDEVFNDPKVLKSY 273
Db 181 TGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTLNRLNTFGDEVFNDPKVLKSY 240
QY 274 A1SDFAVGGRCCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPPFENDRPWRRATAES 333
Db 241 A1SDFAVGGRCCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPPFENDRPWRRATAES 300
QY 334 ASECLPCDCNRSQECYFDPPELYRSTGHGHCNTCRDNTDGAKCERCENFRLGNTTEAC 393
Db 301 ASECLPCDCNRSQECYFDPPELYRSTGHGHCNTCRDNTDGAKCERCENFRLGNTTEAC 360
QY 394 SPCHSPVGSLSLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSTDE 453
Db 361 SPCHSPVGSLSLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSTDE 420
QY 454 CNVETGRCVCKDNVEGNCERCCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGYSVYDI 513
Db 421 CNVETGRCVCKDNVEGNCERCCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGYSVYDI 480
QY 514 SSTFQIDEDGWRVEQRDGESEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYG 573
Db 481 SSTFQIDEDGWRVEQRDGESEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYG 540
QY 574 NLSFSFRVDRDRTRLAEDLVLEGAGLRVSVPLIAQGNSYPSSETTVKYIFRLHEATDYPW 633
Db 541 NLSFSFRVDRDRTRLAEDLVLEGAGLRVSVPLIAQGNSYPSSETTVKYIFRLHEATDYPW 600
QY 634 RPALSPFEQKLLNLTISIKIRGTYSERSAGYLDVTLQSAARPGVPATWVESCTCPVG 693

Db 601 RPALSPFEFQKLLNNLTSIKIRGTYSERSAGYLDVTLQSRPQPGVPATWVESCTCPVG 660
Qy 694 YGGQFCETCLPGYRRETPLSLGYPSPCVLCTCNHSETCDPETYVCDRDNATAGPHCEKCS 753
Db 661 YGGQFCETCLPGYRRETPLSLGYPSPCVLCTCNHSETCDPETYVCDRDNATAGPHCEKCS 720
Qy 754 DGYGDSLTGTSDDCQPCPCPGSSCAIVPKTKEVVCTHCTGTAGKRCCLCDDGYFGDP 813
Db 721 DGYGDSLTGTSDDCQPCPCPGSSCAIVPKTKEVVCTHCTGTAGKRCCLCDDGYFGDP 780
Qy 814 LGSNGPVRLCRPCQCNNDNIDPNAVGNCRNLTGECIKCIYNTAGFYCDRCCKEGFFGNPLAP 873
Db 781 LGSNGPVRLCRPCQCNNDNIDPNAVGNCRNLTGECIKCIYNTAGFYCDRCCKEGFFGNPLAP 840
Qy 874 NPADKCKACACNYGTVOQQSSCNPVGTQCCQLPHVSGRDCGTCDPGYVNLQSGQGCRCRD 933
Db 841 NPADKCKACACNYGTVOQQSSCNPVGTQCCQLPHVSGRDCGTCDPGYVNLQSGQGCRCRD 900
Qy 934 CHALGSTNGQCDIRTGQCEQCPGIGTQHCCERCETNHFHFGPEGCKPCDCHHEGSLSLQCK 993
Db 901 CHALGSTNGQCDIRTGQCEQCPGIGTQHCCERCETNHFHFGPEGCKPCDCHHEGSLSLQCK 960
Qy 994 DDGRCEGFGVGNRCDCQCEENYFYNRSPWQGCPCACRYLVKDKAAEHRVQLQELSLI 1053
Db 961 DDGRCEGFGVGNRCDCQCEENYFYNRSPWQGCPCACRYLVKDKAAEHRVQLQELSLI 1020
Qy 1054 ANLGTGDDMVTDAFEDRLKEAREVTDLLEAQAQVQKVDQNLMDRLQVNSSLSHQSISR 1113
Db 1021 ANLGTGDDMVTDAFEDRLKEAREVTDLLEAQAQVQKVDQNLMDRLQVNSSLSHQSISR 1080
Qy 1114 LQIRNTIETGILAEARSRVSESTEOLIEIASRELEKAKMAANYSIITQPESTGEPPNMT 1173
Db 1081 LQIRNTIETGILAEARSRVSESTEOLIEIASRELEKAKMAANYSIITQPESTGEPPNMT 1140
Qy 1174 LLAEEARLAEHRKQEAADIVRVAKTANETSABAYNLLRLTAGENQTALEIEELNRKYE 1233
Db 1141 LLAEEARLAEHRKQEAADIVRVAKTANETSABAYNLLRLTAGENQTALEIEELNRKYE 1200
Qy 1234 QAKNTSQDLEKQAAARVHEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLD 1293
Db 1201 QAKNTSQDLEKQAAARVHEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLD 1260
Qy 1294 RLIDQKLDYEDLREDMRGKEHEVKNLLEKGAEQQTADQLLARADAALAEAAKGR 1353
Db 1261 RLIDQKLDYEDLREDMRGKEHEVKNLLEKGAEQQTADQLLARADAALAEAAKGR 1320
Qy 1354 STLQEAANDILNNLKDFFRRVNDNKTAAEEALRRIPAINRTTAAANEKTRAEALGNAAA 1413
Db 1321 STLQEAANDILNNLKDFFRRVNDNKTAAEEALRRIPAINRTTAAANEKTRAEALGNAAA 1380
Qy 1414 DATEAKNKAHEAERIAAQAQKATSTKADABRTFGEVTDLDNEVNGMLRQLEEAENELKR 1473
Db 1381 DATEAKNKAHEAERIAAQAQKATSTKADABRTFGEVTDLDNEVNGMLRQLEEAENELKR 1440
Qy 1474 KQDDADQDMMAGMASQAAQAEALNARKAKNSVSSLLSQLNNLLDQLGQDLDVNLKLINE 1533
Db 1441 KQDDADQDMMAGMASQAAQAEALNARKAKNSVSSLLSQLNNLLDQLGQDLDVNLKLINE 1500
Qy 1534 IEGSLNKAKDEMKAASDLDRKVSDDLESEARKQEAAIMDYNRDIAELIKDIHNLEDIKKTLPL 1593
Db 1501 IEGSLNKAKDEMKAASDLDRKVSDDLESEARKQEAAIMDYNRDIAELIKDIHNLEDIKKTLPL 1560
Qy 1594 TGCFTNTPSIEKP 1605
Db 1561 TGCFTNTPSIEKP 1572

RESULT 4
US-09-561-818A-28
; Sequence 28, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:

; APPLICANT: Kortessmaa, Jarrko
; APPLICANT: tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 28
; LENGTH: 1572
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-561-818A-28

Query Match 98.1%; Score 8527; DB 4; Length 1572;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 AMDECADEGGRPQRCMPEFVNAAFNVTVATNTCGTPPEEYCVQTVGTGVTKSCHLCDAG 93
Db 1 AMDECADEGGRPQRCMPEFVNAAFNVTVATNTCGTPPEEYCVQTVGTGVTKSCHLCDAG 60
Qy 94 QOHLQHGAFLTDYNNQADTTWQSQTMLAGVQYVNSINLTLHLGKAFDITYVRLKFHTS 153
Db 61 QOHLQHGAFLTDYNNQADTTWQSQTMLAGVQYVNSINLTLHLGKAFDITYVRLKFHTS 120
Qy 154 RPESFAIYKRTREDGPWIPYQYVSGSCENTYSKANRGFIITGGDEQQAALCTDEFSDISPL 213
Db 121 RPESFAIYKRTREDGPWIPYQYVSGSCENTYSKANRGFIITGGDEQQAALCTDEFSDISPL 180
Qy 214 TCGNVAFTLEGPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVNDPKVLKSYYY 273
Db 181 TCGNVAFTLEGPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVNDPKVLKSYYY 240
Qy 274 AISDPVAGGRCKCNHSHASECVKNEFDKLMCNCKHNTYGVDCCKCLPFFNDRPWRRTAES 333
Db 241 AISDPVAGGRCKCNHSHASECVKNEFDKLMCNCKHNTYGVDCCKCLPFFNDRPWRRTAES 300
Qy 334 ASECLPCDCNGRSQECYFDPPELYRSTGHGHCTNCRDNTDGAKCERCERENFRLGNTEAC 393
Db 301 ASECLPCDCNGRSQECYFDPPELYRSTGHGHCTNCRDNTDGAKCERCERENFRLGNTEAC 360
Qy 394 SPCHCSPVGSLSQCDSDSYGRCSCKPGVWGDKCDRCQPGFHSLSLTAAGCRPCSDPSGSTDE 453
Db 361 SPCHCSPVGSLSQCDSDSYGRCSCKPGVWGDKCDRCQPGFHSLSLTAAGCRPCSDPSGSTDE 420
Qy 454 CNVETGRCVCKDNVEGFNCERCKPGFFNLESSNPKGCTPCFCFCHSSVCTNAVGVSVYDI 513
Db 421 CNVETGRCVCKDNVEGFNCERCKPGFFNLESSNPKGCTPCFCFCHSSVCTNAVGVSVYDI 480
Qy 514 SSTFOIDEDGHRVEQDSEASLEWSSDRQYIAVISDSYFPFYFIAPVKFLGNQVLSYQ 573
Db 481 SSTFOIDEDGHRVEQDSEASLEWSSDRQYIAVISDSYFPFYFIAPVKFLGNQVLSYQ 540
Qy 574 NLSFSFRVDRDRTRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYIFRLHEATDYPW 633
Db 541 NLSFSFRVDRDRTRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYIFRLHEATDYPW 600
Qy 634 RPALSPFEFQKLLNNLTSIKIRGTYSERSAGYLDVTLQSRPQPGVPATWVESCTCPVG 693
Db 601 RPALSPFEFQKLLNNLTSIKIRGTYSERSAGYLDVTLQSRPQPGVPATWVESCTCPVG 660
Qy 694 YGGQFCETCLPGYRRETPLSLGYPSPCVLCTCNHSETCDPETYVCDRDNATAGPHCEKCS 753
Db 661 YGGQFCETCLPGYRRETPLSLGYPSPCVLCTCNHSETCDPETYVCDRDNATAGPHCEKCS 720
Qy 754 DGYGDSLTGTSDDCQPCPCPGSSCAIVPKTKEVVCTHCTGTAGKRCCLCDDGYFGDP 813
Db 721 DGYGDSLTGTSDDCQPCPCPGSSCAIVPKTKEVVCTHCTGTAGKRCCLCDDGYFGDP 780
Qy 814 LGSNGPVRLCRPCQCNNDNIDPNAVGNCRNLTGECIKCIYNTAGFYCDRCCKEGFFGNPLAP 873
Db 781 LGSNGPVRLCRPCQCNNDNIDPNAVGNCRNLTGECIKCIYNTAGFYCDRCCKEGFFGNPLAP 840

QY 874 NPADKCKACACNYGTVQQSSCNPTGQCQCLPHVSGRDCTGDPGYNNLQSGQCERCD 933
Db 841 NPADKCKACACNYGTVQQSSCNPTGQCQCLPHVSGRDCTGDPGYNNLQSGQCERCD 900
QY 934 CHALGSTNGQCDIRTGQCECQPGITGQHCHERCETNHFPGEGCKPCDCHHGSLSLQCK 993
Db 901 CHALGSTNGQCDIRTGQCECQPGITGQHCHERCETNHFPGEGCKPCDCHHGSLSLQCK 960
QY 994 DDGRCECREGFGVGNRCDCQCEENYFYNRSWPGCQCEPCACVRLVKDKAAEHRVKLQLESLLI 1053
Db 961 DDGRCECREGFGVGNRCDCQCEENYFYNRSWPGCQCEPCACVRLVKDKAAEHRVKLQLESLLI 1020
QY 1054 ANLGTGDDMVTDQAFEDRLKEAEREVTDLLREAQEVKDVQNLMDRLQRVNSSLHSQISR 1113
Db 1021 ANLGTGDDMVTDQAFEDRLKEAEREVTDLLREAQEVKDVQNLMDRLQRVNSSLHSQISR 1080
QY 1114 LQIRNTIETGILAEARSRVSTEQLEIASRELEKAKMAANVSITQPESTGEPPNMT 1173
Db 1081 LQIRNTIETGILAEARSRVSTEQLEIASRELEKAKMAANVSITQPESTGEPPNMT 1140
QY 1174 LLAEEARRLAERHKEADDIVRAKTANETSAAEYNLLRTLAGENQTALEIEELNRKYE 1233
Db 1141 LLAEEARRLAERHKEADDIVRAKTANETSAAEYNLLRTLAGENQTALEIEELNRKYE 1200
QY 1234 QAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLD 1293
Db 1201 QAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLD 1260
QY 1294 RLIDQKLXDVEDLREDMRGKEHEVKNLLEKGAEQQTADOLLARADAALKALAEBAKGR 1353
Db 1261 RLIDQKLXDVEDLREDMRGKEHEVKNLLEKGAEQQTADOLLARADAALKALAEBAKGR 1320
QY 1354 STLQEANDILNLLKDFRRVNDNKTAAEEALRRIPAINRTIAEANEKTRQAQLALGNAAA 1413
Db 1321 STLQEANDILNLLKDFRRVNDNKTAAEEALRRIPAINRTIAEANEKTRQAQLALGNAAA 1380
QY 1414 DATEAKNKAHEAERIAASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRLQLEAEANELKR 1473
Db 1381 DATEAKNKAHEAERIAASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRLQLEAEANELKR 1440
QY 1474 KQDDADQDMMAGMASQAAQAEALNARKAKNSVSLLSQLNLLDLQLGQDLDVLDNKLNE 1533
Db 1441 KQDDADQDMMAGMASQAAQAEALNARKAKNSVSLLSQLNLLDLQLGQDLDVLDNKLNE 1500
QY 1534 IEGSLNKADEMKAASDLDRKVSDESEARKQEAAMIDYNRDAIEIIKDIHNLEDIKKTLTP 1593
Db 1501 IEGSLNKADEMKAASDLDRKVSDESEARKQEAAMIDYNRDAIEIIKDIHNLEDIKKTLTP 1560
QY 1594 TGCNFTPSIEKP 1605
Db 1561 TGCNFTPSIEKP 1572

RESULT 5
US-09-562-702A-22
; Sequence 22, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 1609
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-22

Query Match 93.7%; Score 8148; DB 4; Length 1609;
Best Local Similarity 92.8%; Pred. No. 0;
Matches 1493; Conservative 59; Mismatches 53; Indels 4; Gaps 3;

QY 1 NTGGGAAALALQPRGLWPLLAVAL--AAVAGCVRAAMDECADEGGRPQRCMPEFVNAAFN 58
Db 1 MRGSHRAAPALRPRGRLEWFLAVLAAAAACAQAAMDECTDEGGRPQRCMPEFVNAAFN 60
QY 59 VTVVATNTCGTPPEEYCVQGTGVTGVTKSKCHLCDAGQQLHGHGAFLTDYNNQADTTWQ 118
Db 61 VTVVATNTCGTPPEEYCVQGTGVTGVTKSKCHLCDAGQQLHGHGAFLTDYNNQADTTW 120
QY 119 QTMLAGVQYVNSINLTHLGKAFDITYVRLKFHTSRPESFAIYKRTREDGWPWIPYQY 178
Db 121 QTMLAGVQYVNSINLTHLGKAFDITYVRLKFHTSRPESFAIYKRTREDGWPWIPYQY 180
QY 179 SCENTYSKANRGFIRTGDEQALCTDEFSDISPLTGNVAFSTLEGRPSAYNFDNSPVL 238
Db 181 SCENTYSKANRGFIRTGDEQALCTDEFSDISPLTGNVAFSTLEGRPSAYNFDNSPVL 240
QY 239 QEWVTATDIRVTLNRLNTFGDEVFNDPKVLKSYYYAISDFAVGGRCKCNGHASECVK 298
Db 241 QEWVTATDIRVTLNRLNTFGDEVFNDPKVLKSYYYAISDFAVGGRCKCNGHASECVK 300
QY 299 DKLMCNCKHNTYGVDCCKCLPFFNDRPWRRAATAESAECPLCDNCRSGRSGQECYF 358
Db 301 DKLVNCKHNTYGVDCCKCLPFFNDRPWRRAATAESAECPLCDNCRSGRSGQECYF 360
QY 359 TGHGGHCTNCRDNTDGAKCRCRENFRLGNTEACSPCHCSPVGLSTQCDYGRCSCKP 418
Db 361 TGHGGHCTNCRDNTDGAKCRCRENFRLGNTEACSPCHCSPVGLSTQCDYGRCSCKP 420
QY 419 GVMGDKCDRCQPGFHSLTEAGCRPCSDPSGSTDECNVTGRVCVCKDNVEGFNCERCK 478
Db 421 GVMGDKCDRCQPGFHSLTEAGCRPCSDPSGSTDECNVTGRVCVCKDNVEGFNCERCK 480
QY 479 FPNLESSNPKGCTPCFCFGHSSVCTNAVGVSVYDISSTFQIDEDGWRVEQORDGSEAS 538
Db 481 FPNLESSNPRGCTPCFCFGHSSVCTNAVGVSVYDISSTFQIDEDGWRVEQORDGSEAS 540
QY 539 SSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYGONLSFSFRVDRDRRLSAEDLVLE 598
Db 541 SSERQDIAVISDSYFPRYFIAPVKFLGNQVLSYGONLSFSFRVDRDRRLSAEDLVLE 600
QY 599 GLRVSVPLIAQGNSTPSETTVKYIFRLHEATDYPWRPALSPFEFQKLLNLTSLIKIR 658
Db 601 GLRVSVPLIAQGNSTPSETTVKYIFRLHEATDYPWRPALSPFEFQKLLNLTSLIKIR 660
QY 659 SERSAGYLDVTLQSAARPGVPATWVESCTCPVGYGGQFCBETCLPGYRRETSLGPYSP 718
Db 661 SERSAGYLDVTLQSAARPGVPATWVESCTCPVGYGGQFCBETCLPGYRRETSLGPYSP 720
QY 719 CVLCTCNHSETCDPETGVCDRCNRTAGPHCEKCSGDIYVGNSTLGTSSDCQPCPCGSS 778
Db 721 CVLCAACNHSSETCDPETGVCDRCNRTAGPHCEKCSGDIYVGNSTLGTSSDCQPCPCG 780
QY 779 CAIVPKTEVVCTHCPTGTAGKRCCLDDGYFGDPLGNSGNPRLCRPCQCNNDIDPNAVG 838
Db 781 CAWPKTEVVCTNCPTGTTGKRCCLDDGYFGDPLGNSGNPRLCRPCQCNNDIDPNAVG 840
QY 839 NCNRLTGECLKCIYNTAGFYCDRCKEGFFGNPLAPNPADKCKACACN-YGTVQQSSCN 897
Db 841 NCNRLTGECLKCIYNTAGFYCDRCXGDFGNPLAPNPADKCKACACNPGYTMKQSSCN 900
QY 898 VTGQCQCLPHVSGRDCTGDPGYNNLQSGQCERCDCHALGSTNGQCDIRTGQCEQPGI 957

Db 901 VTGQCECLPHVTGQDCGACDPGFYNLQSGQGCRCDCALGSTNGQCDIRTGQCECQPGI 960
QY 958 TGQHCECETNHFHFGPEGCKPCDCHHEGSLSLQCKDDGRCECEGREGVGNRCDCQCEENYF 1017
Db 961 TGQHCECEVNHFGPEGCKPCDCHHEGSLSLQCKDDGRCECEGREGVGNRCDCQCEENYF 1020
QY 1018 YNRSWPGQCECPACRYLVKDKAAEHRVKLQELSLIANLGTGDDMVTDQAFEDRLKEAER 1077
Db 1021 YNRSWPGQCECPACRYLVKDKVADHRVKLQELSLIANLGTGDMVTDQAFEDRLKEAER 1080
QY 1078 EVDLLREAEQVQKVDQNLMDRLQVNSLSHSQISRLQINRNTIETGILAEARARSRVES 1137
Db 1081 EVMDDLREAEQVQKVDQNLMDRLQVNSLSHSQISRLQINRNTIETGILAEARARSRVES 1140
QY 1138 TEQLIEIASRELEKAKM-AANVSITQPESTGEPNNNTLLAEARRLAEHKKQEAADDIVRV 1196
Db 1141 TERLIEIASRELEKAKVAAANVSITQPESTGDPNNNTLLAEARRLAEHKKQEAADDIVRV 1200
QY 1197 AKTANETSAAEAYNLLRLTAGENQTALEIEELNRKYEQAQNISQDLKQAARVHEEAARA 1256
Db 1201 AKTANDTSTEAAYNLLRLTAGENQTALEIEELNRKYEQAQNISQDLKQAARVHEEAARA 1260
QY 1257 GDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLRLIDQKLKDYEDLREDMRGKEHE 1316
Db 1261 GDKAVEIYASVAQLSPDSEALENEANNIKMEAEENLEQLIDQKLKDYEDLREDMRGKEHE 1320
QY 1317 VKNLLKKGKAEQQTADQLLARADAAKALAEAAKKGSRSTLQEAANDILNNLKFDRRVNDN 1376
Db 1321 VKNLLKKGKTEQQTADQLLARADAAKALAEAAKKGSRSTLQEAANDILNNLKFDRRVNDN 1380
QY 1377 KTAABEALRRIPAINRTIABANEKTRAEALALGNAADAATEAKNKAHEAEARIAASAAQKNA 1436
Db 1381 KTAABEALRKIPAINQITTEANEKTRAEALALGNAADAATEAKNKAHEAEARIAASAAQKNA 1440
QY 1437 TSTKADAERTFGEVTDLDNEVNGMLRQLEAEANELKRRKQDDADQDMMAGMASQAQAEAE 1496
Db 1441 TSTKAEAEERTFAEVTDLNEVNNMLKQLEAEAKELKRRKQDDADQDMMAGMASQAQAEAE 1500
QY 1497 LNARKAKNSVSSLLSQNLNLLDQLGQDVTDLNKLNEIEGSLNKADEMKAASDLDRKVSD 1556
Db 1501 INARKAKNSVTSLLSIINDLLESQGLQDVTDLNKLNEIEGTLNKADEMKAASDLDRKVSD 1560
QY 1557 LESEARKQEAAMDYNDRIABEIKDIHNLEDIKKTLPTGCFNTPSIEKP 1605
Db 1561 LENEAKKQEAAMDYNDRIABEIKDIHNLEDIKKTLPTGCFNTPSIEKP 1609

RESULT 6
US-09-561-818A-22
; Sequence 22, Application US/09561818A
; Patent No. 638907
; GENERAL INFORMATION:
; APPLICANT: Kortessmaa, Jarkko
; APPLICANT: Tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 1609
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-818A-22

Query Match 93.7%; Score 8148; DB 4; Length 1609;
Best Local Similarity 92.8%; Pred. No. 0;
Matches 1493; Conservative 59; Mismatches 53; Indels 4; Gaps 3;
QY 1 MTGGGGAALALQPRGLWPLAVL--AAVAGCVRAAMDECADEGGRPQRCMPPEFVNAAFN 58
Db 1 MRGSHRAAPALRPRGLWPLAVLAAAAAGCAQAAMDECTDEGGRPQRCMPPEFVNAAFN 60

QY 59 VTVVATNTCTPPEEYCVQGTGVTGKTSCHLQAGQOHLQGAFLTDYNNQADTTWQOS 118
Db 61 VTVVATNTCTPPEEYCVQGTGVTGKTSCHLQAGQOHLQGAFLTDYNNQADTTWQOS 120
QY 119 QTMLAGVQYVNSINLTLHLGKAFDITYVRLKFTSRPESFAIKRTREDGFWIPYQYYS 178
Db 121 QTMLAGVQYVNSINLTLHLGKAFDITYVRLKFTSRPESFAIKRTREDGFWIPYQYYS 180
QY 179 SCENTYSKANRGFIRTTGGDEQALCTDEFSDISPLTGGNVAFSTLEGPSAYNFDNSPVL 238
Db 181 SCENTYSKANRGFIRTTGGDEQALCTDEFSDISPLTGGNVAFSTLEGPSAYNFDNSPVL 240
QY 239 QEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSYIYVAFSDFAVGGRCCKNGHASECVKNEF 298
Db 241 QEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSYIYVAFSDFAVGGRCCKNGHASECVKNEF 300
QY 299 DKLMCNCKHNTYGVDCCKLPFFNDRPWRRTAEASASECLPCDCNRSQCEYFDPPELYRS 358
Db 301 DKLMCNCKHNTYGVDCCKLPFFNDRPWRRTAEASASECLPCDCNRSQCEYFDPPELYRS 360
QY 359 TGHGHCNCRDNTDGAKCERENFRRLNTEACSPCHCSPVGSLSSTQCDYSGRCCKP 418
Db 361 TGHGHCNCRDNTDGAKCERENFRRLNTEACSPCHCSPVGSLSSTQCDYSGRCCKP 420
QY 419 GVMGKCDRCQPGFHSLTBAGCRPCSDPSGSDTDECNVETGRCVCKDNVEGFNCERCKPG 478
Db 421 GVMGKCDRCQPGFHSLTBAGCRPCSDPSGSDTDECNVETGRCVCKDNVEGFNCERCKPG 480
QY 479 FFNLESSNPKGCTPCPCFCHSSVCTNAVGYSYVDISSTFQIDEDGWRVEORDGSEASLEW 538
Db 481 FFNLESSNPKGCTPCPCFCHSSVCTNAVGYSYVDISSTFQIDEDGWRVEORDGSEASLEW 540
QY 539 SDRQYIAVISDSYFPRIYFIAPVKFLGNQVLSYGONLSFSFRVDRDRTRLSAEDLVLEGA 598
Db 541 SDRQYIAVISDSYFPRIYFIAPVKFLGNQVLSYGONLSFSFRVDRDRTRLSAEDLVLEGA 600
QY 599 GLRVSVPLIAOGNSYPSSETTVKIFRLHEATDYPWRPALSPFFFOKLNNLTSIKIRTY 658
Db 601 GLRVSVPLIAOGNSYPSSETTVKIFRLHEATDYPWRPALSPFFFOKLNNLTSIKIRTY 660
QY 659 SERSAGYLDVTLQSAAPPGVPAWVESCTCPVGGGQFCETCLPGYRRETPLSGPYSP 718
Db 661 SERSAGYLDVTLQSAAPPGVPAWVESCTCPVGGGQFCETCLPGYRRETPLSGPYSP 720
QY 719 CVLCTCNHSETCDPETGVCDCRDNATAGHCKSCSDGYGDSILGTSSDCQPCPCPGSS 778
Db 721 CVLCTCNHSETCDPETGVCDCRDNATAGHCKSCSDGYGDSILGTSSDCQPCPCPGSS 780
QY 779 CAIVPKTEVVCVTHCTGTAGKRCCELCDGDFGDPPLGNSGVPVRLCRPCQCNNDIDPNAVG 838
Db 781 CAIVPKTEVVCVTHCTGTAGKRCCELCDGDFGDPPLGNSGVPVRLCRPCQCNNDIDPNAVG 840
QY 839 NCNRLTGECLKCIYNTAGFYCDRCCKEGFPGNPLAPNPADKCKACACN-YGTVOQOQSSCNP 897
Db 841 NCNRLTGECLKCIYNTAGFYCDRCCKEGFPGNPLAPNPADKCKACACN-YGTVOQOQSSCNP 900
QY 898 VTGQCQCLPHVSGRDCGTCDPGYVNLQSGQGCRCDCCHALGSTNGQCDIRTGQCECQPGI 957
Db 901 VTGQCQCLPHVSGRDCGTCDPGYVNLQSGQGCRCDCCHALGSTNGQCDIRTGQCECQPGI 960
QY 958 TGQHCECETNHFHFGPEGCKPCDCHHEGSLSLQCKDDGRCECEGREGVGNRCDCQCEENYF 1017
Db 961 TGQHCECETNHFHFGPEGCKPCDCHHEGSLSLQCKDDGRCECEGREGVGNRCDCQCEENYF 1020
QY 1018 YNRSWPGQCECPACRYLVKDKAAEHRVKLQELSLIANLGTGDDMVTDQAFEDRLKEAER 1077
Db 1021 YNRSWPGQCECPACRYLVKDKVADHRVKLQELSLIANLGTGDMVTDQAFEDRLKEAER 1080
QY 1078 EVDLLREAEQVQKVDQNLMDRLQVNSLSHSQISRLQINRNTIETGILAEARARSRVES 1137
Db 1081 EVMDDLREAEQVQKVDQNLMDRLQVNSLSHSQISRLQINRNTIETGILAEARARSRVES 1140

QY	1138	TEQLIEIASRELEKAKM-AANVSITQPESTGEPNNMTLLAAEEARRLAEERHKEADDIVRV	1196
Db	1141	TERLIEIASRELEKAKVAAANVSVTQPESTGDPNNMTLLAAEEARKLAEERHKEADDIVRV	1200
QY	1197	AKTANETSAAEAYNLLLRTLAGENQTALAEI EELNRKYEQAKNISQDLEKQAAARVHEEAKRA	1256
Db	1201	AKTANDTSTEAYNLLLRTLAGENQTAFAEIEELNRKYEQAKNISQDLEKQAAARVHEEAKRA	1260
QY	1257	GDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLRLIDQKLKDYEDLREDMRGKEHE	1316
Db	1261	GDKAVEIYASVAQLSPDSETLENEANNIKMEAEENLEQLIDQKLKDYEDLREDMRGKELE	1320
QY	1317	VKNLLEKKGAEQQTADQLLARADAAKALAEAAKKGSRSTLQEANDILNNLKDFDRRVNDN	1376
Db	1321	VKNLLEKKGTEQQTADQLLARADAAKALAEAAKKGGRDTLQEANDILNNLKDFDRRVNDN	1380
QY	1377	KTAAEEALRRIPAINRTIAEANEKTR EAQALGNAAADATEAKNKAAHEAERIAASAAQKNA	1436
Db	1381	KTAAEEALRKIPAINQRTI TEANEKTR EAQOALGSAADATEAKNKAAHEAERIAASVQKNA	1440
QY	1437	TSTKADAERTFGEVTDLDNEVNGMLRQLEEAENELKRKQDDADQDMMAGMASQAAQEAE	1496
Db	1441	TSTKAEARTFAEVTDLDNEVNNMLKQLOEAEKELKRKQDDADQDMMAGMASQAAQEAE	1500
QY	1497	LNARKAKNSVSSLSQNLNLLDQLGQDVTVDLNLKLEIEGSLNKADEMKAASDLDRKVS D	1556
Db	1501	INARKAKNSVTSLSIINDLLEQLGQDVTVDLNLKLEIEGT LNKAKDEMKVSDLDRKVS D	1560
QY	1557	LESEARKOEAAIMDYNRDIAEIIKDIHNLEDIKKTLTGCFNTPTPSIEKP	1605
Db	1561	LENEAKKOEAAIMDYNRDIEEIMKDIRNLEDIRKTLPSGCFNTPTPSIEKP	1609

RESULT 7

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US-09-562-702A-26
; Sequence 26, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 1617
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-562-702A-26

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	Query Match	93.7%;	Score 8148;	DB 4;	Length 1617;
	Best Local Similarity	92.8%;	Pred. No. 0;		
	Matches 1493;	Conservative 59;	Mismatches 53;	Indels 4;	Gaps 3;
QY	1	MTGGRAALALQPRGLWP ¹ LLAVL--AAVAGCVRAAMDECADEGGRPQRCMPPEFVNAAFN	58		
DB	1	MRGSHRAAPALRPRGLWP ¹ VLAVLAAAAAGCAQAAMDECTDEGGRPQRCMPPEFVNAAFN	60		
QY	59	VTWVATNTCGTPPEEYCVQ ¹ TGVTGVTKSCHLCDAGQOHLQHGA ¹ AAFLTDYNNQADTTWQ ¹ S	118		
DB	61	VTWVATNTCGTPPEEYCVQ ¹ TGVTGVTKSCHLCDAGQPHLQHGA ¹ AAFLTDYNNQADTTWQ ¹ S	120		
QY	119	QTMLAGVOYPNSINLT ¹ LHLGKA ¹ FDITYVRLKFHTSRBESFAIYK ¹ RTREDGPWIPYQ ¹ YSG	178		

Db	121	QTMLAGVQYPSSINLTLHLGKAFDITYVRLKFKHTSRPESFAIYKRTREDGPWIPQYISG	180
Qy	179	SCENTYSKANRGFIRTTGGDEQQAALCTDEFSDISPLTTGGNVAFSTLEGRPSAYNFDNSPVL	238
Db	181	SCENTYSKANRGFIRTTGGDEQQAALCTDEFSDISPLTTGGNVAFSTLEGRPSAYNFDNSPVL	240
Qy	239	QEWVTATDIRVTLNRLNTFGDEVFNDPKVLKSYIYAISDFAVGGRCKCNGHASECVKNEF	298
Db	241	QEWVTATDIRVTLNRLNTFGDEVFNDPKVLKSYIYAISDFAVGGRCKCNGHASECMKNEF	300
Qy	299	DKLMCNCKHNTYGVDCBKCLPFFNDRPWRRATABSASECLPCDCNGRSQECYFDPELYRS	358
Db	301	DKLVCNCKHNTYGVDCBKCLPFFNDRPWRRATABSASECLPCDCNGRSQECYFDPELYRS	360
Qy	359	TGHGGHCTNCRDNTDGAKCERCRENFFRLNGTEACSPCHCSPVGSLSLSTQCDSYGRCSCKP	418
Db	361	TGHGGHCTNCQDNTDGAHCERCRENFFRLGNNEACSSCHCSPVGSLSLSTQCDSYGRCSCKP	420
Qy	419	GVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSDTDECNVETGRCVCKDNVEGFNCERCKPG	478
Db	421	GVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSDTDECNVETGRCVCKDNVEGFNCERCKPG	480
Qy	479	FFNLESSNPKGCTPCFCFGHSSVCTNAVGYSVYDISSTFQIDEDGWRVEQRDGSEASLEW	538
Db	481	FFNLESSNPRGCTPCFCFGHSSVCTNAVGYSVYDISSTFQIDEDGWRAEQRDGSEASLEW	540
Qy	539	SSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYQNLSPFSFRVDRDRTRLRSAEDLVLEGA	598
Db	541	SSERQDIAVISDSYFPRYFIAPAKFLGKVLSYQNLSPFSFRVDRDRTRLRSAEDLVLEGA	600
Qy	599	GLRVSVPLIAQNSYSPSETTVKYIFRLHEATDYPWRPALSPFEFQKLLNLTISKIRGTY	658
Db	601	GLRVSVPLIAQNSYSPSETTVKYIFRLHEATDYPWRPALTPFEFQKLLNLTISKIRGTY	660
Qy	659	SERSAGYLLDVTLQSAARPGPVPATWVESCTCPVGYGGQFCETCLPGYRRETSLGPYSP	718
Db	661	SERSAGYLLDVTLASARPGPVPATWVESCTCPVGYGGQFCEMCLSGYRRETSLGPYSP	720
Qy	719	CVLCTCNHSETCDPBTGVCDNRNTAGPHCEKCSGDIYGDSTLTGTSDDCQPCPCGGSS	778
Db	721	CVLCACNGHSETCDPETGVNCNRDNTAGPHCEKCSGDIYGDSTAGTSSDCQPCPCGGSS	780
Qy	779	CAIVPKTKEVVCTHCTGTAGKRCCELCDGDFGDPGLSGNPGVRLCRPCQCNNDIDPNAVG	838
Db	781	CAVVPKTKEVVCTNCPTGTTGKRCELCDGDFGDPGLGRNGPVRLCRLCQCSNDIDPNAVG	840
Qy	839	NCNRLTGECLKCIYNTAGFYCDRCXEGFFGNELAPNPADKCKACACN - YGTVOQOSSCNP	897
Db	841	NCNRLTGECLKCIYNTAGFYCDRCXGDFGNELAPNPADKCKACACNPGYGTMKQOSSCNP	900
Qy	898	VTGQCQCCLPHVSGRDCGTCDPGYYNLQSGQGCERCDCCHALGSTNGQCDIRTGQCECQPGI	957
Db	901	VTGQCECLPHVTGDCGACDPGFYNLQSGQGCERCDCCHALGSTNGQCDIRTGQCECQPGI	960
Qy	958	TGQHCCERCETNHFPGPEGCKPCDCHHEGSLSLQCKDDGRCECREGFVGNRCDCQCEENYF	1017
Db	961	TGQHCCERCEVNHFGPEGCKPCDCHPEGSLSLQCKDDGRCECREGFVGNRCDCQCEENYF	1020
Qy	1018	YNRSWPQCQECPCACYRLVKDAAEHRVKLQELLESILIANLTGDDMTDQAFEDRLKEAER	1077
Db	1021	YNRSWPQCQECPCACYRLVKDKVADHRVKLQELLESILIANLTGDEMVTDQAFEDRLKEAER	1080
Qy	1078	EVTDLLREAQEVKDQDQNLMDRLQRVNSSLHSQISRLQINRNTIETGILAEARARSVES	1137
Db	1081	EVMDLLREAQDVKDQDQNLMDRLQRVNNTLSSQISRLQINRNTIETGILAEARAHVEN	1140
Qy	1138	TEQLIEIASRELEKAKM - AANVSITQPESTGEFPNNMTLLAEAEARRLAERHKQEADDIVRV	1196
Db	1141	TERLIEIASRELEKAKVAAANVSITQPESTGDPNNMTLLAEAEARKLAERHKQEADDIVRV	1200
Qy	1197	AKTANETSAEAYNLLRLRTLAGENQTALEIEELNRKYEQAKNISQDLEKQAARVHEAKRA	1256
Db	1201	AKTANDTSTAAYNLLRLRTLAGENQTALEIEELNRKYEQAKNISQDLEKQAARVHEAKRA	1260

QY 1257 GDKAVIYASVAQLTPVDSALNEANKIKKEADLDRLIDOKLDYEDLREDMRGKEHE 1316
Db 1261 GDKAVIYASVAQLSPDSSTLENEANNIKMEAEENLEQLIDOKLDYEDLREDMRGKELE 1320
QY 1317 VKNLLEKGAEQQTADQLLARADAAKALAEAAKKGSRSTLOEANDILNNLKDFDRRVNDN 1376
Db 1321 VKNLLEKKGTEQQTADQLLARADAAKALAEAAKKGSRSTLOEANDILNNLKDFDRRVNDN 1380
QY 1377 KTAABEALRRIPAINRTTAEANEKTRAEQALGVAADATEAKNKAHEAERIAASAAQKNA 1436
Db 1381 KTAABEALRKIPAINQTITEANEKTRAEQALGVAADATEAKNKAHEAERIAASAVQKNA 1440
QY 1437 TSTKADAERTFGEVTDLDNEVNGMLRQLEEAENELKRKQDDADQDMMWAGMASQAAQEA 1496
Db 1441 TSTKAEARTFAEVTDLNEVNNMLKQLEAEKELKRKQDDADQDMMWAGMASQAAQEA 1500
QY 1497 LNARKAKNSVSSLLSQNLNLDQLGQDLDVNLKNEIEGSLNKADEMKAASDLDRKVS 1556
Db 1501 INARKAKNSVSSLLSIINDLEQLGQDLDVNLKNEIEGTLNKADEMKAASDLDRKVS 1560
QY 1557 LESAARKQEAAMIDYNRDIAEIIKDIHNLEDIKKTLPTGCFTNTPSIEKP 1605
Db 1561 LENAARKQEAAMIDYNRDIEIIMKDIRNLEDIRKTLPSGCFNTPSIEKP 1609

RESULT 8

US-09-562-702A-24
; Sequence 24, Application US/09562702A
; Patent No. 6632790

GENERAL INFORMATION:

; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B

; CURRENT APPLICATION NUMBER: US/09/562,702A

; CURRENT FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: 60/155,945

; PRIOR FILING DATE: 1999-09-24

; PRIOR APPLICATION NUMBER: 60/143,289

; PRIOR FILING DATE: 1999-07-12

; PRIOR APPLICATION NUMBER: 60/139,198

; PRIOR FILING DATE: 1999-06-15

; PRIOR APPLICATION NUMBER: 60/131,720

; PRIOR FILING DATE: 1999-04-30

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: Patent in Ver. 2.0

; SEQ ID NO 24

; LENGTH: 1576

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-562-702A-24

Query Match 92.5%; Score 8043; DB 4; Length 1576;

Best Local Similarity 93.3%; Pred. No. 0;

Matches 1470; Conservative 57; Mismatches 47; Indels 2; Gaps 2;

QY 32 RAAMDECADEGGRPQRCMPEFVNAAFNVTVVATNTCGTPPEEYCVQTVGTGVTKSCHLCD 91
Db 1 QAAMDECTDEGGRPQRCMPEFVNAAFNVTVVATNTCGTPPEEYCVQTVGTGVTKSCHLCD 60
QY 92 ACQOHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYPNSINLTLHLGKAFDITYVRLKPH 151
Db 61 ACQPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYPSSINLTLHLGKAFDITYVRLKPH 120
QY 152 TSRPESFAIKRTRDGPWIPYQYSGSCENTYSKANRGFIRTGDEQQALCTDESDIS 211
Db 121 TSRPESFAIKRTRDGPWIPYQYSGSCENTYSKANRGFIRTGDEQQALCTDESDIS 180
QY 212 PLTGGNVAFSTLEGRPSAYNFDSNPLQEWVTATDIRVTNLRLNTFGDEVNPKVLSY 271
Db 181 PLTGGNVAFSTLEGRPSAYNFDSNPLQEWVTATDIRVTNLRLNTFGDEVNPKVLSY 240
QY 272 YYAISDFAVGGRCKNGHASECVKNEFDKLMCNCKNTYGVDCCKLPFFNDRPWRATA 331

Db 241 YYAISDFAVGGRCKNGHASECMKNEFDKLVNCKNTYGVDCCKLPFFNDRPWRATA 300
QY 332 ESASECLPCDCNCRSGOEYFDELYRSTGHGGHCITNCRDNTDGAKCERCENPRLGNTE 391
Db 301 ESASECLPCDCNCRSGOEYFDELYRSTGHGGHCITNCRDNTDGAKCERCENPRLGNNE 360
QY 392 ACSPCHCSPVGSLSLSTQCDSYGRCSCKPGVMGDKDRCPGFHSLTEAGCRPCSDPSSGT 451
Db 361 ACSSCHCSPVGSLSLSTQCDSYGRCSCKPGVMGDKDRCPGFHSLTEAGCRPCSDPSSGI 420
QY 452 DECNVETGRCVCKDNVEGFNCERCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGYSVY 511
Db 421 DECNVETGRCVCKDNVEGFNCERCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGYSVY 480
QY 512 DISSTFQIDEDGWRVEQDRDSSEASLEWSSDRQYIAVISDSYFFRYFIAPVKFLGNQVLSY 571
Db 481 SISSTFQIDEDGWRVEQDRDSSEASLEWSSDRQYIAVISDSYFFRYFIAPVKFLGNQVLSY 540
QY 572 GQNLFSFVRVDRRDLRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYIFRLHEATDY 631
Db 541 GQNLFSFVRVDRRDLRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYIFRLHEATDY 600
QY 632 PWRPALSPFEFQKLLNLTSTKIRGTYSERSAGYDDVDTLQASRPGPGVATWVESCTCP 691
Db 601 PWRPALTPFEFQKLLNLTSTKIRGTYSERSAGYDDVDTLQASRPGPGVATWVESCTCP 660
QY 692 VGYGGQFCETCLPGYRRRETPSLGYPSPCVLCTCNHSETCDPETGVCDNRDNTAGPHCEK 751
Db 661 VGYGGQFCETCLPGYRRRETPSLGYPSPCVLCTCNHSETCDPETGVCDNRDNTAGPHCEK 720
QY 752 CSDGYGDSSTLTSSDCCQPCPCPGSSCAIVPKTKVCHTCPTGTAGKCELCDDGYFG 811
Db 721 CSDGYGDSSTLTSSDCCQPCPCPGSSCAIVPKTKVCHTCPTGTAGKCELCDDGYFG 780
QY 812 DPLGNGPVRLCRPCQCNNDIDPNAVGNCRNLTGECCLKIYNTAGFYCDRCKEGFFGNPL 871
Db 781 DPLGNGPVRLCRPCQCNNDIDPNAVGNCRNLTGECCLKIYNTAGFYCDRCKEGFFGNPL 840
QY 872 APNPADKCKACACN-YGTVOQSSCNPVTVGQCCQLPHVSGRDCGTCDFGYNLSQGGCE 930
Db 841 APNPADKCKACACN-PYGTVMQSSCNPVTVGQCCQLPHVSGRDCGTCDFGYNLSQGGCE 900
QY 931 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCECETNHFHFGPEGCKPCDCHEGSLSL 990
Db 901 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCECETNHFHFGPEGCKPCDCHEGSLSL 960
QY 991 QCKDDGRCECREGFGVGNRCDCQCEENYFYNRSWPGQCECPACVRLVKDKAAEHRVKLQELE 1050
Db 961 QCKDDGRCECREGFGVGNRCDCQCEENYFYNRSWPGQCECPACVRLVKDKAAEHRVKLQELE 1020
QY 1051 SLIANLGTGDDMTDQAFEDRLKEAEREVTDLLEAQQEVKQVQDQNLMDRLQVNSLSHSQ 1110
Db 1021 SLIANLGTGDDMTDQAFEDRLKEAEREVTDLLEAQQEVKQVQDQNLMDRLQVNSLSHSQ 1080
QY 1111 ISRLQIRNTIETGILAEARARSRVSTEQILIEIASRELEKAKM-AANVSITQPESTGEP 1169
Db 1081 ISRLQIRNTIETGILAEARARSRVSTEQILIEIASRELEKAKM-AANVSITQPESTGEP 1140
QY 1170 NNMTLLAEERARLAERHKEADDIIVRVAKTANETSAAEAYNLLRLTLAGENQTALEIEELN 1229
Db 1141 NNMTLLAEERARLAERHKEADDIIVRVAKTANETSAAEAYNLLRLTLAGENQTALEIEELN 1200
QY 1230 RKYEOAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSALNEANKIKKEA 1289
Db 1201 RKYEOAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSALNEANKIKKEA 1260
QY 1290 ADLRLIDQKLDYEDLREDMRGKEHEVKNLLEKGAEQQTADQLLARADAAKALAEAA 1349
Db 1261 ENLEQLIDQKLDYEDLREDMRGKEHEVKNLLEKGAEQQTADQLLARADAAKALAEAA 1320
QY 1350 KGRSTLQEAANDILNNLKDFDRRVNDNKTAAEALRRIPAINRTTAEANEKTRAEQALG 1409

Db 1321 KKGRDTLQEAANDILNNLKDPDRRVNDNKTAAABEALRKIPAINQTITEANEKTRAAQALG 1380
QY 1410 NAAADATEAKNKAHEABERIASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAEN 1469
Db 1381 SAAADATEAKNKAHEABERIASAVQKNATSTKABABERTFAEVTDLNNEVNNMLKQLEAEK 1440
QY 1470 ELKRQDDADQDMMAGMASQAAQAEAEELNARKAKNSVSSLLSQNLNLLDQLGQDLDVTLN 1529
Db 1441 ELKRQDDADQDMMAGMASQAAQAEAEINARKAKNSVTSLLSIINDLLEQLGQDLDVTLN 1500
QY 1530 KLNIEGSLNKADEMKASDLDRKVSLESEARKQEAAMIDYNRDIAEIIKDIHNLEDIK 1589
Db 1501 KLNIEGTLNKADEMKVSDLDLRKVSLENEAKQEAAMIDYNRDIEEIMKDIRNLEDIR 1560
QY 1590 KTLPTGCFNTPSIEKP 1605
Db 1561 KTLPSGCFNTPSIEKP 1576

RESULT 9

US-09-561-818A-24
; Sequence 24, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortessmaa, Jarrko
; APPLICANT: Tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 1576
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-818A-24

Query Match 92.5%; Score 8043; DB 4; Length 1576;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 1470; Conservative 57; Mismatches 47; Indels 2; Gaps 2;

QY 32 RAAMDECADEGGRPQRCMPEFVNAAFNVTVVATNCTGTPPEEYCVQGTGVTGKSKCHLCD 91
Db 1 QAAAMDECTDEGGRPQRCMPEFVNAAFNVTVVATNCTGTPPEEYCVQGTGVTGKSKCHLCD 60
QY 92 AGQQLQHGAFLTDYNNQADTTWQSQTMLAGVQYPNSINTLHLGKAFDITYVRLKFH 151
Db 61 AGQPHLQHGAFLTDYNNQADTTWQSQTMLAGVQYPSSINTLHLGKAFDITYVRLKFH 120
QY 152 TSRPESFAIYKRTREDGPWIPYQYYSGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDIS 211
Db 121 TSRPESFAIYKRTREDGPWIPYQYYSGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDIS 180
QY 212 PLTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNRLNLTGDEVFNDPKVLKSY 271
Db 181 PLTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNRLNLTGDEVFNDPKVLKSY 240
QY 272 YYAISDFAVGGRCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKCLPFFNDRPWRRATA 331
Db 241 YYAISDFAVGGRCKNGHASECMKNEFDKLVCNCKHNTYGVDCCKCLPFFNDRPWRRATA 300
QY 332 ESASECLPCDCNGRSQECYFDPPELYRSTGHGHCNTCRDNTDGAKCRCRENFRLGNTE 391
Db 301 ESASECLPCDCNGRSQECYFDPPELYRSTGHGHCNTCRDNTDGAHCRCRENFRLGNNE 360
QY 392 ACSCHCSPVGLSTQCDSYGRCSCKPGVMGDKDRQCPGFHSLTEAGRCPCSDPSGST 451
Db 361 ACSCHCSPVGLSTQCDSYGRCSCKPGVMGDKDRQCPGFHSLTEAGRCPCSDPSGSI 420
QY 452 DECNVETGRCVKONVEGFNCERCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGYSVY 511
Db 421 DECNVETGRCVKONVEGFNCERCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGYSVY 480

QY 512 DISSTFQIDEDGWRVEQRDGSEASLEWSSDRQYIAVISDSYFPRYFIAPVKELGNQVLSY 571
Db 481 SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPRYFIAPKFLGKQVLSY 540
QY 572 GQNLFSFRVDRRDLRLSAEDLVLEGAGLRVSVPLIAQNSYPSSETTVKYIFRLHEATDY 631
Db 541 GQNLFSFRVDRRDLRLSAEDLVLEGAGLRVSVPLIAQNSYPSSETTVKYIFRLHEATDY 600
QY 632 PWRPALSPFEFQKLLNLTISIKIRGTYSSAGVLDVTLQSAARPGVPATWVESCTCP 691
Db 601 PWRPALTPFEFQKLLNLTISIKIRGTYSSAGVLDVTLASARPGVPATWVESCTCP 660
QY 692 VGYGQCFETCLPGYRRTPSLGPPYSPCVLCTCNHSETCDPETGVCDNRDNTAGPHCEK 751
Db 661 VGYGQCFCEMCLSGYRRTPNLGPPYSPCVLCAACNHSETCDPETGVCDNRDNTAGPHCEK 720
QY 752 CSDGYGDSLTGTSSDCQPCPCPGGSSCAIVPKTBVVVCTHCPTGTAGKRCCLCDDGYFG 811
Db 721 CSDGYGDSLTGTSSDCQPCPCPGGSSCAVVPKTBVVVCTNCPTGTTGKRCCLCDDGYFG 780
QY 812 DPLGNGPVLRCRQCQNDNIDPNAVGNCRNLGTGELCKIYNTAGFYCDRCKEGFFGNPL 871
Db 781 DPLGRNGPVLRLCRLCQCSNIDPNAVGNCRNLGTGELCKIYNTAGFYCDRCCKDGFEGNPL 840
QY 872 APNPADKCKACACN-YGTVQQSSCNPNVTGQCQCCLPHVSGRDCGCTDPGYYNLQSGQGE 930
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QY 931 RCDCHALGSTNGQCDIRTGQCECQPGITGOHCERCETNHFHFGPEGCKPCDCHHESLSL 990
Db 901 RCDCHALGSTNGQCDIRTGQCECQPGITGOHCERCETNHFHFGPEGCKPCDCHHESLSL 960
QY 991 QCKDDGRCECREGFVGNRCDQCEENYFYNRSWPGQCECPACYRLVKDKAAEHRVKLOELE 1050
Db 961 QCKDDGRCECREGFVGNRCDQCEENYFYNRSWPGQCECPACYRLVKDKVADHRVKLOELE 1020
QY 1051 SLTANLGTGDDMTDQAFEDRLKEABEREVTDLLRBAQEVKVDQNLMDRLQRVNSSLHSQ 1110
Db 1021 SLTANLGTGDEMTDQAFEDRLKEABEREVMDLLRBAQVDKVDQNLMDRLQRVNSSLSSQ 1080
QY 1111 ISRLQNRNTIETGILABRARSVESTEOQLIEIASRELEKAKM-AANVSITQPESTGEP 1169
Db 1081 ISRLQNRNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSITQPESTGDP 1140
QY 1170 NNMTLLAEARRLAERHKOEADDIVRVAKTANETSAEAYNLLRLTLAGENQALIEBELN 1229
Db 1141 NNMTLLAEARLAEARHKOEADDIVRVAKTANDTSTEAYNLLRLTLAGENQATFEIENLN 1200
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Db 1201 RKYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDSETLENEANNIKWEA 1260
QY 1290 ADLRLIDQKLKDYEDLREDMRGKEHEVKNLLEKGAEQQTADQLLARADAALAEAEA 1349
Db 1261 ENLEQLIDQKLKDYEDLREDMRGKEHEVKNLLEKGTKEQQTADQLLARADAALAEAEA 1320
QY 1350 KKGRSTLQEAANDILNNLKDPDRRVNDNKTAAEEALERRIPAINRTIAEANEKTRAAQALG 1409
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QY 1410 NAAADATEAKNKAHEABERIASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAEN 1469
Db 1381 SAAADATEAKNKAHEABERIASAVQKNATSTKABABERTFAEVTDLNNEVNNMLKQLEAEK 1440
QY 1470 ELKRQDDADQDMMAGMASQAAQAEAEELNARKAKNSVSSLLSQNLNLLDQLGQDLDVTLN 1529
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QY 1530 KLNIEGSLNKADEMKASDLDRKVSLESEARKQEAAMIDYNRDIAEIIKDIHNLEDIK 1589
Db 1501 KLNIEGTLNKADEMKVSDLDLRKVSLENEAKQEAAMIDYNRDIEEIMKDIRNLEDIR 1560

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991	Q	C	K	D	D	G	R	C	E	R	E	G	F	V	G	N	R	C	D	Q	C	E	E	N	F	Y	N	R	S	W																															

RESULT 11
US-09-845-583A-10

		Sequence 10, Application US/09845583A			
		Patent No. 6635616			
		GENERAL INFORMATION:			
		APPLICANT: Burgeson, Robert			
		APPLICANT: Brunken, William Joseph			
		APPLICANT: Champlaud, Marie-France			
		APPLICANT: Hunter, Dale			
		TITLE OF INVENTION: LAMININ 15 AND USES THEREOF			
		FILE REFERENCE: 10287-056001			
		CURRENT APPLICATION NUMBER: US/09/845,583A			
		CURRENT FILING DATE: 2001-04-30			
		PRIOR APPLICATION NUMBER: 2000-05-01			
		PRIOR FILING DATE: 2000-05-01			
		NUMBER OF SEQ ID NOS: 18			
		SOFTWARE: FastSeq for Windows Version 4.0			
		SEQ ID NO 10			
		LENGTH: 1587			
		TYPE: PRT			
		ORGANISM: Mus musculus			
		US-09-845-583A-10			
		Query Match 41.4%; Score 3596.5; DB 4; Length 1587;			
		Best Local Similarity 43.8%; Pred. No. 5.2e-207;			
		Matches 707; Conservative 258; Mismatches 571; Indels 77; Gaps 24;			
QY	20	LLAVLAAGVAVRAAMDECADEGGRPQRCMPEFVNAFNVTVATNTCGTPPEEYCVQTG	79		
Db	12	LLAPRAAGAG-----MGACYDGAGRPQRCPLPVFENAAFGRLAQASHTCGSPEDFCPHVG	66		
QY	80	VTGVTKSCHLDCAQQHLOHGAFLTDVNNQADTTWQSQTMLAGVQYVNSINLTLLHGK	139		
Db	67	AAGAGAHQRCQDAADPQRHNASYLTDFHSQDESTWQSPSMAFGVQYPTSVNITLRLGK	126		
QY	140	AFDITYVRLKFHTSRPESFAIYKRTREDGEWIPYQYYSGCSENTYSKANRGFIRTTGGDEQ	199		
Db	127	AYEITYVRLKFHTSRPESFAIYKRSRADGEWEPYQYFASCSQKTYGRPEGQYLRPGEDER	186		
QY	200	QALCTDEFSDISPLTGGNVAFSTLEGPSAYNFEDNSPVLQEWTTATDIRVTNLRLNTFGD	259		
Db	187	VAFCTSEFSDISPLSGGNVAFSTLEGPSAYNFEEESPGLOEWTVSTELLISLDRLNTFGD	246		
QY	260	EVFNDPKVLKSYIYAISDFAVGGRCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKCLP	319		
Db	247	DIFDKPKVLQSYIYAVSDFSVGGRCKNGHASECGPDVAGQLACRCQHNTTGTDCERCCLP	306		
QY	320	FFNDRPWRRATAESASECLPCDCNRSQECVDFDPELYRSTGHGHCHTCNRDNTDGAKCER	379		
Db	307	FFQDRPWARGTAAEAHECLPCNCSGRSECTFDRELFRSTGHGRCHHCHRDHTAGPHCER	366		
QY	380	CRENFFRLGNTEACSPCHCSPVGLSTQDSYGRCSCKPGVMGDKDCRCQPGFHSLTEAG	439		
Db	367	CQENFYHWDPRMPCQPCDCQSAGSLHLQCDTGTCAKPTVTGKWCDCRCLPGFHSLSSEG	426		
QY	440	CRPCSDPSGSTDECNVETGRVCCKONVEGFNCERCKPGFFNLESSNPKGCTPCFCFGHS	499		
Db	427	CRPCTCNPAGSLDTC DPRSGRCPCCKENVEGNLCDCRCRPGTFNLQPHNPAGCSSCFCYGHS	486		
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Db	487	KVCASTAQFQVHHILSDFFHQAGGWWARSVGGSEHSPQWSPN-----GVLLSPDEEEELTA	542		
QY	560	PVKFLGNQVLSYQNLFSFRVDRDRRLSABDLVLEGAGLRVSVPLIAQGNNSYPSETTV	619		
Db	543	PGKFLGDQRFYSYQGPLILTFRVPPGDSPLPVQ-LRLEGTGLALS--LRHSSLSGPQDARA	599		
QY	620	KVIFRLH---EATDYPWRPALSPFEFQKLLNNLTSIKIRGTYSERSAG--YLDDEVTLQSA	674		
Db	600	SQGGRAQVPLQETSEDVAPPLPPFFHFQRLLANLTSRLRVSPGSPAGPVFLTEVRLTSA	659		
QY	675	RPFGVPATWVESCTCPVYGGQFCETCLPGVRETPSLGYPSPCVLCTCNHGHSETCDPE	734		
Db	660	RPGLSPASWVEICSCPTGYTGQFCESCAPGYKREMPQGGPYASCVPCTCNQHG-TCDPN	718		

RESULT 12
US-09-561-709B-3
; Sequence 3, Application US/09561709B
; Patent No. 6682911
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Champlaud, Marie-France
; APPLICANT: Olson, Pamela
; APPLICANT: Koch, Manuel
; APPLICANT: Brunken, William
; TITLE OF INVENTION: LAMININS AND USES THEREOF
; FILE REFERENCE: 10287-060001

735 TGVCDCRDNTAGPHCEKCSDDGYVGDSTLTGSSDCQPCPCPGSSCAIVPKTKVVCTHCP 794
719 TGICVCSHHTEGSPSCERCLPGFYGNPFAGQADDCQPCPCGQSACTTIPESGEVCTHCP 778
795 TGTAGRCRCELDDGYFGDPLGNSGVPRLCRPCQCNNDNIDPNAVGNRLTGECLCKIYNT 854
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855 AGFYCDRCCKEGFFGNPLAPNPADKCKACACN-YGTVQQSSSCNVPVTQCQCCLPHVSGRDC 913
839 TGDHCEHCQEGFYGSALAPRPADKCMPCSCHPQGSVSEQMPCDPVTGQCSCLPHVTARDC 898
914 GTCDPGYNLSQGGCERCDCCHALGSTNGQCDIRTGQCECQPGITGQHCHERCETNHFVG 973
899 SRCYPGFFDLPQGRGCRSCKCHPLGSQEDQCHPKTGCTCRPGVTGQACDRCOLGFFGSS 958
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1019 LVKEETAKLKLRLTTEGWLQSGDCGSPWGLDILLGEAPRGDVYQGH-----LLPGARE 1074
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1487 MASQAAQAEALNARKAKNSVSSLLSQNLNLDQLGQDLD--VDLNKLNIEGSLNKAKDE 1544
1476 LS-----EMEQQIRESRISLEKDIETLSSELLARLGLSLDTHQAPQALNETQWALERLQ 1530
1545 M-KASDLDRKVSDESEARKQEAAMDMYNDIAEIIKDIHNLEDIKTLPTGC 1596
1531 LGSPGSLQKLSLLEQESQQELQIQGFESDLAEIRADKQNLKLEAILHSLPENC 1583

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; CURRENT APPLICATION NUMBER: US/09/561,709B
; CURRENT FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 09/168,949
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: US 60/061,609
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1587
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-709B-3

Query Match      41.4%; Score 3596.5; DB 4; Length 1587;
Best Local Similarity 43.8%; Pred. No. 5.2e-207;
Matches 707; Conservative 258; Mismatches 571; Indels 77; Gaps 24;

Qy 20 LLAVLAAGVAVRAAMDECADEGRPQRCMPPEFVNAFNVVATNTCGTPPEEYCVQTG 79
Db 12 LLAPRAAGAG-----MGACYDGAAGPQRCPLPVFENAAFGRLAQASHTCGSPPEDFCPHVG 66

Qy 80 VTGVTKSHLCHLDAQQHLQHAFLTDYNNQADTTWQSQTMLAGVQYPNINLTLHLGK 139
Db 67 AAGAGAHQRCDAADPQRHNASYLTDFHSQDESTWQSPSMAFGVQYPTSVNITRLGK 126

Qy 140 AFDITYVLKFTSRPESFAIYKTRDGPWIPYQYSSGSCENTYSKANRGFIRTTGGDEQ 199
Db 127 AYEITYVLKFTSRPESFAIYKSRADGPWEYQYFASQKTYGRPEGQYLRPGEDER 186

Qy 200 QALCTDEFSDISPLTGGNVAFSITLGRPSAYNFEDNSPVLOEWVTATDIRVTILRLNTEFGD 259
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Db 307 FFQDRPWARGTAABAAHECLPCNCSGRSEECTFDELFERSTGHGRCHHCRDHTAGHCER 366

Qy 380 CRENFRLGNTEACSPCHCSPVGLSTQCDSYGRCSCKPQVMDGDKDCRCQPGFHSLSLEAG 439
Db 367 CQENFYHWPMPQPCDCQASGLHLQCDTGTCACTPTVTGWKDCRCLPGFHSLSLEGG 426

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Qy 500 SVCTNAVGSYVDISSTFQIDEDGWRVQORDGSEASLEWSSDRQYIAVISDSYFPRYFIA 559
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Qy 560 PVKFLGNQVLSYGQNLSPSFRVDRRDTRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTV 619
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Db 660 RPLSLPPASWVEICSCPTGYTGQFCESCAPGYKREMPQGGPYASCVPCTCNQHG-TCDPN 718

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Qy 795 TGTAGKRCCLDDGYFGDPLGSGNGPVRLCRPCQNDNIDPNAVGNCRNLTGECLKCIYNT 854
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Db 1299 ATLQTE---PLTMARSRLTATFASQLHQGARAALTOASSSVQAAATVTVMGARTLL 1355

Qy 1368 DFDRRVNDNKTAAEEALRRIPAINRTIAEANEKTRQAQLALGNAADAAATEAKNKAHE 1427
Db 1356 GMKLQFPFPKQDQALQKADSVSDLLADTRKTKQAERMLGNAAPLSSSAKKKGREAV 1415

Qy 1428 IASAAQKNAITSTKADAERTFGEVTDLDNEVNGMLRQL-EEAENELKRRKQDDADQDM 1486
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Qy 1487 MASQAQAEALNARKAKNSVSSLLSQLNNLLDQLGQDLD--VDLNLKLEIEGSLNKAX 1544
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Qy 1545 M-KASDLDRKVSLESEARKQEAAMDNRYNDIAEIIKDIHNLEDIKKTLPTGC 1596
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RESULT 13
US-08-317-450B-13
; Sequence 13, Application US/08317450B
; Patent No. 5660982
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Kallunki, Pekka
; APPLICANT: Pyke, Charles
; TITLE OF INVENTION: Laminin Chains: Diagnostic and
; TITLE OF INVENTION: Therapeutic Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & ALLEGRETTI, LTD.
; STREET: Ten South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
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TYPE: amino acid		Query Match		28.5%; Score 2476.5; DB 1; Length 1111;	
TOPOLOGY: linear		Best Local Similarity		39.4%; Pred. No. 4e-140;	
MOLECULE TYPE: protein		Matches 481; Conservative 215; Mismatches 389; Indels 137; Gaps 12;			
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QY	377	CERCRENFFRLNGNTEACSPCHCSPVGSLSLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHS	436		
DB	65	CEKCKNGFYRHRDRCLPCNCNSKGSLSARCDNSGRCSCKPGVTGARCDRCLPGFFHMLT	124		
QY	437	EAGC-----RPCSCDPSGSTDECNVETGRVCXKDNVEGFNCERCKPGFFNLESSNPK	488		
DB	125	DAGCTQDQRLDLSKDCDPAAGPC--DAGRCVCKPAVTGERCDRCRSGYNLDGGNPE	182		
QY	489	GCTPCFCFGHSSVCTNAVGYSVYDISSTFQIDEDGWRVEQORDGSEASLEWSSDRQYIAV	548		
DB	183	GCTQCFCYGHSAACRSAAEYSVHKITSTFHQDVGWKAVQRNGSPAKLQWSQRHQDVFS	242		
QY	549	SDSYFPRYFIAPVKFLGNQVLSYQNLSPSFRVDRDRTRLAEDLVLEGAGLRVSVPLIA	608		
DB	243	AQRLDPVYFVAPAKFLGNQOVSYGQSLSPDYRVDRGGRHPSAHDVILEGAGLRITAPLMP	302		
QY	609	QGNYSYSETTVKIFYRLHEATDYPWRPALSPFQKLLNNLTSIKIRGTYSERSAGYLDD	668		
DB	303	LGKTLPCGLTKTYTFRLNEHPNNWSPQLSYFEYRRLRLNLTAIRATYGEYSTGYIDN	362		
QY	669	VTQSARPPGVPATWVESCTCPVGYGGQFCETCLPGYRRETSLGPSPCVLCTCNHGS	728		
DB	363	VTLISARPVSGAPAPVVEQCICPVGYKGQFCQDCASGYKRDSARLPGFGTCIPCNCG-G	421		
QY	729	ETCDPETGVCDORDNTAGPHCEKCSGDGYVYGDSTLGTSSDCQPCPCGGSSCAIVPKTKEV	788		
DB	422	GACDPDTGDCYSGDENPDIEACDPIGFYNDP--HDPRSCKPCPCHNGFSCSVIPETEEV	479		
QY	789	VCTHCPTGTAGKRCCLCDDGYFGDPLGNSGPPVRLCRPCQCNDNIDPNAVGNCRNLGEC	848		
DB	480	VCNNCPPGVTGARCELCA	539		
QY	849	KCIYNTAGFYCDRCKEGFFGNPLAPNPADKCKACACACNYGTVQQSSCNPVTGQCCLPHV	908		
DB	540	KCIHNTAGIYCDQCKAGYFGDPLAPNPADKCRACNCN-----	576		
QY	909	SGRDCGTCDPGYYNLQSGQGCERCDC	968		
DB	577	-----	576		
QY	969	HFGFGECKPCDCHHEGSLSLQCKDDGRCECREGFVGNRCDOCEENYFYNRSWPGCQEC	1028		
DB	577	-----PMGSEP-----VGRSDGTVCVKPFGGPNCEH-----GAFSC	609		
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DB	610	PACYNQVKIQMDQFMQQLQRMELISKACQGGDGVVPDTELEGRMQQAEQALQDILRDAQI	669		
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QY	1208	YNLLLRTL-----AGENQTALEIEELNRYEQAKNISQDLEKQAARVHVEAKRAGDKA	1260		
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QY	1261	VEIYASVAQLTFVDSEALE-NEANKIKKEAADLRLIDQKLKDYEDLREDMRGKEHEVKN	1319
Db	849	LRLLDVSPLOGVSDQSFQVEEAKRIKQKADSLSSLVTRHMDEFKRTQKNLGNWKEEAQ	908
QY	1320	LLEKGKAEQQTADOLLARADAALAAEAAKGRSTLQEAANDILNNLKDFFDRRVNDNKTA	1379
Db	909	LQNGKSGREKSDQLLSRANLAKSRAQEAALSMGNATFFEYESILKNLREFDLQVDNRKAE	968
QY	1380	AEALRRIPAINRTIAEANEKTRQAQLALGNAADAAATEAKNKAHEAERIAAAQKNATST	1439
Db	969	ABEAMKRLSYISOKVSDASDKTQQAERALGSAADAAQRAKNGAGEALEISSEIEIGSL	1028
QY	1440	KADAERTFGEVTDLDNEVNGMLRQLEEAENELKRKQDDADQDMMAGMASQAQAELNA	1499
Db	1029	NLEANTVADGALAMEKGLASLXKSEMREVEGELEKELEFDTNMDAVQMVITEAQKVDTRA	1088
QY	1500	RKAKNSVSSLLSQLNNLLDQLG	1521
Db	1089	KNAGVTIQDTLNTLDGLLHLMG	1110

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Job time : 19.1415 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:56:24 ; Search time 40.8326 Seconds
(without alignments)
10937.572 Million cell updates/sec

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Perfect score: 8694
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	8694	100.0	1605	14	US-10-037-182-18	Sequence 18, Appl
2	8627	99.2	1607	9	US-09-938-275-10	Sequence 10, Appl
3	8527	98.1	1572	14	US-10-037-182-20	Sequence 20, Appl
4	8148	93.7	1609	14	US-10-037-182-14	Sequence 14, Appl
5	8148	93.7	1609	14	US-10-299-058-12	Sequence 12, Appl
6	8144	93.7	1609	9	US-09-938-275-11	Sequence 11, Appl
7	8144	93.7	1609	15	US-10-372-683-36	Sequence 36, Appl
8	8043	92.5	1576	14	US-10-037-182-16	Sequence 16, Appl
9	3596.5	41.4	1587	9	US-09-845-583-10	Sequence 10, Appl
10	3596.5	41.4	1587	12	US-10-262-839-210	Sequence 210, App
11	3593.5	41.3	1575	12	US-10-262-839-212	Sequence 212, App
12	3193	36.7	1557	15	US-10-369-493-6816	Sequence 6816, Ap
13	2592	29.8	1193	12	US-10-392-113-14	Sequence 14, Appl
14	2592	29.8	1193	14	US-10-171-311-115	Sequence 115, App
15	2592	29.8	1193	14	US-10-053-662A-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1

US-10-037-182-18

; Sequence 18, Application US/10037182

; Publication No. US20030044899A1

; GENERAL INFORMATION:

; APPLICANT: Tryggvason, Karl

; APPLICANT: Doi, Masayuki

; APPLICANT: Thyboll, Jill

; TITLE OF INVENTION: Recombinant Laminin 10

; FILE REFERENCE: 99-274-F

; CURRENT APPLICATION NUMBER: US/10/037,182

; CURRENT FILING DATE: 2001-12-21

; PRIOR APPLICATION NUMBER: 60/257,449

; PRIOR FILING DATE: 2000-12-21

; PRIOR APPLICATION NUMBER: 60/279,282

; PRIOR FILING DATE: 2001-03-28

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 18

; LENGTH: 1605

; TYPE: PRT

; ORGANISM: Mus musculus

US-10-037-182-18

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			Gaps	0;
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Db	61	VVATNTCGTPPEEYCVQTGVTGVTYSCHLCLDAGQQHLOHGAFLTDYNNQADTTWQSQI	120	
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Db 121 MLAGVQYPNSINLTILHLGKAFDITYVRLKFHTSRPESFAIYKRTREDGPWIPYQYYSGSC 180

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Db 181 ENTYSKANRGFIRTTGGDEQALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFDSNPSVLQE 240

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Db 241 WVTATDIRVTNLRLNTFGDEVFNDPKVLKSYYYAISDFAVGGRCKCNHGASECVKNEFDK 300

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Db 361 HGGHCTNCRDNTDGAKCERENFRRLGNTAECSPCHCSPVGSLSSTQCDSYGRCSCKPGV 420

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Db 481 NLESSNPKGCTPCFCFGHSSVCTNAVGYSVYDISSTFQIDEDGWRVEQRCSEASLEWSS 540

QY 541 DROYIAVISDSYFPRYFIAPVKFLGNQVLSYQNLFSFRVDRDRDTRLSABDLVLEGAGL 600

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RESULT 2

US-09-938-275-10

; Sequence 10, Application US/09938275

; Patent No. US20020111309A1

; GENERAL INFORMATION:

; APPLICANT: Gerardo Castillo

; APPLICANT: Alan Snow

; TITLE OF INVENTION: Therapeutic and Diagnostic Applications

; FILE OF INVENTION: of Laminin and Laminin-Derived Protein Fragments

; FILE REFERENCE: PROTEO.P03

; CURRENT APPLICATION NUMBER: US/09/938,275

; CURRENT FILING DATE: 2001-08-16

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 10

; LENGTH: 1607

; TYPE: PRT

; ORGANISM: Mus Musculus

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: Swissprot P02468

; DATABASE ENTRY DATE: 1989-07-01

US-09-938-275-10

Query Match 99.2%; Score 8627; DB 9; Length 1607;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 1598; Conservative 2; Mismatches 5; Indels 2; Gaps 2;

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Db 1081 TDLLEAQAQEVKVDQNLMDRLQVNSLHSLQISLQINRNTIETGILAEARSRVESTE 1140
QY 1140 QLIETASRELEKAKM-AANYVITQPESTGEPNNTLLAEAEARRLAERHKEAADDIVRVAK 1198
Db 1141 QLIETASRELEKAKMAAANYVITQPESTGEPNNTLLAEAEARRLAERHKEAADDIVRVAK 1200
QY 1199 TANETSABAYNLLRLTAGENQTALEIEELNRKYEQAQNIQSODLEKQAAARVHEAKRAGD 1258
Db 1201 TANETSABAYNLLRLTAGENQTALEIEELNRKYEQAQNIQSODLEKQAAARVHEAKRAGD 1260
QY 1259 KAVETIASVAQLTPVDSEALENEANKIKKEAADLRLIDQKLKYEDLREDMRGKEHEVK 1318
Db 1261 KAVETIASVAQLTPVDSEALENEANKIKKEAADLRLIDQKLKYEDLREDMRGKEHEVK 1320
QY 1319 NLEKGAEQQTADQLLARADAALAEAAKKGSRSTLQEAANDILNLDKDFDRRVNDNKT 1378
Db 1321 NLEKGAEQQTADQLLARADAALAEAAKKGSRSTLQEAANDILNLDKDFDRRVNDNKT 1380
QY 1379 AAEALRRIPAINRTIAEANEKTRQAALGNAADATEAKNKAHEAERIASAAQKNATS 1438

Db 1381 AAEALRRIPAINRTIAEANEKTRQAALGNAADATEAKNKAHEAERIASAVQKNATS 1440
QY 1439 TKADAERTFGEVTDLDNEVNGMLRQLLEAEANELKRKQDDADQDMMAGMASQAQAQEAELN 1498
Db 1441 TKADAERTFGEVTDLDNEVNGMLRQLLEAEANELKRKQDDADQDMMAGMASQAQAQEAELN 1500
QY 1499 ARKAKNSVSSLLSOLNNLLDQLGQDLDVTLNKLNEIEGSLNKADEMKAESDLDRKVSLE 1558
Db 1501 ARKAKNSVSSLLSOLNNLLDQLGQDLDVTLNKLNEIEGSLNKADEMKAESDLDRKVSLE 1560
QY 1559 SEARKQEAAMINDYNRDIAEIIKDIHNLEDIKKTLPFGCFNTPSIEKP 1605
Db 1561 SEARKQEAAMINDYNRDIAEIIKDIHNLEDIKKTLPFGCFNTPSIEKP 1607

RESULT 3

US-10-037-182-20
; Sequence 20, Application US/10037182
; Publication No. US20030044899A1
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Doi, Masayuki
; APPLICANT: Thyboll, Jill
; TITLE OF INVENTION: Recombinant Laminin 10
; FILE REFERENCE: 99-274-F
; CURRENT APPLICATION NUMBER: US/10/037,182
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,449
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/279,282
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 20
; LENGTH: 1572
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-037-182-20

Query Match 98.1%; Score 8527; DB 14; Length 1572;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 AMDECADEGGPQRCMPEFVNAFNVVATNTCGTPPEYCVQGTGVTGKSKHLCDAAG 93
Db 1 AMDECADEGGPQRCMPEFVNAFNVVATNTCGTPPEYCVQGTGVTGKSKHLCDAAG 60
QY 94 QHQLHGAAFLTDYNNQADTTWQSQTMLAGVQYVNSINLTLLHKGAFDITYVRLKFHTS 153
Db 61 QHQLHGAAFLTDYNNQADTTWQSQTMLAGVQYVNSINLTLLHKGAFDITYVRLKFHTS 120
QY 154 RPESFAIYKTRTREDGPIPIQYIYSGSCENTYSKANRGFIRTTGGDEQQALCTDEFSISPL 213
Db 121 RPESFAIYKTRTREDGPIPIQYIYSGSCENTYSKANRGFIRTTGGDEQQALCTDEFSISPL 180
QY 214 TGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTILNRLNTFGDEVFNDPKVLKSY 273
Db 181 TGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTILNRLNTFGDEVFNDPKVLKSY 240
QY 274 AISDFAVGGRCCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPFFNDRPWRRTAES 333
Db 241 AISDFAVGGRCCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPFFNDRPWRRTAES 300
QY 334 ASECLPCDCNRSQECYFDPPELYRSTGHGHCNTCRDNTDGAKECRERENFRRLGNTAEC 393
Db 301 ASECLPCDCNRSQECYFDPPELYRSTGHGHCNTCRDNTDGAKECRERENFRRLGNTAEC 360
QY 394 SPCHCSPVGLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLSLTAAGCRPCSCDFSGSTDE 453
Db 361 SPCHCSPVGLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLSLTAAGCRPCSCDFSGSTDE 420
QY 454 CNVETGRCVCKDNVEGFNCERCKPGFFNLESSNPKXGTCFCFCHGSSVCTNAVGSYVDI 513

Db 421 CNVETGRCVCKDNVEGFNCERCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGSVYDI 480
QY 514 SSTFQIDEDGWRVEQDGESEASLEWSSDROYIAVISDSYFPYFIAPVKFLGNQVLSYGQ 573
Db 481 SSTFQIDEDGWRVEQDGESEASLEWSSDROYIAVISDSYFPYFIAPVKFLGNQVLSYGQ 540
QY 574 NLSFSFRVDRDRTRLSAEDLVLEGAGLRVSVELIAQNSYSPSETTVKYIFRLHEATDYPW 633
Db 541 NLSFSFRVDRDRTRLSAEDLVLEGAGLRVSVELIAQNSYSPSETTVKYIFRLHEATDYPW 600
QY 634 RPALSPFEFQKLLNLTISKIRGTYSERSAGYLDVTLQ SARPGVPATWVESCTCPVG 693
Db 601 RPALSPFEFQKLLNLTISKIRGTYSERSAGYLDVTLQ SARPGVPATWVESCTCPVG 660
QY 694 YGGQFCETCLPGYRRETPSLGYPSPCVLCTCNHSETCDPETGVCDNRDNTAGPHCEKCS 753
Db 661 YGGQFCETCLPGYRRETPSLGYPSPCVLCTCNHSETCDPETGVCDNRDNTAGPHCEKCS 720
QY 754 DGYVGDSTLGTSSDCQPCPGSSCAIVPKTKBVVCTHCPTGTAGKRCCLCDDGYFGDP 813
Db 721 DGYVGDSTLGTSSDCQPCPGSSCAIVPKTKBVVCTHCPTGTAGKRCCLCDDGYFGDP 780
QY 814 LGSNGPVRLRCPQCNDNIDPNAVGNCRNLGTGELCKIYNTAGFYCDRCCKEGFFGNPLAP 873
Db 781 LGSNGPVRLRCPQCNDNIDPNAVGNCRNLGTGELCKIYNTAGFYCDRCCKEGFFGNPLAP 840
QY 874 NPADKCKACACNYGTVQOQSSCNPVGTQCQCLPHVSGRDCGTCDPGYVNLQSGQCERCDC 933
Db 841 NPADKCKACACNYGTVQOQSSCNPVGTQCQCLPHVSGRDCGTCDPGYVNLQSGQCERCDC 900
QY 934 CHALGSTNGQCDIRTGQCEQCPGITGQHCHERCETNHFGFEGPEGCKPCDCHHEGSLSLQCK 993
Db 901 CHALGSTNGQCDIRTGQCEQCPGITGQHCHERCETNHFGFEGPEGCKPCDCHHEGSLSLQCK 960
QY 994 DDGRCECREGFGVGNRCDQCEENFYFNRSWPGGCECPACRYLVKDKAAEHRVKLQLESLI 1053
Db 961 DDGRCECREGFGVGNRCDQCEENFYFNRSWPGGCECPACRYLVKDKAAEHRVKLQLESLI 1020
QY 1054 ANLGTGDDMVTDQAFEDRLKEABREVTDLLREAEQVKDQVQNLMDRLQVNSSLSHSQISR 1113
Db 1021 ANLGTGDDMVTDQAFEDRLKEABREVTDLLREAEQVKDQVQNLMDRLQVNSSLSHSQISR 1080
QY 1114 LQNTIRNTIEETGILAEARSRVESTEQLEIEIASRELEKAKMAANVSITQPESTGEPNNMT 1173
Db 1081 LQNTIRNTIEETGILAEARSRVESTEQLEIEIASRELEKAKMAANVSITQPESTGEPNNMT 1140
QY 1174 LLAEARRLAERHKQEAADDIVRVAKTANETSAAEYNLLRLTLAGENQTALEIEELNRKYE 1233
Db 1141 LLAEARRLAERHKQEAADDIVRVAKTANETSAAEYNLLRLTLAGENQTALEIEELNRKYE 1200
QY 1234 QAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLD 1293
Db 1201 QAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLD 1260
QY 1294 RLIDQKLKDYEDLREDMRGKEHEVKNLLEKGAEQQTADQLLARADAALAEAAKKGR 1353
Db 1261 RLIDQKLKDYEDLREDMRGKEHEVKNLLEKGAEQQTADQLLARADAALAEAAKKGR 1320
QY 1354 STLQEANDILNNLKDFRRVNDNKTAAEALRRIPAINRTIAEANETREAQLALGNAAA 1413
Db 1321 STLQEANDILNNLKDFRRVNDNKTAAEALRRIPAINRTIAEANETREAQLALGNAAA 1380
QY 1414 DATEAKNKAHEAERIAASAAQKNATSTKADAERTFGEVTDLDNEVGMRLQLEEAENELKR 1473
Db 1381 DATEAKNKAHEAERIAASAAQKNATSTKADAERTFGEVTDLDNEVGMRLQLEEAENELKR 1440
QY 1474 QODDADQDMMAGMASQAQAEALNARKAKNSVSSLLSOLNNLLDQLGQDQTDVLDNKLNE 1533
Db 1441 QODDADQDMMAGMASQAQAEALNARKAKNSVSSLLSOLNNLLDQLGQDQTDVLDNKLNE 1500
QY 1534 IEGSLNKAKDEMKAASDLDRKVSLESEARKQEAAIMDYNRDIAEIIKDIHNLEDIKKTLTP 1593

Db 1501 IEGSLNKAKDEMKAASDLDRKVSLESEARKQEAAIMDYNRDIAEIIKDIHNLEDIKKTLTP 1560
QY 1594 TGCFTNTPSIEKP 1605
Db 1561 TGCFTNTPSIEKP 1572
RESULT 4
US-10-037-182-14
; Sequence 14, Application US/10037182
; Publication No. US20030044899A1
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Doi, Masayuki
; APPLICANT: Thyboll, Jill
; TITLE OF INVENTION: Recombinant Laminin 10
; FILE REFERENCE: 99-274-F
; CURRENT APPLICATION NUMBER: US/10/037,182
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,449
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/279,282
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 1609
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-037-182-14
Query Match 93.7%; Score 8148; DB 14; Length 1609;
Best Local Similarity 92.8%; Pred. No. 0;
Matches 1493; Conservative 59; Mismatches 53; Indels 4; Gaps 3;
QY 1 MTGGGAAALALQPRGLWPLLAVL--AAVAGCVRAAMDECADEGGRPQRCMPEFVNAAFN 58
Db 1 MRGSHRAAPALRPRGLWPVLAVLAAAAAGCAQAAAMDECTDEGGRPQRCMPEFVNAAFN 60
QY 59 VTIVATNTCGTPPEEYCVQGTGVTGKTSCHLCAAGQHLQHGAAFLTDYNNQADTTWQOS 118
Db 61 VTIVATNTCGTPPEEYCVQGTGVTGKTSCHLCAAGQHLQHGAAFLTDYNNQADTTWQOS 120
QY 119 QTMLAGVQYPNSINLTLLHGKAFDITYVRLKFTSRPESFAIYKRTREDGWPWIPYQYISG 178
Db 121 QTMLAGVQYPSSINLTLLHGKAFDITYVRLKFTSRPESFAIYKRTREDGWPWIPYQYISG 180
QY 179 SCENTYSKANRGFIRTGDEQALCTDEFSDISPLTGGNVAFSTLEGPSAYNFDNSPVL 238
Db 181 SCENTYSKANRGFIRTGDEQALCTDEFSDISPLTGGNVAFSTLEGPSAYNFDNSPVL 240
QY 239 QEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSYIYAIISDFAVGGRCKCNHASECMKNEF 298
Db 241 QEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSYIYAIISDFAVGGRCKCNHASECMKNEF 300
QY 299 DKLMCNCKHNTYGVDCCKLPFFNDRPWRRTAEASASECLPCDCNGRSQECYFDPPELYRS 358
Db 301 DKLVNCKHNTYGVDCCKLPFFNDRPWRRTAEASASECLPCDCNGRSQECYFDPPELYRS 360
QY 359 TGHGGHCTNCRDNTDGAKCERCENFFRLGNTAEACSPCHSPVGSLSLSTQCDSYGRCSCKP 418
Db 361 TGHGGHCTNCRDNTDGAKCERCENFFRLGNTAEACSPCHSPVGSLSLSTQCDSYGRCSCKP 420
QY 419 GVMGDKCDRCQPGFHSLSLTAEGCRPCSDPSGSTDECNVETGRCVCKDNVEGFNCERCKPG 478
Db 421 GVMGDKCDRCQPGFHSLSLTAEGCRPCSDPSGSTDECNVETGRCVCKDNVEGFNCERCKPG 480
QY 479 FFNLESSNPKGCTPCFCFGHSSVCTNAVGSYVYDISSTFOIDEDGWRVEQDGESEASLEW 538
Db 481 FFNLESSNPKGCTPCFCFGHSSVCTNAVGSYVYDISSTFOIDEDGWRVEQDGESEASLEW 540
QY 539 SDDRQYIAVISDSYFPYFIAPVKFLGNQVLSYQNLSPFRVDRDTRLAEDLVLEGA 598

Db 541 SSERQDIAVISDSYFPRYFIAPAKFLGKQVLSYQNLSPFSFRVDRDRTRLSAEDLVLEGA 600

Qy 599 GLRVSVPLIAQGNYSYSETTVKYIFRLHEATDYPWRPALSPFEFQKLLNLTISIKIRGTY 658

Db 601 GLRVSVPLIAQGNYSYSETTVKYVFRLEATDYPWRPALTPFEFQKLLNLTISIKIRGTY 660

Qy 659 SERSAGYLDVTLQSAARPGVGPATWVESCTCPVGYGGQFCETCLPGYRRETSLGPYSP 718

Db 661 SERSAGYLDVTLASARPGVGPATWVESCTCPVGYGGQFCSEMCLSGYRRETNLGPYSP 720

Qy 719 CVLCTCNHSETCDPETGVCDNRDNTAGPHCEKSDGYGDSLTGSSDCQPCPCGGSS 778

Db 721 CVLCACNGHSETCDPETGVCDNRDNTAGPHCEKSDGYGDSLTGSSDCQPCPCGGSS 780

Qy 779 CAIVPKTKEVVCTHCTGTAGKRCCLDDGYFGDPLGSGNPVRLCRPCQNDNIDPNAVG 838

Db 781 CAVVPKTKEVVCTNCPTGTTGKRCCLDDGYFGDPLGRNPVRLCRLCQCSNDIDPNAVG 840

Qy 839 NCNRLTGECLKCIYNTAGFYCDRCCKEGFFGNPLAPNADKCKACACN-YGTVQQSSCNP 897

Db 841 NCNRLTGECLKCIYNTAGFYCDRCCKGFFGNPLAPNADKCKACNPNPYGTMKQQSSCNP 900

Qy 898 VTGQCQCLPHVSGRDCGTCDPGYNYLQSGQGBRCDCHALGSTNGQCDIRTGQCECQPGI 957

Db 901 VTGQCECLPHVTQDCGACDPGFYNYLQSGQGBRCDCHALGSTNGQCDIRTGQCECQPGI 960

Qy 958 TGOHCERCETNHFSGPBGKPCDCHHEGSLSLQCKDDGRCECREGFVGNRCDQCEENYF 1017

Db 961 TGOHCERCEVNHFGPBGKPCDCHPEGSLSLQCKDDGRCECREGFVGNRCDQCEENYF 1020

Qy 1018 YNRSWPGQCECPACRYLVKDAAEHRVKLQELLESILANLGTGDDMVTDOAFEDRLKEAER 1077

Db 1021 YNRSWPGQCECPACRYLVKDVADHRVKLQELLESILANLGTGDEMVTDOAFEDRLKEAER 1080

Qy 1078 EVTDLLREAQEVKDVQNLMDRLQRVNSSLHSQISRLQNIENRTIETGILAEARSRVES 1137

Db 1081 EVMDLLREAQDVKDVQNLMDRLQRVNNTLSSQISRLQNIENRTIETGNLAEQARAHVEN 1140

Qy 1138 TEQLIEIASRELEKAKM-AANVSITQPESTGEFNNMTLLAEAEARRLAERHKQEADDIVRV 1196

Db 1141 TERLIEIASRELEKAKVAAANVSITQPESTGTFNNMTLLAEAEARKLAERHKQEADDIVRV 1200

Qy 1197 AKTANETSAAEYNLLRTLAGEHOTALEIEELNRYEQAKNISQDLEKQAAARVHEEAKRA 1256

Db 1201 AKTANDTSTEAYNLLRTLAGEHOTAFEIEELNRYEQAKNISQDLEKQAAARVHEEAKRA 1260

Qy 1257 GDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLDRLLDQKLKYEDLREDMRGKEHE 1316

Db 1261 GDKAVEIYASVAQLSPDSETLENEANNIKMEAEENLEQLIDQKLKYEDLREDMRGKELE 1320

Qy 1317 VKNLLEKGAEOQTADQLLARADAAKALAEAAKKGRSTLQEBANDILNLLKDFDRRVNDN 1376

Db 1321 VKNLLEKKGKTEQQTADQLLARADAAKALAEAAKKGRDRTLQEBANDILNLLKDFDRRVNDN 1380

Qy 1377 KTAABEALRRIPAINRTIAEANEKTREAOALGNAADATEAKNKAHEAEERIASAAQKNA 1436

Db 1381 KTAABEALRKIPAINQITTEANEKTREAOQALGSAADATEAKNKAHEAEERIASAVQKNA 1440

Qy 1437 TSTKADAERTFGEVTDLDNEVNGMLRQLEEAENELKXKQDDADQDMMAGMASQAAQAEAE 1496

Db 1441 TSTKAEARTFAEVTDLDDNEVNNMLKQLEAEKELKXKQDDADQDMMAGMASQAAQAEAE 1500

Qy 1497 LNARKAKNSVSSLLSQNLNLLDQLGQDVTDLNKLNEIEGSLNKADEMKAESDLDKRVSD 1556

Db 1501 LNARKAKNSVTSLLSIINDLLEQLGQDVTDLNKLNEIEGTLNKADEMKVSDLDKRVSD 1560

Qy 1557 LESEARKQEAAMIDYNRDIAEIIKDIHNLEDIKKTLPTGCFNTPSIEKP 1605

Db 1561 LENEAKQEAAMIDYNRDIEEIMKDIRNLEDIRKTLPSGCFNTPSIEKP 1609

; Sequence 12, Application US/10299058
; Publication No. US20030103975A1
; GENERAL INFORMATION:
; APPLICANT: JONES, JONATHAN C.R.
; APPLICANT: GONZALES, MEREDITH
; TITLE OF INVENTION: MODULATION OF ANGIOGENESIS AND ENDOTHELIALIZATION
; FILE REFERENCE: 1720-1-002 CIP
; CURRENT APPLICATION NUMBER: US/10/299,058
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/706,235
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: 60/163,199
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1609
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-299-058-12

Query Match 93.7%; Score 8148; DB 14; Length 1609;
Best Local Similarity 92.8%; Pred. No. 0;
Matches 1493; Conservative 59; Mismatches 53; Indels 4; Gaps 3;

Qy 1 MTGGRAALALQPRGLWPLJAVL--AAVAGCVRAAMDECADEGGRPQRCMPEFVNAAFN 58

Db 1 MRGSHRAAPALRPRGLWPLVAVLAAAAAGCAQAAMDECTDEGGRPQRCMPEFVNAAFN 60

Qy 59 VTIVATNTCGTPPEEYCVQTGVTGKTSCHLCDACQOHLQHGAAFLTDYNNQADTTWQS 118

Db 61 VTIVATNTCGTPPEEYCVQTGVTGKTSCHLCDACQOHLQHGAAFLTDYNNQADTTWQS 120

Qy 119 QTMLAGVQYPNNSINLTHLGKAFDITYVRLKFHTSRPESFAIYKRTREDGWPYQYYSG 178

Db 121 QTMLAGVQYPPSSINLTHLGKAFDITYVRLKFHTSRPESFAIYKRTREDGWPYQYYSG 180

Qy 179 SCENTYSKANRGFIRTGDEQOALCTDEFSDISPLTGGNVAFSTLEGPSAYNFDNSPVL 238

Db 181 SCENTYSKANRGFIRTGDEQOALCTDEFSDISPLTGGNVAFSTLEGPSAYNFDNSPVL 240

Qy 239 QEWYTATDIRVTNLNLTGDEVFNDPKVLKSYYYAISDFAVGGRCKCNHGASECVKNEF 298

Db 241 QEWYTATDIRVTNLNLTGDEVFNDPKVLKSYYYAISDFAVGGRCKCNHGASECMKNEF 300

Qy 299 DKLMCNCKHNTYGVDCCKLPFFNDRPWRRAATAESASECLPCDNGRSQECYFDPPELYRS 358

Db 301 DKLVNCKHNTYGVDCCKLPFFNDRPWRRAATAESASECLPCDNGRSQECYFDPPELYRS 360

Qy 359 TGHGGHCTNCRDNTDGAKCERCENFRRLGNTACSPCHSPVGSLSQCDSYGRCSCKP 418

Db 361 TGHGGHCTNCQDNTDGAHCERCENFRRLGNNACSSCHSPVGSLSQCDSYGRCSCKP 420

Qy 419 GVMGDKCDRCQPGFHSLTEAGCRPCSDPSGSDTDECNVETGRCVCCKDNVEGFNCERCKPG 478

Db 421 GVMGDKCDRCQPGFHSLTEAGCRPCSDPSGSDTDECNVETGRCVCCKDNVEGFNCERCKPG 480

Qy 479 FNNLESSNPKGCTPCFCFGHSSVCTNAVGSVYDIISSFTQIDEDGWRVEORDGSEASLEW 538

Db 481 FNNLESSNPRGCTPCFCFGHSSVCTNAVGSVYISISSTFQIDEDGWRVEORDGSEASLEW 540

Qy 539 SSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYQNLSPFSFRVDRDRTRLSAEDLVLEGA 598

Db 541 SSERQDIAVISDSYFPRYFIAPAKFLGKQVLSYQNLSPFSFRVDRDRTRLSAEDLVLEGA 600

Qy 599 GLRVSVPLIAQGNYSYSETTVKYIFRLHEATDYPWRPALSPFEFQKLLNLTISIKIRGTY 658

Db 601 GLRVSVPLIAQGNYSYSETTVKYVFRLEATDYPWRPALTPFEFQKLLNLTISIKIRGTY 660

Qy 659 SERSAGYLDVTLQSAARPGVGPATWVESCTCPVGYGGQFCETCLPGYRRETSLGPYSP 718

Db 661 SERSAGYLDVTLASARPGVGPATWVESCTCPVGYGGQFCSEMCLSGYRRETNLGPYSP 720

QY 719 CVLCTCNHGHSETCDPETGVCDRCRDNNTAGPHCEKSDGYGDSLTGTSSDCQPCPCPGSS 778
Db 721 CVLCAACNGHSETCDPETGVNCNCRDNNTAGPHCEKSDGYGDSLTGTSSDCQPCPCPGSS 780
QY 779 CAIVPKTKEVWCTHPTGTAGKRCCLCDDGYFGDPLGSGNPGVRLCRPCQCNNDIDPNAVG 838
Db 781 CAVVPKTKEVWCTNCPTGTTGKRCCLCDDGYFGDPLGSGNPGVRLCRLCQCSNDIDPNAVG 840
QY 839 NCNRLTGECLKCIYNTAGFYCDRCCKEGFFGNPLAPNADKCKACACN-YGTVQQSSCNP 897
Db 841 NCNRLTGECLKCIYNTAGFYCDRCCKEGFFGNPLAPNADKCKACNPNYGTWKQSSCNP 900
QY 898 VTGQCQCLPHVSGRDCGTCDPGYNNLQSGQCRCRCDHALGSTNGQCQDRTGQCECQPGI 957
Db 901 VTGQCECLPHVTGQDCGACDPGFYNLQSGQCRCRCDHALGSTNGQCQDRTGQCECQPGI 960
QY 958 TGQHCERCETNHFPGPEGCKPCDCHHEGSLSLQCKDDGRCECREGFVGNRCDOCEENYF 1017
Db 961 TGQHCERCETNHFPGPEGCKPCDCHHEGSLSLQCKDDGRCECREGFVGNRCDOCEENYF 1020
QY 1018 YNRSWPGCQCECPACRYLVKDKAAEHRVKLQELSLIANLGTGDDMTDQAFEDRLKEAER 1077
Db 1021 YNRSWPGCQCECPACRYLVKDKVADHRVKLQELSLIANLGTGDEMVTQAFEDRLKEAER 1080
QY 1078 EVTDLLREAEVKDQVQDQNLMDRLQVNSLHQSISRLQINRTIETGILAEARARSVES 1137
Db 1081 EVMDLLREAQDQVQDQNLMDRLQVNNLTSSQISRLQINRTIETGILAEARAHVEN 1140
QY 1138 TEQLTETIASRELEKAKM-AANVSIQPESTGEPNNTLLAEAEARRLAERHKQAEADDIVRV 1196
Db 1141 TERLTETIASRELEKAKAAANVSQTPESTGDPNNTLLAEAEARKLAERHKQAEADDIVRV 1200
QY 1197 AKTANETSAAEAYNLLRLTAGENQTALEIEELNRKYEQAKNISQDLEKQAARVHEEAKRA 1256
Db 1201 AKTANDTSTAEAYNLLRLTAGENQTAFAIEELNRKYEQAKNISQDLEKQAARVHEEAKRA 1260
QY 1257 GDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLRLIDQKLKYEDLREDMRGKEHE 1316
Db 1261 GDKAVEIYASVAQLSPLDSETLENEANNIKMEAEENLEQLIDQKLKYEDLREDMRGKELE 1320
QY 1317 VKNLLEKGAEQQTADQLLARADAALAEAAKKGRTLQEANDILNLLKDFDRRVNDN 1376
Db 1321 VKNLLEKGTQEQQTADQLLARADAALAEAAKKGRTLQEANDILNLLKDFDRRVNDN 1380
QY 1377 KTAABEALRRIPAINRTIAEANEKTRQAQLALGNAAADATEAKNKAHEAERIASAAQKNA 1436
Db 1381 KTAABEALRKIPAINQTI TEANEKTRQAQALGSAADATEAKNKAHEAERIASAVQKNA 1440
QY 1437 TSTKADARTFGEVTDLDNEVNGMLRQLEEAENELKRDQDADQDMMAGMASQAAQAE 1496
Db 1441 TSTKAEARTFAEVTDLNEVNNMLKQLEAEKELKRDQDADQDMMAGMASQAAQAE 1500
QY 1497 LNARKAKNSVSSLLSQLNNLLDQLGQDQDVLNKLNEIEGSLNKAKDEMKAASDLDRKVS 1556
Db 1501 INARKAKNSVTSLLSIINDLLEQLGQDQDVLNKLNEIEGTLNKAKDEMKVSDLDRKVS 1560
QY 1557 LESEARKQEAAMNDYNRDIAEIIKDHNLEDIKKTLPFGCFNTPSIEKP 1605
Db 1561 LENEAKQEAAMNDYNRDIEEIMKDINLEDIRKTLPSGCFNTPSIEKP 1609

RESULT 6
US-09-938-275-11
; Sequence 11, Application US/09938275
; Patent No. US2002011309A1
; GENERAL INFORMATION:
; APPLICANT: Gerardo Castillo
; APPLICANT: Alan Snow
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications
; TITLE OF INVENTION: of Laminin and Laminin-Derived Protein Fragments
; FILE REFERENCE: PROTEO.P03
; CURRENT APPLICATION NUMBER: US/09/938,275
; CURRENT FILING DATE: 2001-08-16

; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1609
; TYPE: PRT
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Swissprot P11047
; DATABASE ENTRY DATE: 1991-11-01
US-09-938-275-11

Query Match 93.7%; Score 8144; DB 9; Length 1609;
Best Local Similarity 92.7%; Pred. No. 0;
Matches 1492; Conservative 59; Mismatches 54; Indels 4; Gaps 3;

QY 1 MTGGRAALALQPRGLWPLLAVL--AAVAGCVRAAMDECADEGGRPQRCMPEFVNAAFN 58
Db 1 MRGSHRAAPALRPRGLWPVLAVLAAAAAGCAQAAMDECTDEGGRPQRCMPEFVNAAFN 60
QY 59 VTVVATNTCGTPPEEYCVQGTGVTGKSCHLCDAGQQLQHGAFLTDYNNQADTTWQS 118
Db 61 VTVVATNTCGTPPEEYCVQGTGVTGKSCHLCDAGQQLQHGAFLTDYNNQADTTWQS 120
QY 119 QTMLAGVQYPSINLTLHLKAFDITYVRLKFHTSRPESFAIYKRTREDGWPWIPYQYSG 178
Db 121 QTMLAGVQYPSINLTLHLKAFDITYVRLKFHTSRPESFAIYKRTREDGWPWIPYQYSG 180
QY 179 SCENTYSKANRGFIRTGDEQALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFDNSPVL 238
Db 181 SCENTYSKANRGFIRTGDEQALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFDNSPVL 240
QY 239 QEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSYIYAIISDPAVGGRCCKNGHASECVKNEF 298
Db 241 QEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSYIYAIISDPAVGGRCCKNGHASECVKNEF 300
QY 299 DKLMCNCKHNTYGVDCCKLPFFNDRPWRRTAEASASECLPCDCNGRSQCXYEDPELYRS 358
Db 301 DKLVGNCKHNTYGVDCCKLPFFNDRPWRRTAEASASECLPCDCNGRSQCXYEDPELYRS 360
QY 359 TGHGHTNCRDNTDGAKCECRENFRLGNTEACSPCHCSVPSLSLSTQCDSYGRCSCKP 418
Db 361 TGHGHTNCQDNTDGAHCRERENFRLGNEACSCSCHSPVGSLSLSTQCDSYGRCSCKP 420
QY 419 GVMGDKDRCPQGFHSLTEAGCRPCSDPSGSDTECNVETGRCVKONVEGNCERCKPG 478
Db 421 GVMGDKDRCPQGFHSLTEAGCRPCSDPSGSDTECNVETGRCVKONVEGNCERCKPG 480
QY 479 FFNLESSNPKGCTPCFCFGHSSVCTNAVGSVYDISSTFQIDEDGWRVEQRDGSEASLEW 538
Db 481 FFNLESSNPRGCTPCFCFGHSSVCTNAVGSVYDISSTFQIDEDGWRVEQRDGSEASLEW 540
QY 539 SDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYQNLSPFRVDRDRLSAEDLVLEGA 598
Db 541 SSERQDIAVISDSYFPRYFIAPAKFLGKQVLSYQNLSPFRVDRDRLSAEDLVLEGA 600
QY 599 GLRVSVPLIAQNSYPSSETTVKIFRLHEATDYPPRPALSPFQKLLNNLTSIKIRGTY 658
Db 601 GLRVSVPLIAQNSYPSSETTVKIFRLHEATDYPPRPALTPPFQKLLNNLTSIKIRGTY 660
QY 659 SERSAGYLDVTLQARPGVPATWVESCTCPVGYGGQFCETCLPGYRRETSLGPYSP 718
Db 661 SERSAGYLDVTLASARPGVPATWVESCTCPVGYGGQFCMCLSGYRRETSLGPYSP 720
QY 719 CVLCTCNHGHSETCDPETGVCDRCRDNNTAGPHCEKSDGYGDSLTGTSSDCQPCPCPGSS 778
Db 721 CVLCAACNGHSETCDPETGVNCNCRDNNTAGPHCEKSDGYGDSLTGTSSDCQPCPCPGSS 780
QY 779 CAIVPKTKEVWCTHPTGTAGKRCCLCDDGYFGDPLGSGNPGVRLCRPCQCNNDIDPNAVG 838
Db 781 CAVVPKTKEVWCTNCPTGTTGKRCCLCDDGYFGDPLGSGNPGVRLCRLCQCSNDIDPNAVG 840
QY 839 NCNRLTGECLKCIYNTAGFYCDRCCKEGFFGNPLAPNADKCKACACN-YGTVQQSSCNP 897

Db 841 NCNRLTGECLKCIYNTAGFYCDRCCKDGFPGNPLAPNPADKCKACNCNPGYTMKQSSCNP 900

QY 898 VTGQCQCCLPHVSGRDCGTCDPGYYNLQSGQCERCDCCHALGSTNGQCDIRTGQCECQPGI 957

Db 901 VTGQCECLPHVTGQDCGACDPGFYNLQSGQCERCDCCHALGSTNGQCDIRTGQCECQPGI 960

QY 958 TGOHCERCETNHFPGPEGCKPCDCHHGGSLQCKDDGRCECEGFGVGNRCDCQCEENYF 1017

Db 961 TGOHCERCEVNHFGPEGCKPCDCHHGGSLQCKDDGRCECEGFGVGNRCDCQCEENYF 1020

QY 1018 YNRSWPGCQCEPACRYRLVKDAAEHVRVKLQELSLIANLTGTDMDVTDQAFEDRLKEAER 1077

Db 1021 YNRSWPGCQCEPACRYRLVKDADHRVKLQELSLIANLTGTDMDVTDQAFEDRLKEAER 1080

QY 1078 EVTDLLREAEVKVDQONLMDRLQRVNSSLHSQISRLQNRNTIETGILAEARARSRVES 1137

Db 1081 EVMDLLREAEVKVDQONLMDRLQRVNSSLSSQISRLQNRNTIETGNLAEQARAHVEN 1140

QY 1138 TEOLIEIASRELEKAKM-AANVSITQPESTGEPNNMTLLAEAEARPLAERHKQAEADDIVRV 1196

Db 1141 TERLIEIASRELEKAKVAAANVSITQPESTGEPNNMTLLAEAEARKLAERHKQAEADDIVRV 1200

QY 1197 AKTANETSAEAYNLLRLTLAGENQTALEIEELNRKYEQAQKNSQDLEKQAARVHEEAkra 1256

Db 1201 AKTANDTSTEAYNLLRLTLAGENQTAFEIEELNRKYEQAQKNSQDLEKQAARVHEEAkra 1260

QY 1257 GDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLRLIDQKLKDYEDLREDMRGKEHE 1316

Db 1261 GDKAVEIYASVAQLSPDSETLENEANNIKMEAEENLEQLIDQKLKDYEDLREDMRGKELE 1320

QY 1317 VKNLLEKGAEOQTADQLLARADAAKALAEBAKKGRRSTLQEAANDILNNLKFDRRVNDN 1376

Db 1321 VKNLLEKGTQEQOTADQLLARADAAKALAEBAKKGRRDTLQEAANDILNNLKFDRRVNDN 1380

QY 1377 KTAEEEEALRRIPAINRTIAEANEKTRAEQALGNAADAATEAKNKAHEAERIASAAQKNA 1436

Db 1381 KTAEEEEALRKIPAINQTI TEANEKTRAEQALGSAADAATEAKNKAHEAERIASAVQKNA 1440

QY 1437 TSTKADAERTFGEVTDLDNEVNGMLRQLBEAEENELKRKQDDADQDMMAGMASQAAQAE 1496

Db 1441 TSTKAEARTFAEVTDLNEVNNMLKQLQEAELKRKQDDADQDMMAGMASQAAQAE 1500

QY 1497 LNARKAKNSVSSLSQLNNLLDOLGOLDTVDLNKLNEIEGSLNKADEMKA SLDLRKVS D 1556

Db 1501 INARKAKNSVTSLSIINDLLEQLGOLDTVDLNKLNEIEGTLNKADEMKA SLDLRKVS D 1560

QY 1557 LESEARKQEAAMNDYNRDIAEIIKDIHNLEDIKTTLPTGCFNTPSIEKP 1605

Db 1561 LENEAKQEAAMNDYNRDIEEIMKDIRNLEDIRKTLPSGCFNTPSIEKP 1609

RESULT 7

US-10-372-683-36

; Sequence 36, Application US/10372683

; Publication No. US20040009171A1

; GENERAL INFORMATION:

; APPLICANT: GERRITSEN, MARY E.

; APPLICANT: PEALE JR., FRANKLIN V.

; APPLICANT: WU, THOMAS D.

; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA

; FILE REFERENCE: P1928R1P1

; CURRENT APPLICATION NUMBER: US/10/372,683

; CURRENT FILING DATE: 2003-02-21

; PRIOR APPLICATION NUMBER: US 10/271,690

; PRIOR FILING DATE: 2002-10-16

; PRIOR APPLICATION NUMBER: US 60/344,534

; PRIOR FILING DATE: 2001-10-18

; NUMBER OF SEQ ID NOS: 49

; SEQ ID NO 36

; LENGTH: 1609

; TYPE: PRT

; ORGANISM: Homo sapien

US-10-372-683-36

Query Match 93.7%; Score 8144; DB 15; Length 1609;

Best Local Similarity 92.7%; Pred. No. 0;

Matches 1492; Conservative 59; Mismatches 54; Indels 4; Gaps 3;

QY 1 MTGGGRAALALQPRGLWPLLAVL--AAVAGCVRAAMDECADEGGRPQRCMPEFVNAAFN 58

Db 1 MRGSHRAAPALRPRGLWPLLAVLAAAAAGCAQAAAMDECTDEGGPRQRCMPEFVNAAFN 60

QY 59 VTVVATNTCGTPPEEYCVQTVGTGVTGKSHCLCDAGQOHLQHGAAFLTDYNNQADTTWQOS 118

Db 61 VTVVATNTCGTPPEEYCVQTVGTGVTGKSHCLCDAGQPHLQHGAAFLTDYNNQADTTWQOS 120

QY 119 QTMLAGVQYPNSINLTHLGKAFDITYVRLKFHTSRPESFAIYKRTREDDGFWIPYQYYS 178

Db 121 QTMLAGVQYPSSINLTHLGKAFDITYVRLKFHTSRPESFAIYKRTREDDGFWIPYQYYS 180

QY 179 SCENTYSKANRGFIRTTGGDEQQAALCTDEFSDISPLTGGNVAFSTLEGPSAYNFDNSPVL 238

Db 181 SCENTYSKANRGFIRTTGGDEQQAALCTDEFSDFSPLTGGNVAFSTLEGPSAYNFDNSPVL 240

QY 239 QEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSYYYAISDFAVGGRCKNCNGHASECVKNEF 298

Db 241 QEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSYYYAISDFAVGGRCKNCNGHASECMKNEF 300

QY 299 DKLMCNCKHNTYVDCEKCLPFENDRPWRRAATAESASECLPCDCNGRSQECYFDPPELYRS 358

Db 301 DKLVNCCKHNTYVDCEKCLPFENDRPWRRAATAESASECLPCDCNGRSQECYFDPPELYRS 360

QY 359 TGHGGHCTNCRDNTDGAKCERCENFRRLGNTAEACSPCHCSPVGSLSLTCDSYGRCSCKP 418

Db 361 TGHGGHCTNCQDNTDGAHCERCENFRRLGNNAEACSSCHCSPVGSLSLTCDSYGRCSCKP 420

QY 419 GWMGDKCDRCQPGFHSLTEAGCRPCSDPSGSTDECNVETGRCVCKDNVEGFNCERCKPG 478

Db 421 GWMGDKCDRCQPGFHSLTEAGCRPCSDPSGSDENCNVETGRCVCKDNVEGFNCERCKPG 480

QY 479 FFNLESSNPKGCTPCFCFHSSVCTNAVGVSVYDISSTFQIDEDGWRVEQRDGESEASLEW 538

Db 481 FFNLESSNPRGCTPCFCFHSSVCTNAVGVSVYDISSTFQIDEDGWRABQRDGESEASLEW 540

QY 539 SSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYGQNLFSFRVDRDRTRLSEAEDLVLEGA 598

Db 541 SSERQDIAVISDSYFPRYFIAPAKFLGKQVLSYGQNLFSFRVDRDRTRLSEAEDLVLEGA 600

QY 599 GLRVSVPLIAQGNYSYSETTVKYIFRLHEATDYPWRPALSPFQKLNLTSTIKIRGTY 658

Db 601 GLRVSVPLIAQGNYSYSETTVKYVFLHEATDYPWRPALTPFEFQKLNLTSTIKIRGTY 660

QY 659 SERSAGYLDVTLQSAARPGPVATWVESCTCPVGYGGQFCETCLPGYRRETSLGYPSP 718

Db 661 SERSAGYLDVTLASARPGPVATWVESCTCPVGYGGQFCMCLSGYRRETSLGYPSP 720

QY 719 CVLCTCNGHSETCDPBTGVCDRCRDNTAGPHCEKCSDDGYGDSLTGTSDDCQPCPCPGSS 778

Db 721 CVLCACNGHSETCDPBTGVCDRCRDNTAGPHCEKCSDDGYGDSLTGTSDDCQPCPCPGSS 780

QY 779 CAIVPKTKEVVCTHCTGTAGKRCCELCDGDFGDPPLGSGNGPVRLCRCPCCNDNIDPNAVG 838

Db 781 CAVVPKTKEVVCTNCTGTTGKRCCELCDGDFGDPPLGSGNGPVRLCRLCQSDNIDPNAVG 840

QY 839 NCNRLTGECLKCIYNTAGFYCDRCCKEGFFGNPLAPNPADKCKACACN-YGTVQQQSSCNP 897

Db 841 NCNRLTGECLKCIYNTAGFYCDRCCKOGFFGNPLAPNPADKCKACNCPYGTWKQQSSCNP 900

QY 898 VTGQCQCCLPHVSGRDCGTCDPGYYNLQSGQCERCDCCHALGSTNGQCDIRTGQCECQPGI 957

Db 901 VTGQCECLPHVTGQDCGACDPGFYNLQSGQCERCDCCHALGSTNGQCDIRTGQCECQPGI 960

QY 958 TGOHCERCETNHFPGPEGCKPCDCHHGGSLQCKDDGRCECEGFGVGNRCDCQCEENYF 1017

Db 961 TGOHCERCEVNHFGPEGCKPCDCHHGGSLQCKDDGRCECEGFGVGNRCDCQCEENYF 1020

QY 1018 YNRSWPGCQECPCACVRLVKDKAAEHRVKLOELESLIANLGTGDDMTDQAFEDRLKEAER 1077
Db 1021 YNRSWPGCQECPCACVRLVKDKVADHRVKLOELESLIANLGTGDEMVTDQAFEDRLKEAER 1080
QY 1078 EVDTLLEAREAEVQVDQNLMDRLQRVNSSLHSQISRLQIRNIRNTIETGILAEARARSVES 1137
Db 1081 EVMDDLREAOQVDQVDQNLMDRLQRVNSSLHSQISRLQIRNIRNTIETGILAEARAHVEN 1140
QY 1138 TEQLIEIASRELEKAKM-AANVSITQPESTGEENMTLLAEAEARRLAERHKQAEADDIVRV 1196
Db 1141 TERLIEIASRELEKAKVAAANVSITQPESTGDPNNMTLLAEAEARKLAERHKQAEADDIVRV 1200
QY 1197 AKTANETSAAEYNLLRLTAGENQTALEIEBELNRKYEQAKNISQDLEKQAAARVHEEAKRA 1256
Db 1201 AKTANDTSTEAYNLLRLTAGENQTALEIEBELNRKYEQAKNISQDLEKQAAARVHEEAKRA 1260
QY 1257 GDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLRLIDQKLKDYEDLREDMRGKEHE 1316
Db 1261 GDKAVEIYASVAQLSPDSELENEANNIKMEAEENLEQLIDQKLKDYEDLREDMRGKELE 1320
QY 1317 VKNLLEKGAEQQTADQLLARADAATAKALAEAAKGRSTLQEAANDILNNLKDFDRRVNDN 1376
Db 1321 VKNLLEKGTQQTADQLLARADAATAKALAEAAKGRDTLQEAANDILNNLKDFDRRVNDN 1380
QY 1377 KTAAEALRRIPAINRTIAEANEKTRQAALGNAAADATEAKNKAHEABERIASAAQKNA 1436
Db 1381 KTAAEALRKIPAINQTITEANEKTRQAALGSAADATEAKNKAHEABERIASAVQKNA 1440
QY 1437 TSTKADAERTFGEVTDLDNEVNGMLRQLEEAENELKQKDDADQDMMWAGMASAAQAEAE 1496
Db 1441 TSTKAEARTFAEVTDLNEVNNMLKQLOEAEKELKQKDDADQDMMWAGMASAAQAEAE 1500
QY 1497 LNARKAKNSVSSLLSQNLNLLDQLGQDQDQDQDQDQDQDQDQDQDQDQDQDQDQDQDQD 1556
Db 1501 INARKAKNSVTSLLSIINDLEQLGQDQDQDQDQDQDQDQDQDQDQDQDQDQDQDQDQD 1560
QY 1557 LESEARKQEAAMIDYNRDIAEILKIDHNEIDIKTLPTGCFNTPSIEKP 1605
Db 1561 LENEAKQEAAMIDYNRDIEEIMKDINLEDIRKTLPSGCFNTPSIEKP 1609

RESULT 8
US-10-037-182-16
; Sequence 16, Application US/10037182
; Publication No. US20030044899A1
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Doi, Masayuki
; APPLICANT: Thyboll, Jill
; TITLE OF INVENTION: Recombinant Laminin 10
; FILE REFERENCE: 99-274-F
; CURRENT APPLICATION NUMBER: US/10/037,182
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,449
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/279,282
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 1576
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-037-182-16

Query Match 92.5%; Score 8043; DB 14; Length 1576;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 1470; Conservative 57; Mismatches 47; Indels 2; Gaps 2;
QY 32 RAAMDECADEGGRPQRCMPEFVNAAFNVTVVATNCGTPPEEYCVQGTGVTGYSCHLCD 91
Db 1 QAAMDECTDEGGRPQRCMPEFVNAAFNVTVVATNCGTPPEEYCVQGTGVTGYSCHLCD 60

QY 92 ACQQLHQGAFLTDYNNQADTTWQSQTMLAGVQVPSINLTLHLGKAFDITYVRLKPH 151
Db 61 ACQPHLQGAFLTDYNNQADTTWQSQTMLAGVQVPSINLTLHLGKAFDITYVRLKPH 120
QY 152 TSRPESFAIYKRTREDGPWIPYQYYSGSCENTYSKANRGFIRTTGGDEQCALCTDEFSDIS 211
Db 121 TSRPESFAIYKRTREDGPWIPYQYYSGSCENTYSKANRGFIRTTGGDEQCALCTDEFSDIS 180
QY 212 PLTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSY 271
Db 181 PLTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSY 240
QY 272 YVAISDFAVGGRCKCNCHGSHASECVKNEFDKLMCNKXNTYGVDCCKLPFFNDRPWRATA 331
Db 241 YVAISDFAVGGRCKCNCHGSHASECMKNEFDKLVNCKXNTYGVDCCKLPFFNDRPWRATA 300
QY 332 ESASECLPCDCNGRSQECYFDPPELYRSTGHGGHCTNCRDNTDGAKCERCERENFRLGNT 391
Db 301 ESASECLPCDCNGRSQECYFDPPELYRSTGHGGHCTNCRDNTDGAKCERCERENFRLGNT 360
QY 392 ACSPECHCSPVGLSTQCDYSYGRCSCKPGVMGDKDRCPGFHSLTEAGCRPCSCDPSGST 451
Db 361 ACSPECHCSPVGLSTQCDYSYGRCSCKPGVMGDKDRCPGFHSLTEAGCRPCSCDPSGST 420
QY 452 DECNVETGRVCVKONVEGFNCERCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVYSVY 511
Db 421 DECNVETGRVCVKONVEGFNCERCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVYSVY 480
QY 512 DISSTFQIDEDGWRVEQDQSEASLEWSSDRQYIAVISDSYFPRIYPIAPVKFLGNQVLSY 571
Db 481 SISSTFQIDEDGWRVEQDQSEASLEWSSDRQYIAVISDSYFPRIYPIAPVKFLGNQVLSY 540
QY 572 GQNLSPSFRVDRRDLRLSAEDLVLEGAGLRVSVPLIAQNSYPSSETTVKYIFRLHEATDY 631
Db 541 GQNLSPSFRVDRRDLRLSAEDLVLEGAGLRVSVPLIAQNSYPSSETTVKYIFRLHEATDY 600
QY 632 PWRPALSPFEFQKLLNNLTSIKIRGTYSERSAGVLDVLTQASARPGVPGVATWVESCTCP 691
Db 601 PWRPALTPFEFQKLLNNLTSIKIRGTYSERSAGVLDVLTQASARPGVPGVATWVESCTCP 660
QY 692 VGYGQFCETCLPGYRRTPSLGYPSPCVLCTCNHSETCDPETGVCDNRDNTAGPHCEK 751
Db 661 VGYGQFCETCLPGYRRTPSLGYPSPCVLCTCNHSETCDPETGVCDNRDNTAGPHCEK 720
QY 752 CSDGYGDSLTGTSSDCQPCPCPGSSCAIVPKTKBHVCTHCPTGTAGKRCCLDDGYFG 811
Db 721 CSDGYGDSLTGTSSDCQPCPCPGSSCAIVPKTKBHVCTHCPTGTAGKRCCLDDGYFG 780
QY 812 DPLSGNPVRLCRPCQCNNDNPDNAVGNCRNLTEGLCKIYNTAGFYCDRCKEGFGNPL 871
Db 781 DPLSGNPVRLCRPCQCNNDNPDNAVGNCRNLTEGLCKIYNTAGFYCDRCKEGFGNPL 840
QY 872 APNPADKCKACACN-YGTVQOQSSCNPNVTGQCCLPHVSGRDCGTCDPGYVNLQSGQCE 930
Db 841 APNPADKCKACACNPNYGTWKQSSCNPNVTGQCCLPHVSGRDCGTCDPGYVNLQSGQCE 900
QY 931 RCDCHALGSTNGQCDIRTGQCECQPGITGOHCERCETNHFHFGPEGCKPCDCHHESLSL 990
Db 901 RCDCHALGSTNGQCDIRTGQCECQPGITGOHCERCETNHFHFGPEGCKPCDCHHESLSL 960
QY 991 QCKDDGRCCEGREGFVGNRCQCEENYFYNRSWPGCQECPCACVRLVKDKAAEHRVKLOELE 1050
Db 961 QCKDDGRCCEGREGFVGNRCQCEENYFYNRSWPGCQECPCACVRLVKDKVADHRVKLOELE 1020
QY 1051 SLIANLGTGDDMTDQAFEDRLKEAEREVTDLLREAOEVKQVDQNLMDRLQRVNSSLHSQ 1110
Db 1021 SLIANLGTGDEMVTDQAFEDRLKEAEREVMDDLREAOQVQVDQNLMDRLQRVNSSLSSQ 1080
QY 1111 ISRLQIRNTIETGILAEARARSVESTEOLEIASRELEKAKM-AANVSITQPESTGEP 1169
Db 1081 ISRLQIRNTIETGILAEARARSVESTEOLEIASRELEKAKVAAANVSITQPESTGDP 1140
QY 1170 NNMTLLAEARLAERHKQAEADDIVRVAKTANETSAAEYNLLRLTAGENQTALEIEBELN 1229

Db 1141 NMVTLAEEARKLAERHKQEAADIVRVAKTANDTSTEAYNLLRLTLAGENQTAPEIEELN 1200
Qy 1230 RKVEQAKNISQDLEKQOARVHEBAKRAQDKAVEIYASVAQLTPVDSEALENEANKIKKEA 1289
Db 1201 RKVEQAKNISQDLEKQOARVHEBAKRAQDKAVEIYASVAQLSPDSETLENEANNIKMEA 1260
Qy 1290 ADJLELIDOKLKDYEDLREDMRGHEHEVKNLLEKGAEOQTADQLLARADAAKALAEAA 1349
Db 1261 ENLEQIDOKLKDYEDLREDMRGKELEVKNLLEKKGTEQOTADQLLARADAAKALAEAA 1320
Qy 1350 KKGRSTLOEANDILNLLKDFDRVNDNKTAEEALRRIPAINRTIAEANEKTRERQALG 1409
Db 1321 KKGRDTLOEANDILNLLKDFDRVNDNKTAEEALRKIPAINQITIEANEKTRERQALG 1380
Qy 1410 NAAADATEAKNKAHEAERIAASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAEN 1469
Db 1381 SAAADATEAKNKAHEAERIAASAVQKNATSTKAAEERTFAEVTDLNEVNNMLKQIQEAEK 1440
Qy 1470 ELKRQDDADQDMMAGMASQAAQAEALNARKAKNSVSSLLSQLNLLDQLGQDQDVTDLN 1529
Db 1441 ELKRQDDADQDMMAGMASQAAQAEALNARKAKNSVTSLLSIINDLLEQLGQDQDVTDLN 1500
Qy 1530 KLEIEGSLNKADEMKAASDLDRKVSDDLESEARKQEAALMDYNRDIAEIIKDIHNLEDIK 1589
Db 1501 KLEIEGTLNKAKDEMKVSDLRKVSDDLENEAKKQEAALMDYNRDIEEIMKDIRNLEDIR 1560
Qy 1590 KTLPTGCFNTPSIEKP 1605
Db 1561 KTLPSGCFNTPSIEKP 1576

RESULT 9

US-09-845-583-10
; Sequence 10, Application US/09845583
; Patent No. US20020142954A1
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Brunken, William Joseph
; APPLICANT: Champliand, Marie-France
; APPLICANT: Hunter, Dale
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
; FILE REFERENCE: 10287-056001
; CURRENT APPLICATION NUMBER: US/09/845,583
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/200,863
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1587
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-845-583-10

Query Match 41.4%; Score 3596.5; DB 9; Length 1587;
Best Local Similarity 43.8%; Pred. No. 2.2e-201;
Matches 707; Conservative 258; Mismatches 571; Indels 77; Gaps 24;
Qy 20 LLAVLAAGCVRAAMDECADEGGRPQRCMPPEFVNAAFNVTVVATNTCGTPPEEYCVQTG 79
Db 12 LLAPRAAGAG-----MGACYDGAAGRPQRCPLPVFENAAFGRLAQASHTCGSPPEDFCPHVG 66
Qy 80 VTGVTKSHCLDAGQOHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYPNSINLTILHGK 139
Db 67 AAGAGAHQRCDAADPQRHNASYLTDFHSQDESTWQSPSMAFGVQYPTSVNITLRLGK 126
Qy 140 AFDITYRLKFHTSRPESFAIYKRTREDGPWIPYQYISGSCENTYSKANRGFIRTTGGDEQ 199
Db 127 AYEITYRLKFHTSRPESFAIYKRSRADGPWEPIQYFASCKQTYGRPEGQYLRPGEDE 186
Qy 200 QALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFNDNSPVLQEWVVTATDIRVTNRLNTFGD 259

Db 187 VAFCTSEFSDISPLSGGNVAFSTLEGRPSAYNFEESPGLQEWVTSTELLISLDRLNTFGD 246
Qy 260 EVFNDPKVLKSYYYAISDFAVGGRCKCNGHASECVKNEFDKLMCNCKHNTYGVDCCKCLP 319
Db 247 DIFKDPKVLQSYYYAVSDFSVGGRCKCNGHASECGPDVAGLACRCQHNTTGTDCERCCLP 306
Qy 320 FFNDRPWRATAESASECLPCDCNGRSQECYFDPPELYRSTGHGHCNCRDNTDGAACER 379
Db 307 FFQDRPWARGTAEAHAHECLPCNCSGRSEECTFDRELFRSTGHGRCHCRDHTAGPHCER 366
Qy 380 CRENFFRLGNTEACSPCHCSPVGSLSLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAG 439
Db 367 CQENFYHWDPRMPCQPCDQOSAGSLHLQCDDTGTCAKPTVTGWKCDRCLPGFHSLSSEGG 426
Qy 440 CRPCSCDPSGSTDECNVETGRVCVKNVGEFNCERCKPGFNLESSNPKGCTPCFCFGHS 499
Db 427 CRPCTCNFAGSLDTC DPRSGRCPCKENVEGNLDCRCPGTGNLQPHNPAGCSCFCYGH 486
Qy 500 SVCTNAVGSVYDIDISSTFQIDEDGWRVEQORDGSEASLEWSSDRQYIAVISDSYFFRYFIA 559
Db 487 KVCASTAQFQVHHILSDFHQGAEGWARSVGGSEHSPQWSPN-----GVLLSPEDEEELTA 542
Qy 560 PVKFLGNQVLSYGQNLFSFRVDRDRTRLAEDLVLEGAGLRVSVPLIAQGNYSYPSETTV 619
Db 543 PGKFLGDQRFSGYQPLILTFRVPPGDSPLPVQ-LRLEGTGLALS--LRHSSLSGPDARA 599
Qy 620 KYIFRLH---EATDYPWRPALSPFEFQKLNNLTSIKIRGTYSERSAG--YLDDVTLQSA 674
Db 600 SQGGRAGVPLQETSEADVAPLPPEFHFQRLLANLTSLRVSPGPSPAGVPVFLTEVRLTSA 659
Qy 675 RPPGVPATWVESCTCPVGYGGQFCETCLPGYRRRETPLSGYSPCVLCTCNHGHSETCDPE 734
Db 660 RPLGLSPPASWVEICSCPTGYTGQFCESCAPGYKREMPQGGPYASCVPCTCNQHG-TCDPN 718
Qy 735 TGVCDCRDNTAGPHCEKCSGYIGDSTLTGSSDCQPCPCPGSSCAIVPKTKVVVCTHCP 794
Db 719 TGICVCSHTEGSPSCERCLPGFYGNPFAGQADDCCQPCPCQSQSACTTIPESGEVVCTHCP 778
Qy 795 TGTAGKRCELDDGYFGDPLGSGNPVRLCRPCQCNDNIDBNVAGNCNRLTGECLKCIYNT 854
Db 779 PGQRRRCCEVCDGFFGDPGLFLGHPPQCHQCQCSGNVDNAVGNCDPLSGHCLRLCHNT 838
Qy 855 AGFYCDRCCKEGFFGNPLAPNPADKCKACACN-YGTVOQQSSCNPVGTGQCCLPHVSGRDC 913
Db 839 TGDHCEHQEGFYGSALAPRPADKCMPCSCHPQGSVSEQMPCDPVTGQCSCPLHVTARD 898
Qy 914 GTCDPGYNLOSQGGCERCDCCHALGSTNGQCDIRTGQCEQCPGIGTQHCERCETNHFPG 973
Db 899 SRCYPGFFDLQPGRCRSCKCHPLGSEDQCHPKTGCTCPCPVGTVGQACDRCOLGFFGSS 958
Qy 974 PEGCKPCDCHHEGSLSLQCKDDGRCECREGFGVGNRCQCEENYFYNRSPWPGCQECPCYR 1033
Db 959 IKGCRACRCSPLGAASAQCHYNGTVCVRPGFEGYKCDRCHYNEFFLTADGTHCQCCPCYA 1018
Qy 1034 LVKDKAAEHRVKLQELLESILANLGTGD-----DMVTDAQFEDRLKEAEREVTDLLREAQ 1088
Db 1019 LVKEETAKLAKARLTLTGWLQSDCGSPWGPLDILLGEAPRGDVYQGH-----LLPGARE 1074
Qy 1089 VKDQDQNLMDRLQVRNSSLHSQISRLQNRNTIETGILAEARARSRVESTEQLIETASRE 1148
Db 1075 A-----FLEQMMGLEGAVKAREQLRLNKGARCAQAGSQKTCQLADLEAVLESSEEE 1128
Qy 1149 -LEKAKMAANVSITQPESTGEFNNMTLLAEARRLAERHKQEAADDIVRVAKTANETSAAE 1207
Db 1129 ILHAAAILASLEIPQ-EGPSQPTKWSHLAEARALARSHRDATKIAATAWRALLASNTS 1187
Qy 1208 YNLLRLTAGENQTALEIE-ELNRKYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYAS 1266
Db 1188 YALLWNLL--EGRVALETORDLEDRYQEVQAAQKALRTAVAEVLPEAE-----SVLAT 1238
Qy 1267 VAQL-----TPVDSEA--LENEANKIKKEAADLRLIDQKLKDYEDLRE 1308
Db 1239 VQQVGADTAPYALLASPGALPQKRAEDLGLKAKALEKTVASQWQMATEAARTLQATAAQ 1298

QY 1309 -DMRGKEHEVKNLLEKGAEQQTADQLLARADAAKALAEAAKKGRSTLQEAANDILNNLK 1367
Db 1299 ATLQRTE---PLTWARSRLTATFASQLHQGARAALTOASSSVQAATVTVMGARTLLADLE 1355
QY 1368 DFDRRVNDNKTAAEAEALRRIPAINRTIABANEKTRQAQLALGNAAADATEAKNKAHEAER 1427
Db 1356 GMKLQFPRPKDQAALQKADSVSDRLLDTRKKTQKAERMLGNAAPLSSSAKKGREAEV 1415
QY 1428 IASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQL-EEAENELKRRKQDDADQDDMMAG 1486
Db 1416 LAKDSAKLAKALLRERKQAHRRASRLTSQTATLQOASQQVLASEARRQEEAEAEVAG 1475
QY 1487 MASQAAQAEALNARKAKNSVSSLLSQLNLLDQLGLDTP--VDLNKLNEIEGSLNKAKDE 1544
Db 1476 LS-----EMEQQIRRESRISLEKDIETLSELLARLGLSLDTHQAPQAALNETQWALERLRLQ 1530
QY 1545 M-KASDLDRKVSDESEARKQEAAMIDYNRDIAEIIKDIHNLEDIKKTLPTGC 1596
Db 1531 LGSPGSLQKLSLLEQESQQELQIQGFESDLAEIRADKQNLLEAILHSLPENC 1583

RESULT 10

US-10-262-839-210

; Sequence 210, Application US/10262839

; Publication No. US20040038877A1

; GENERAL INFORMATION:

; APPLICANT: Alsobrook, John,

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; APPLICANT: Li, Li,

; APPLICANT: Miller, Charles,

; APPLICANT: Patturajan, Meera,

; APPLICANT: Reiger, Daniel,

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; APPLICANT: Zerhusen, Brian,

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; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

; FILE REFERENCE: 21402-462A

; CURRENT APPLICATION NUMBER: US/10/262,839

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; PRIOR FILING DATE: 2002-04-12

; PRIOR APPLICATION NUMBER: 60/327,342

; PRIOR FILING DATE: 2001-10-05

; PRIOR APPLICATION NUMBER: 60/328,044

; PRIOR FILING DATE: 2001-10-09

; PRIOR APPLICATION NUMBER: 60/328,849
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/374,738
; PRIOR FILING DATE: 2002-04-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 367
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 210
; LENGTH: 1587
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-839-210

Query Match 41.4%; Score 3596.5; DB 12; Length 1587;
Best Local Similarity 43.8%; Pred. No. 2.2e-201;
Matches 707; Conservative 258; Mismatches 571; Indels 77; Gaps 24;

QY 20 LLAVLAAVAGCVRAAMDECADEGGRPQRCNPFVNAAFNTVVAATNTTCGTPPEEYCVQTG 79
Db 12 LLAPRAAGAG-----MGACYDGAGRPQRCCLPVFENAAFGRLAQASHTCGSPPEDFCPHVG 66
QY 80 VTGVTKSCHLCDAGQQHLQHGAFLTDYNNQADTTWQSQTMLAGVQYPNSINLTLLHLGK 139
Db 67 AAGAGAHQCQRCDAAADPPQRHNNASYLTDFHSQDESTWQSPSMAFGVQYPTSVNITLRLGK 126
QY 140 AFDITYVRLKFTSRPESFAIYKRTREDGWIPYQYYSGCENTYSKANRGFIRTTGGDEQ 199
Db 127 AYEITYVRLKFTSRPESFAIYKRSRADGPWEFYQFYSASCOQTYGRPEGQYLRPGEDER 186
QY 200 QALCTDEFSDISPLTGGNVAFSTLEGPSAXNFDSNPLVQLQEWVTAIDIRVTLNRLNTPGD 259
Db 187 VAFCTSEFSDISPLSGGNVAFSTLEGPSAXNFESPGQLQEWVSTELLISLDRLNTFGD 246
QY 260 EVFNDPKVLKSYVYVAISDFAVGGRCKCNHGHASECVKNEFDKLMCNKHNTYGVDCCKCLP 319
Db 247 DIFKDPKVLQSYVYVAVDFSVGGRCKCNHGHASECGPDVAGQLACRCQHNTTGTDCERCLP 306
QY 320 FFNDRPWRRATAESASECLPCDCNGRSQECYFDPPELYRSTGHGHCNTCRDNTDGAKCER 379
Db 307 FFQDRPWARGTAEAAHECLPCNCSGRSECTFDRELFRSTGHGGRCHCRDHTAGPHCER 366
QY 380 CRENFFRLGNTAECSPCHSPVGLSTQCDYGRCSCKPGVMGDKDCRCQPGFHSLTEAG 439
Db 367 CQENFYHWDPRMPCQPCDCQASAGSLHLQCDDTGTCAKPTVTGWKCDRCLPGFHSLSEGG 426
QY 440 CRPCSDPSGSTDECNVETGRCVCKDNVEGFNCERCKPGFFNLESSNPKGCTPCFCFGHS 499
Db 427 CRPCTCNPAGSLDTC DPRSGRCPCKENVEGNLCDRCRPGTGNLQHPNAGSCSSCFCYGHS 486
QY 500 SVCTNAVGYSVYDISFTFQIDEDGWRVEQRDQSEASLEWSSDRQYIAVISDSYFPRYFIA 559
Db 487 KVCASTAQFQVHHILSDFHQGAEGWARSVGSSEHSPQWSPN----GVLSPDEEELTA 542
QY 560 PVKFLGNQVLSYGNLSFSFRVDRDRDTRLASADLVLEGAGLRVSVPLIAQGNYSYPSETTV 619
Db 543 PKKFLGDQRFYSYGQPLILTFRVPPGDSPLPVQ-LRLEGTGLALS--LRHSSLGSPQDARA 599
QY 620 KYIFRLH---EATDYPWRPALSPFEFQKLLNLTISKIRGTYSERSAG--YLDDEVTLQSA 674
Db 600 SQGGAQVPLQETSEDVAPPLPPFFHFQRLLANLTSLRLVSPGPSAGPVFLTEVRLTSA 659
QY 675 RPPGVPATWVESCTCPVYGGQFCETCLPGYRRETSLGYPSPCVLCTCNHSETCDPE 734
Db 660 RPLSLPPASWVEICSCPTGYTGQFCESCAPGYKREMPQGGPYASCVPCTCNQHG-TCDPN 718
QY 735 TGVCDCRDNTAGPHCEKCSDDGYGDSTLGTSSDCQPCPCPGGSSCAIVPKTKEVVCTHCP 794
Db 719 TGICVCSHHTEGPSCERCLPGFYGNPFAGQADDCCQPCPCPGQSACTTIPESGEVVCTHCP 778
QY 795 TGTAGKRCELDDGYFGDPLGNSGNPVRLLCRPCQNDNIDPNAVGNCRNLTGECCLKCIYNT 854
Db 779 PGQGRRCCEVCDDGFFGDLGLFGLFHPQPHQCCQSGNVDPNAVGNCDPLSGHCLRLHNT 838

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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:58 ; Search time 14.7709 Seconds
(without alignments)
10452.141 Million cell updates/sec

Title: US-10-037-182-18
Perfect score: 8694
Sequence: 1 MTGGGRAALALQPRGLWPL.....EDIKTLPTGCFNTPSIEKP 1605

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8627	99.2	1607	1 MMSB2	laminin gamma-1 ch
2	8144	93.7	1609	1 MMHUB2	laminin gamma-1 ch
3	3469	39.9	1639	1 MMFFB2	laminin gamma-1 ch
4	3193	36.7	1557	2 T28811	hypothetical prote
5	2591	29.8	1193	2 A44018	laminin B2t chain
6	2400.5	27.6	1192	2 S69000	laminin gamma 2 ch
7	1812.5	20.8	3106	1 S53868	laminin alpha-2 ch
8	1784	20.5	3084	1 MMSA	laminin alpha-1 ch
9	1742	20.0	3075	2 S14458	laminin alpha-1 ch
10	1682	19.3	1786	1 MMHUB1	laminin beta-1 cha
11	1661.5	19.1	1786	1 MMSB1	laminin beta-1 cha
12	1655.5	19.0	1790	1 MMFFB1	laminin beta-1 cha
13	1632	18.8	2823	2 T23064	hypothetical prote
14	1632	18.8	2823	2 F87908	protein T22A3.8 [i
15	1632	18.8	3102	2 T43291	laminin alpha chai
16	1625.5	18.7	1808	2 T15099	hypothetical prote
17	1592	18.3	1801	1 MMRTS	laminin beta-2 cha
18	1568	18.0	1798	2 S53869	laminin beta-2 cha
19	1475.5	17.0	1797	2 A55677	laminin beta-2 cha
20	1455	16.7	3712	2 S18253	laminin alpha-1 ch
21	1384	15.9	3672	2 T23433	hypothetical prote
22	1384	15.9	3704	2 T37316	probable laminin a
23	1347.5	15.5	3635	2 T10053	laminin alpha 5 ch
24	1162	13.4	606	2 A54665	netrin-1 precursor
25	1045	12.0	581	2 B54665	netrin-2 precursor
26	986.5	11.3	612	2 JH0799	laminin-related pr
27	939.5	10.8	1170	2 A53612	laminin B1k chain
28	905	10.4	1168	2 I56985	kalinin B1 - mouse
29	903.5	10.4	4391	2 A38096	perlecan precursor

30	877.5	10.1	3707	2 S18252	heparan sulfate pr
31	637.5	7.3	1160	2 F88369	protein unc-52 [im
32	637.5	7.3	2295	2 C88369	protein unc-52 [im
33	637.5	7.3	3375	2 T19821	hypothetical prote
34	619	7.1	1751	1 MMHUMH	laminin alpha-2 ch
35	590	6.8	1620	2 T27283	hypothetical prote
36	586	6.7	1816	1 S68960	laminin alpha-4 ch
37	555.5	6.4	1574	2 T13954	MEGF6 protein - ra
38	551	6.3	1111	2 T26972	hypothetical prote
39	514	5.9	1713	2 A55347	adhesive ligand ep
40	490	5.6	400	2 T46383	hypothetical prote
41	477	5.5	2471	2 A49128	cell-fate determin
42	471	5.4	303	2 B45067	laminin B1 chain -
43	466.5	5.4	2703	1 A24420	notch protein - fr
44	466	5.4	2318	2 S45306	notch 3 protein -
45	459.5	5.3	2352	2 T30201	Notch homolog prot

ALIGNMENTS

RESULT 1

MMMSB2
laminin gamma-1 chain precursor mouse
N;Alternate names: laminin chain B2
C;Species: Mus musculus (house mouse)
C;Date: 28-Feb-1986 #sequence revision 30-Jun-1991 #text change 10-Dec-1999
C;Accession: A28469; A27729; A28082; S02680; S05327; S02037; A02870; S13544; S14552
R;Sasaki, M.; Yamada, Y.
J. Biol. Chem. 262, 17111-17117, 1987
A;Title: The laminin B2 chain has a multidomain structure homologous to the B1 chain.
A;Reference number: A28469; MUID:88059118; PMID:3680290
A;Accession: A28469
A;Molecule type: mRNA
A;Residues: 1-1607 <SAS>
A;Cross-references: EMBL:J03484; NID:G198694; PIDN:AAA39405.1; PID:G293688
R;Duckin, M.E.; Bartos, B.B.; Liu, S.H.; Phillips, S.L.; Chung, A.E.
Biochemistry 27, 5198-5204, 1988
A;Title: Primary structure of the mouse laminin B2 chain and comparison with laminin B1.
A;Reference number: A27729; MUID:89000737; PMID:3167041
A;Accession: A27729
A;Molecule type: mRNA
A;Residues: 1-263, 'D', 265-336, 'C', 338-446, 'PS', 449-661, 'S', 663-885, 887-1155, 1157-1433, 'A'
A;Cross-references: EMBL:J02930; NID:G198702; PIDN:AAA39408.1; PID:G293691
A;Note: the authors translated the codon TAT for residue 544 as Asp and GCG for residue
R;Ogawa, K.; Burbelo, P.D.; Sasaki, M.; Yamada, Y.
J. Biol. Chem. 263, 8384-8389, 1988
A;Title: The laminin B2 chain promoter contains unique repeat sequences and is active in
A;Reference number: A28082; MUID:88228071; PMID:2836421
A;Accession: A28082
A;Molecule type: DNA
A;Residues: 1-215, 'A', 217-239 <OGA>
A;Cross-references: EMBL:J03749; NID:G198704; PIDN:AAA39409.1; PID:G554184
R;Fujiwara, S.; Shinkai, H.; Deutzmann, R.; Paulsson, M.; Timpl, R.
Biochem. J. 252, 453-461, 1988
A;Title: Structure and distribution of N-linked oligosaccharide chains on various domain
A;Reference number: S02678; MUID:88326259; PMID:2458101
A;Accession: S02680
A;Molecule type: protein
A;Residues: 227-238 <FUJ>
R;Hartl, L.; Oberbaeumer, I.; Deutzmann, R.
Eur. J. Biochem. 173, 629-635, 1988
A;Title: The N-terminus of laminin A chain is homologous to the B chains.
A;Reference number: S00624; MUID:88225080; PMID:3267223
A;Accession: S05327
A;Molecule type: protein
A;Residues: 227-238;387-393, 'F', 395-405;881-912;1022-1034 <HAR>
R;Deutzmann, R.; Huber, J.; Schmetz, K.A.; Oberbaeumer, I.; Hartl, L.
Eur. J. Biochem. 177, 35-45, 1988
A;Title: Structural study of long arm fragments of laminin. Evidence for repetitive C-te
A;Reference number: S01790; MUID:89030693; PMID:3181157
A;Accession: S02037
A;Molecule type: protein

QY 1259 KAVEIYASVAQLTPVDSEALENEANKIKKEAADLRLIDQKLXDYEDLREDMRGKEHEVK 1318
Db 1261 KAVEIYASVAQLTPVDSEALENEANKIKKEAADLRLIDQKLXDYEDLREDMRGKEHEVK 1320
QY 1319 NLLEKGAEOQTADQLLARADAAKALAEBAKKGKRGSTLQEAANDILNLLKDFDRRVNDNKT 1378
Db 1321 NLLEKGAEOQTADQLLARADAAKALAEBAKKGKRGSTLQEAANDILNLLKDFDRRVNDNKT 1380
QY 1379 AAEALRRIPAINRTIAEANEKTRQAQLALGNAAADATEAKNKAHEAERIAASAAQKNATS 1438
Db 1381 AAEALRRIPAINRTIAEANEKTRQAQLALGNAAADATEAKNKAHEAERIAASAVQKNATS 1440
QY 1439 TKADAERTFGEVTDLDNEVNGMLRQLEEAENELKRKQDDADQDMMAGWASQAAQAEALN 1498
Db 1441 TKADAERTFGEVTDLDNEVNGMLRQLEEAENELKRKQDDADQDMMAGWASQAAQAEALN 1500
QY 1499 ARKAKNSVSSLLSQNLNLLDQLGQDTPVDLNKLNIEIGSLNKAKDEMKASDLDRKVSdle 1558
Db 1501 ARKAKNSVSSLLSQNLNLLDQLGQDTPVDLNKLNIEIGSLNKAKDEMKASDLDRKVSdle 1560
QY 1559 SEARKOEAAIMDYNRDIAIHKDIHNLEDIKKTLPTGCFNTPSIEKP 1605
Db 1561 SEARKOEAAIMDYNRDIAIHKDIHNLEDIKKTLPTGCFNTPSIEKP 1607
RESULT 2
MMHUB2
laminin gamma-1 chain precursor - human
N;Alternate names: laminin chain B2
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text_change 10-Dec-1999
C;Accession: S13548; A28158; S13549; B34961; S14664; S23567
R;Kallunki, T.; Ikonen, J.; Chow, L.T.; Kallunki, P.; Tryggvason, K.
J. Biol. Chem. 266, 221-228, 1991
A;Title: Structure of the human laminin B2 chain gene reveals extensive divergence from
A;Reference number: S13548; MUID:91093128; PMID:1985895
A;Accession: S13548
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1609 <KAL>
A;Cross-references: GB:M55217; NID:g186937
A;Note: the nucleotide sequence was submitted to GenBank, February 1991
R;Pikkarainen, T.; Kallunki, T.; Tryggvason, K.
J. Biol. Chem. 263, 6751-6758, 1988
A;Title: Human laminin B2 chain. Comparison of the complete amino acid sequence with the
A;Reference number: A28158; MUID:88198245; PMID:3360804
A;Accession: A28158
A;Molecule type: mRNA
A;Residues: 1-211, '1', 213-1609 <PIK>
A;Cross-references: EMBL:J03202; NID:g186916; PIDN:AAA59488.1; PID:g307107
R;Fukushima, Y.; Pikkarainen, T.; Kallunki, T.; Eddy, R.L.; Byers, M.G.; Haley, L.L.; He
Cytogenet. Cell Genet. 48, 137-141, 1988
A;Title: Isolation of a human laminin B2 (LAMB2) cDNA clone and assignment of the gene b
A;Reference number: S13549; MUID:89169663; PMID:3234037
A;Accession: S13549
A;Molecule type: mRNA
A;Residues: 1393-1609 <FUK>
A;Cross-references: EMBL:M27654; NID:g186923; PIDN:AAA59489.1; PID:g186924
R;Olsen, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki,
Lab. Invest. 60, 772-782, 1989
A;Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 cha
A;Reference number: A34961; MUID:89280632; PMID:273383
A;Accession: B34961
A;Molecule type: mRNA
A;Residues: 868-1551, 'N', 1553-1609 <OLS>
R;Santos, C.L.S.; Sabbaga, J.; Brentani, R.
DNA Seq. 1, 275-277, 1991
A;Title: Differences in human laminin B2 sequences.
A;Reference number: S14664; MUID:92216129; PMID:1806043
A;Accession: S14664
A;Molecule type: mRNA
A;Residues: 1282-1609 <SAN>
A;Cross-references: EMBL:X13939; NID:g34237; PIDN:CAA32122.1; PID:g34238

R;Vuolteenaho, R.; Kallunki, T.; Chow, L.; Ikonen, J.; Pikkarainen, T.; Tryggvason, K.
in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp. 175-193, Academic P
A;Title: Genes for the human laminin B1 and B2 chains.
A;Reference number: S23566
A;Accession: S23567
A;Molecule type: DNA
A;Residues: 801-1481, 'R', 1483-1609 <VUO>
A;Note: mRNA was also sequenced
C;Genetics:
A;Gene: GDB:LAMC1; LAMB2
A;Cross-references: GDB:120136; OMIM:150290
A;Map position: 1q31-1q31
A;Introns: 140/1; 241/3; 285/2; 341/1; 404/1; 443/2; 476/2; 522/1; 563/1; 626/2; 664/1;
/3; 1525/1
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C;Function:
A;Description: interact with cells and with other basement membrane proteins to promote
C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular
F;1-33/Domain: signal sequence #status predicted <SIG>
F;34-1609/Product: laminin gamma-1 chain #status predicted <MAT>
F;34-285/Domain: VI <DOM6>
F;286-504/Domain: V <DOM5>
F;286-339/Domain: laminin-type EGF-like homology <LE01>
F;342-395/Domain: laminin-type EGF-like homology <LE02>
F;398-442/Domain: laminin-type EGF-like homology <LE03>
F;445-492/Domain: laminin-type EGF-like homology <LE04>
F;495-504/Domain: laminin-type EGF-like homology #status atypical <LE05>
F;505-689/Domain: IV <DOM4>
F;690-1034/Domain: III <DOM3>
F;690-721/Domain: laminin-type EGF-like homology #status atypical <LE06>
F;724-770/Domain: laminin-type EGF-like homology <LE07>
F;773-825/Domain: laminin-type EGF-like homology <LE08>
F;828-881/Domain: laminin-type EGF-like homology <LE09>
F;884-932/Domain: laminin-type EGF-like homology <LE10>
F;935-980/Domain: laminin-type EGF-like homology <LE11>
F;983-1028/Domain: laminin-type EGF-like homology <LE12>
F;1035-1609/Domain: II/I <DOM1>
F;1035-1609/Region: heptad repeats
F;40-50/Disulfide bonds: #status predicted
F;60,134,576,650,1022,1107,1161,1175,1205,1223,1241,1380,1395,1439/Binding site: carbohy
F;1031,1034,1600/Disulfide bonds: interchain #status predicted
Query Match 93.7%; Score 8144; DB 1; Length 1609;
Best Local Similarity 92.7%; Pred. No. 3.3e-302;
Matches 1492; Conservative 59; Mismatches 54; Indels 4; Gaps 3;
QY 1 MTGGGRAALALQPRGLWPLLAVL--AAVAGCVRAAMDECADEGGRPQRCMPEFVNAAFN 58
Db 1 MRGSHRAAPALRPRGRLWPVLAVLAAAAAAGCAQAAMDECTDEGGRPQRCMPEFVNAAFN 60
QY 59 VTVVATNTCGTPPEEYCVQGTGVTKSCHLCDAGQHLQHGAFLTDYNNQADTTWQWS 118
Db 61 VTVVATNTCGTPPEEYCVQGTGVTKSCHLCDAGQHLQHGAFLTDYNNQADTTWQWS 120
QY 119 QTMLAGVQYPNSINLTLLHLGKAFDITYVRLKFHTSRPESFAIYKRTREDGPWIPYQYISG 178
Db 121 QTMLAGVQYPSSINLTLLHLGKAFDITYVRLKFHTSRPESFAIYKRTREDGPWIPYQYISG 180
QY 179 SCENTYSKANRGFIRTTGGDEQALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFNDSFVL 238
Db 181 SCENTYSKANRGFIRTTGGDEQALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFNDSFVL 240
QY 239 QEWVTATDIRVTNLRLNTFGDEVENDPKVLKSYYYAISDFAVGGRCKNGHASECVKNEF 298
Db 241 QEWVTATDIRVTNLRLNTFGDEVENDPKVLKSYYYAISDFAVGGRCKNGHASECMKNEF 300
QY 299 DKLMCNCKHNTYGVDCCKLPFFNDRPWRRATAESASECLPCDCNGRSQECYFDPPELYRS 358
Db 301 DKLVNCNCKHNTYGVDCCKLPFFNDRPWRRATAESASECLPCDCNGRSQECYFDPPELYRS 360
QY 359 TGHGGHCTNCRDNTDGAKCERCERENFFRLGNTEACSPCHSPVGSLSLTCDSYGRCSCKP 418

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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:26:08 ; Search time 9.12547 Seconds
(without alignments)
9158.169 Million cell updates/sec

Title: US-10-037-182-18
Perfect score: 8694
Sequence: 1 MTGGRAALALQPRGLWPL.....EDIKKTLPTGCFNTPSIEKP 1605

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8627	99.2	1607	1 LMG1_MOUSE	P02468 mus musculus
2	8144	93.7	1609	1 LMG1_HUMAN	P11047 homo sapien
3	3596.5	41.4	1587	1 LMG3_HUMAN	Q9Y6N6 homo sapien
4	3500	40.3	1581	1 LMG3_MOUSE	Q9R0B6 mus musculus
5	3476	40.0	1639	1 LMG1_DROME	P15215 drosophila
6	3176	36.5	1535	1 LML1_CAEL	Q18823 caenorhabdi
7	2592	29.8	1193	1 LMG2_HUMAN	Q13753 homo sapien
8	2475	28.5	1191	1 LMG2_MOUSE	Q61092 mus musculus
9	1812.5	20.8	3106	1 LMA2_MOUSE	Q60675 mus musculus
10	1795.5	20.7	3110	1 LMA2_HUMAN	P24043 homo sapien
11	1784	20.5	3084	1 LMA1_MOUSE	P19137 mus musculus
12	1742	20.0	3075	1 LMA1_HUMAN	P25391 homo sapien
13	1682	19.3	1786	1 LMB1_HUMAN	P07942 homo sapien
14	1661.5	19.1	1786	1 LMB1_MOUSE	P02469 mus musculus
15	1656.5	19.1	1790	1 LMB1_DROME	P11046 drosophila
16	1592	18.3	1801	1 LMB2_RAT	P15800 rattus norv
17	1562	18.0	1798	1 LMB2_HUMAN	P55268 homo sapien
18	1552	17.9	1799	1 LMB2_MOUSE	Q61292 mus musculus
19	1455	16.7	3712	1 LMA_DROME	Q00174 drosophila
20	1396	16.1	3718	1 LMA5_MOUSE	Q61001 mus musculus
21	1384	15.9	3672	1 LML2_CAEL	Q21313 caenorhabdi
22	1356.5	15.6	3695	1 LMA5_HUMAN	Q15230 homo sapien
23	1167	13.4	604	1 NET1_MOUSE	Q09118 mus musculus
24	1163.5	13.4	604	1 NET1_HUMAN	Q95631 homo sapien
25	1162.5	13.4	3333	1 LMA3_MOUSE	Q61789 mus musculus
26	1162	13.4	606	1 NET1_CHICK	Q90922 gallus gall
27	1045	12.0	581	1 NET2_CHICK	Q90923 gallus gall
28	986.5	11.3	612	1 UNC6_CAEL	P34710 caenorhabdi
29	949.5	10.9	1172	1 LMB3_HUMAN	Q13751 homo sapien
30	904	10.4	1168	1 LMB3_MOUSE	Q61087 mus musculus
31	903.5	10.4	4391	1 PGBM_HUMAN	P98160 homo sapien
32	883	10.2	727	1 NETA_DROME	Q24567 drosophila
33	877.5	10.1	3707	1 PGBM_MOUSE	Q05793 mus musculus

34	853	9.8	793	1	NETB_DROME	Q24568 drosophila
35	637.5	7.3	3375	1	UN52_CAEL	Q06561 caenorhabdi
36	623.5	7.2	539	1	NTG1_MOUSE	Q8r490 mus musculus
37	585	6.7	1816	1	LMA4_HUMAN	Q16363 homo sapien
38	574.5	6.6	1816	1	LMA4_MOUSE	P97927 mus musculus
39	566.5	6.5	530	1	NTG2_HUMAN	Q96cw9 homo sapien
40	532	6.1	589	1	NTG2_MOUSE	Q8r4f1 mus musculus
41	514	5.9	1713	1	LMA3_HUMAN	Q16787 homo sapien
42	479	5.5	2470	1	NTC2_MOUSE	Q35516 mus musculus
43	477	5.5	2471	1	NTC2_RAT	Q9qW30 rattus norv
44	471	5.4	303	1	LMB1_CHICK	Q01635 gallus gall
45	469.5	5.4	2703	1	NOTC_DROME	P07207 drosophila

ALIGNMENTS

RESULT 1
LMG1_MOUSE
ID LMG1_MOUSE STANDARD; PRT; 1607 AA.
AC P02468;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Laminin gamma-1 chain precursor (laminin B2 chain).
GN LAMC1 OR LAMC-1 OR LAMB-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88059118; PubMed=3680290;
RA Sasaki M., Yamada Y.;
RT "The laminin B2 chain has a multidomain structure homologous to the B1 chain."
RL J. Biol. Chem. 262:17111-17117(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89000737; PubMed=3167041;
RA Durkin M.E., Bartsch-B., Liu S.-H., Phillips S.L., Chung A.E.;
RT "Primary structure of the mouse laminin B2 chain and comparison with laminin B1."
RL Biochemistry 27:5198-5204(1988).
RN [3]
RP SEQUENCE OF 1-239 FROM N.A.
RX MEDLINE=88228071; PubMed=2836421;
RA Ogawa K., Burelo P.D., Sasaki M., Yamada Y.;
RT "The laminin B2 chain promoter contains unique repeat sequences and is active in transient transfection."
RL J. Biol. Chem. 263:8384-8389(1988).
RN [4]
RP SEQUENCE OF 1391-1607 FROM N.A.
RX MEDLINE=85051302; PubMed=6209134;
RA Barlow D.P., Green N.M., Kurkinen M., Hogan B.L.M.;
RT "Sequencing of laminin B chain cDNAs reveals C-terminal regions of coiled-coil alpha-helix."
RL EMBO J. 3:2355-2362(1984).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 771-932.
RX MEDLINE=96196434; PubMed=8648630;
RA Stetefeld J., Mayer U., Timpl R., Huber R.;
RT "Crystal structure of three consecutive laminin-type epidermal growth factor-like (LE) modules of laminin gamma1 chain harboring the nidogen binding site."
RL J. Mol. Biol. 257:644-657(1996).
RN [6]
RP STRUCTURE BY NMR OF 824-881.
RX MEDLINE=96196435; PubMed=8648631;
RA Baumgartner R., Cziisch M., Mayer U., Poeschl E., Huber R., Timpl R., Holak T.A.;
RT "Structure of the nidogen binding LE module of the laminin gamma1 chain in solution."

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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:25:32 ; Search time 42.7526 Seconds
(without alignments)
10415.614 Million cell updates/sec

Title: US-10-037-182-16
Perfect score: 8544
Sequence: 1 QAMDECTDEGRPQRCMPE.....EDIRKTLPSGCFNTPSIEKP 1576

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	8544	100.0	1576	3 AAB19802	Aab19802 Human lam
2	8544	100.0	1576	3 AAB48453	Aab48453 Human lam
3	8544	100.0	1576	5 ABB81595	Abb81595 Human lam
4	8544	100.0	1584	3 AAB19804	Aab19804 Human lam
5	8544	100.0	1609	3 AAB19801	Aab19801 Human lam
6	8544	100.0	1609	3 AAB48452	Aab48452 Human lam
7	8544	100.0	1609	5 ABB81594	Abb81594 Human lam
8	8544	100.0	1609	7 ADC01887	Adc01887 Human lam
9	8544	100.0	1617	3 AAB19803	Aab19803 Human lam
10	8540	100.0	1609	2 AAW50898	Aaw50898 Human lam
11	8043	94.1	1605	3 AAB19805	Aab19805 Mouse lam
12	8043	94.1	1605	3 AAB48454	Aab48454 Mouse lam
13	8043	94.1	1605	5 ABB81596	Abb81596 Mouse lam
14	8042	94.1	1607	2 AAW50897	Aaw50897 Mouse lam
15	8038	94.1	1572	3 AAB19806	Aab19806 Mouse lam
16	8038	94.1	1572	3 AAB48455	Aab48455 Mouse lam
17	8038	94.1	1572	5 ABB81597	Abb81597 Mouse lam
18	3602	42.2	1587	3 AAB40917	Aab40917 Human ORF
19	3600	42.1	1587	5 AAM50361	Aam50361 Mouse lam
20	3600	42.1	1587	6 ABR58467	Abr58467 Human NOV
21	3598	42.1	1575	6 ABR58468	Abr58468 Human NOV
22	3463.5	40.5	1524	2 AAY15458	Aay15458 Human lam
23	3440	40.3	1639	4 ABB59807	Abb59807 Drosophil
24	2637	30.9	1193	2 AAR91427	Aar91427 Kalinin/1
25	2637	30.9	1193	3 AAB48468	Aab48468 Human lam

26	2637	30.9	1193	5 AAE14712	Aae14712 Human lam
27	2637	30.9	1193	5 AAO14992	Aao14992 Laminin g
28	2637	30.9	1193	6 ABR48214	Abr48214 Human bla
29	2637	30.9	1193	6 ABU56513	Abu56513 Lung canc
30	2637	30.9	1193	6 ABU56696	Abu56696 Lung canc
31	2637	30.9	1193	6 ABR92103	Abr92103 Human cer
32	2637	30.9	1193	6 ADA74120	Ada74120 Human lam
33	2630	30.8	1172	3 AAB48469	Aab48469 Human lam
34	2629	30.8	1193	3 AAB48470	Aab48470 Human lam
35	2622	30.7	1172	3 AAB48471	Aab48471 Human lam
36	2612.5	30.6	1190	6 ADA74091	Ada74091 Equine la
37	2516.5	29.5	1111	2 AAR91428	Aar91428 Kalinin/1
38	2516.5	29.5	1111	5 AAE14713	Aae14713 Human lam
39	2516.5	29.5	1111	5 AAO14993	Aao14993 Laminin g
40	2454.5	28.7	1171	3 AAB48473	Aab48473 Mouse lam
41	2454.5	28.7	1192	3 AAB48472	Aab48472 Mouse lam
42	2454.5	28.7	1192	5 AAE14711	Aae14711 Mouse lam
43	2454.5	28.7	1192	6 ADA74121	Ada74121 Murine la
44	2355.5	27.6	1171	2 AAW26583	Aaw26583 Rat hemid
45	1782.5	20.9	3084	4 AAE11215	Aae11215 Mouse lam

ALIGNMENTS

RESULT 1
AAB19802
ID AAB19802 standard; protein; 1576 AA.
XX
AC AAB19802;
XX
DT 05-MAR-2001 (first entry)
XX
DE Human laminin 2 mature gamma-1 chain.
XX
KW Laminin 2; human; nerve regeneration; angiogenic; cell adhesion;
KW degenerative muscle disorder; muscular dystrophy; cell therapy.
XX
OS Homo sapiens.
XX
PN WO200066730-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US011378.
XX
PR 30-APR-1999; 99US-0131720P.
PR 15-JUN-1999; 99US-0139198P.
PR 12-JUL-1999; 99US-0143289P.
PR 24-SEP-1999; 99US-0155945P.
XX
PA (UTYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
PI Yurchenco P;
XX
DR WPI; 2000-687537/67.
DR N-PSDB; AAA88902.
XX
PT Purified laminin 2 protein, useful for research and therapeutic purposes
PT including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.
XX
PS Claim 5; Page 251-256; 305pp; English.
XX
CC The present sequence is that of human laminin 2 gamma-1 chain mature
CC protein. Laminin-2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and
CC gamma-1 (100 kDa) chains. It is thought to be specifically required for
CC stabilizing myotubes during skeletal muscle development, and for
CC preventing apoptosis. Genetic defects in its structure or expression are
CC associated with a major type of congenital muscular dystrophy. Laminin 2
CC is also thought to be important in Schwann cell/basal lamina
CC interactions. The invention provides laminin 2 alpha-2, beta-1 and gamma-
CC 1 chain polypeptides (see AAB19791-806) and the polynucleotides encoding

PR 30-APR-1999; 99US-0131720P.
PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.
PR 11-FEB-2000; 2000US-0182012P.
XX
PA (BIOS-) BIOSTRATUM INC.
XX
XX Kortessmaa J, Tryggvason K;
PI
XX
DR WPI; 2000-687539/67.
DR N-PSDB; AAC83714.
XX
PT Purified laminin 8 protein, useful for research and therapeutic purposes
PT including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.
XX
XX
PS Claim 5; Page 214-218; 245pp; English.
XX
CC The present sequence is a laminin 8 polypeptide chain. Laminins are a
CC family of heterotrimeric glycoproteins that function via binding
CC interactions with neighbouring cell receptors and by forming laminin
CC networks. They are signalling molecules which influence cellular
CC function. Laminin 8 is useful for treating injuries to tissue of
CC mesenchymal origin, such as bone, cartilage, tendon, and ligament,
CC treating injuries to vascular tissue, promoting cell attachment and
CC migration, ex vivo cell therapy, improving the biocompatibility of
CC medical devices, and preparing improved cell culture devices and media.
CC Laminin 8 is also useful for promoting re-endothelialisation at the site
CC of vascular injuries, improving the take of grafts, improving the
CC biocompatibility of medical devices, treating neural injuries (neural
CC regeneration), regulating angiogenesis, and promoting cell attachment and
CC migration
XX
SQ Sequence 1576 AA;
Query Match 100.0%; Score 8544; DB 3; Length 1576;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QAAMDECTDEGGRPQRCMPEFVNAAFNVTVVATNTCGTPPEEYCVQGTGVTKSCHLCD 60
Db 1 QAAMDECTDEGGRPQRCMPEFVNAAFNVTVVATNTCGTPPEEYCVQGTGVTKSCHLCD 60
Qy 61 AGQPHLQHGAFLTDYNNQADTTWQSQTMLAGVQYDPSINLTLLHLGKAFDITYVRLKFH 120
Db 61 AGQPHLQHGAFLTDYNNQADTTWQSQTMLAGVQYDPSINLTLLHLGKAFDITYVRLKFH 120
Qy 121 TSRPESFAIYKRTREDGPWIPYQYYSGCSENTYSKANRGFI RTGGDEQQALCTDEFSDIS 180
Db 121 TSRPESFAIYKRTREDGPWIPYQYYSGCSENTYSKANRGFI RTGGDEQQALCTDEFSDIS 180
Qy 181 PLTGGNVAFSTLEGRRPSAYNFDNSPVLQEWVTATDIRVTNRLNTFGDEVNDPKVLKSY 240
Db 181 PLTGGNVAFSTLEGRRPSAYNFDNSPVLQEWVTATDIRVTNRLNTFGDEVNDPKVLKSY 240
Qy 241 YYAISDFAVGGRCKCNHGHASECMKNEFDKLVNCNKHNTYGVDCCKLPFFNDRPWRATA 300
Db 241 YYAISDFAVGGRCKCNHGHASECMKNEFDKLVNCNKHNTYGVDCCKLPFFNDRPWRATA 300
Qy 301 ESASECLPCDCNRSQECYFDPPELYRSTGHGGHCTNCQNTDGAHCRCRNFRLGNNE 360
Db 301 ESASECLPCDCNRSQECYFDPPELYRSTGHGGHCTNCQNTDGAHCRCRNFRLGNNE 360
Qy 361 ACSSCHGSPVGSLSLSTQCDSYGRCSCKPGVMGDKCDRCQDPGFHSLTEAGCRPCSDPSGSI 420
Db 361 ACSSCHGSPVGSLSLSTQCDSYGRCSCKPGVMGDKCDRCQDPGFHSLTEAGCRPCSDPSGSI 420
Qy 421 DECNVETGRVCVCKDNVEGNCERCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGSVY 480
Db 421 DECNVETGRVCVCKDNVEGNCERCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGSVY 480
Qy 481 SISSTFQIDEDGWAEQRDGSEASLEWSSERQDIAVISDYFPFYFIAPAKFLGKQVLSY 540

Db 481 SISSTFQIDEDGWAEQRDGSEASLEWSSERQDIAVISDYFPFYFIAPAKFLGKQVLSY 540
Qy 541 GQNLFSFSFRVDRRDTLSAEDLVLEGAGLRVSUPLIAQGNISYPSETTVKYVFRLHEATDY 600
Db 541 GQNLFSFSFRVDRRDTLSAEDLVLEGAGLRVSUPLIAQGNISYPSETTVKYVFRLHEATDY 600
Qy 601 PWRPALTPPEFQKLLNLTISKIRGTYSERSAGYLDVTLASARPGVGPATWVESCTCP 660
Db 601 PWRPALTPPEFQKLLNLTISKIRGTYSERSAGYLDVTLASARPGVGPATWVESCTCP 660
Qy 661 VGYGGQFCMCLSGYRRETPNLGPYSPCVLACNHSSETCDPETGVNCNRDNTAGPHCEK 720
Db 661 VGYGGQFCMCLSGYRRETPNLGPYSPCVLACNHSSETCDPETGVNCNRDNTAGPHCEK 720
Qy 721 CSDGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKBVCTNCPTGTTGKRCCLCDDGYFG 780
Db 721 CSDGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKBVCTNCPTGTTGKRCCLCDDGYFG 780
Qy 781 DPLGRNGPVRLCRLCQCSNDIDPNVAGNCNRLTGECLKCIYNTAGFYCDRCCKDGFNGNPL 840
Db 781 DPLGRNGPVRLCRLCQCSNDIDPNVAGNCNRLTGECLKCIYNTAGFYCDRCCKDGFNGNPL 840
Qy 841 APNPADKCKACNCPYGTWKQSSCNPNVTGQCECLPHVTGQDCGACDPGFYNLQSGQGCE 900
Db 841 APNPADKCKACNCPYGTWKQSSCNPNVTGQCECLPHVTGQDCGACDPGFYNLQSGQGCE 900
Qy 901 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCHERCEVNHFGFEGEGCKPCDCHPEGSLSL 960
Db 901 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCHERCEVNHFGFEGEGCKPCDCHPEGSLSL 960
Qy 961 QCKDDGRCECREGVGNRCDOCEENFYNRSWPGCQBCPACRYLVKDKVADHRVKLQLELE 1020
Db 961 QCKDDGRCECREGVGNRCDOCEENFYNRSWPGCQBCPACRYLVKDKVADHRVKLQLELE 1020
Qy 1021 SLIANLGTGDEMVTDOAFEDRLKEAREVMDLLREADVQDVQDNLMRLQRVNNTLSQ 1080
Db 1021 SLIANLGTGDEMVTDOAFEDRLKEAREVMDLLREADVQDVQDNLMRLQRVNNTLSQ 1080
Qy 1081 ISRLQNRNTIETGNLAEQARAHVENTERLIEIASHELEKAKVAAANVSVTQPESTGDP 1140
Db 1081 ISRLQNRNTIETGNLAEQARAHVENTERLIEIASHELEKAKVAAANVSVTQPESTGDP 1140
Qy 1141 NNMTLLAEARKLAEHRHKEADDIRVAKTANDTSTEAYNLLRRTLAGENQTAFEIEELN 1200
Db 1141 NNMTLLAEARKLAEHRHKEADDIRVAKTANDTSTEAYNLLRRTLAGENQTAFEIEELN 1200
Qy 1201 RKYEQAKNISQDLEKQAARVHBEAKRAGDKAVEIYASVAQLSPDLSETLENEANNKMEA 1260
Db 1201 RKYEQAKNISQDLEKQAARVHBEAKRAGDKAVEIYASVAQLSPDLSETLENEANNKMEA 1260
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Qy 1381 SAAADATEAKNKAHEAERIAASAVQKNATSTKAAEERTFAEVTDL DNEVNNMLKQLOEAEK 1440
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Qy 1441 ELKRRQDDADQDMMAGMASQAAQEAIEINARKAKNSVTSLLSI INDLLEQLGQDVTVDLN 1500
Db 1441 ELKRRQDDADQDMMAGMASQAAQEAIEINARKAKNSVTSLLSI INDLLEQLGQDVTVDLN 1500
Qy 1501 KLNEIEGTLNKAKDEMKSVDLRKVSVDLENEAKKQEAAMDNDRDIEEIMKDIRNLEDIR 1560
Db 1501 KLNEIEGTLNKAKDEMKSVDLRKVSVDLENEAKKQEAAMDNDRDIEEIMKDIRNLEDIR 1560
Qy 1561 KTLPSGCCENTPSIEKP 1576
Db 1561 KTLPSGCCENTPSIEKP 1576

RESULT 3

AB81595
ID AB81595 standard; protein; 1576 AA.
XX AC AB81595;
XX DT 19-SEP-2002 (first entry)
XX DE Human laminin 10 third chain protein sequence SEQ ID NO:16.

XX KW Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;
XX KW tissue repair development; laminin; healing; vascular tissue;
XX KW re-endothelialisation; vascular injury; cell attachment; cell stasis;
XX KW proliferation; migration.

XX OS Homo sapiens.

XX PN WO200250111-A2.

XX PD 27-JUN-2002.

XX PF 21-DEC-2001; 2001WO-US051035.

XX PR 21-DEC-2000; 2000US-0257449P.

XX PR 28-MAR-2001; 2001US-0279282P.

XX PR 13-NOV-2001; 2001US-00279282.

XX PA (BIOS-) BIOSTRATUM INC.

XX PI Tryggvason K, Doi M, Thyboll J;

XX DR WPI; 2002-557650/59.

XX DR N-PSDB; ABQ72913.

XX PT New human laminin-10 proteins, useful for accelerating the healing of
PT vascular tissue, improving the biocompatibility of grafts, or for
PT promoting re-endothelialization at the site of vascular injuries.

XX PS Claim 9; Page 177-182; 231pp; English.

XX CC The present invention describes human laminin alpha 5. Also described is
CC an isolated laminin 10. Laminin 10 has vulnery activity. Laminins are
CC useful in maintaining cell/tissue phenotype as well as promoting cell
CC growth and differentiation in tissue repair development. Specifically,
CC laminin 10 can be used for accelerating the healing injuries of vascular
CC tissue, improving the biocompatibility of grafts useful for treating such
CC injuries, for promoting re-endothelialisation at the site of vascular
CC injuries, and promote cell attachment and subsequent cell stasis,
CC proliferation, differentiation, and/or migration. The present sequence
CC represents a third chain protein of laminin 10, from the present
CC invention

XX SQ Sequence 1576 AA;

Query Match 100.0%; Score 8544; DB 5; Length 1576;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QAAMDECTDEGGRPQRCMPEFVNAAFNVTVATNTCTGTPPEEYCVQGTGVTKSKLCLD 60
DB 1 QAAMDECTDEGGRPQRCMPEFVNAAFNVTVATNTCTGTPPEEYCVQGTGVTKSKLCLD 60
QY 61 AGQPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQVPSINLTLLHGXAFDITYVRLKFX 120
DB 61 AGQPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQVPSINLTLLHGXAFDITYVRLKFX 120
QY 121 TSRPESFAIKYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTGDEQALCTDEFSDIS 180
DB 121 TSRPESFAIKYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTGDEQALCTDEFSDIS 180
QY 181 PLTGGNVAFSTLEGRPSAYNFDSNPSVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSY 240

DB 181 PLTGGNVAFSTLEGRPSAYNFDSNPSVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSY 240
QY 241 YYAISDFAVGGRCKNGHASECMKNEFDKLVCKNCKHNTYGVDCCKECLPFENDRPWRRATA 300
DB 241 YYAISDFAVGGRCKNGHASECMKNEFDKLVCKNCKHNTYGVDCCKECLPFENDRPWRRATA 300
QY 301 ESASECLPCDCNCRSGRQECYFDPPELYRSTGHGGHCTNCQDNTDGAHCRCRENFRLGNNE 360
DB 301 ESASECLPCDCNCRSGRQECYFDPPELYRSTGHGGHCTNCQDNTDGAHCRCRENFRLGNNE 360
QY 361 ACSSCHCSPVGSLSSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLSLTEAGCRPCSCDPSGSI 420
DB 361 ACSSCHCSPVGSLSSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLSLTEAGCRPCSCDPSGSI 420
QY 421 DECNVETGRCVCKDNVEGFNCERCCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGSVY 480
DB 421 DECNVETGRCVCKDNVEGFNCERCCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGSVY 480
QY 481 SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFFRYFIAPAKFLGKQVLSY 540
DB 481 SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFFRYFIAPAKFLGKQVLSY 540
QY 541 GQNLFSFRVDRDRRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYVFLHEATDY 600
DB 541 GQNLFSFRVDRDRRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYVFLHEATDY 600
QY 601 PWRPALTPFEFQKLLNNLTISKIRGTYSERSAGYLDVTLASARPGVPATWVESCTCP 660
DB 601 PWRPALTPFEFQKLLNNLTISKIRGTYSERSAGYLDVTLASARPGVPATWVESCTCP 660
QY 661 VGYGGQFCMCLSGYRRRETNLGPYSPCVLCACNGHSETCDPETGVNCRDNTAGPHCEK 720
DB 661 VGYGGQFCMCLSGYRRRETNLGPYSPCVLCACNGHSETCDPETGVNCRDNTAGPHCEK 720
QY 721 CSDGYGDSSTAGTSDCQPCPCPGSSCAVWPKTKEVVTCTGTTGKRCCELCDGDFG 780
DB 721 CSDGYGDSSTAGTSDCQPCPCPGSSCAVWPKTKEVVTCTGTTGKRCCELCDGDFG 780
QY 781 DPLGRNGPVLRLCQCSNIDPNVAGNCNRLTGECLKCIYNTAGFYCDRCCKDGFENPL 840
DB 781 DPLGRNGPVLRLCQCSNIDPNVAGNCNRLTGECLKCIYNTAGFYCDRCCKDGFENPL 840
QY 841 APNPADKCKACNCPYGTMTKQSSCNPTVGTQCECLPHVTGDCGACDPPGYNLQSGQCE 900
DB 841 APNPADKCKACNCPYGTMTKQSSCNPTVGTQCECLPHVTGDCGACDPPGYNLQSGQCE 900
QY 901 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCEVNHFGFEGCKPCDCHPEGSLSL 960
DB 901 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCEVNHFGFEGCKPCDCHPEGSLSL 960
QY 961 QKDDGRCECEGFVGNRCDCQCEENYFYNRSPWPGCQCEPACRYLVKQVADHRYKLQELE 1020
DB 961 QKDDGRCECEGFVGNRCDCQCEENYFYNRSPWPGCQCEPACRYLVKQVADHRYKLQELE 1020
QY 1021 SLIANLGTGDEMVTDAQFEDRLKEAEREVMDLLREAOVDKVDQNLMDRLQVRNNTLSSQ 1080
DB 1021 SLIANLGTGDEMVTDAQFEDRLKEAEREVMDLLREAOVDKVDQNLMDRLQVRNNTLSSQ 1080
QY 1081 ISRLQIRNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSVTQESTGDP 1140
DB 1081 ISRLQIRNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSVTQESTGDP 1140
QY 1141 NNMNTLLAEARKLAERHKEADDIRVAKTANDTSTEYNLLRLTLRGTAFIEELN 1200
DB 1141 NNMNTLLAEARKLAERHKEADDIRVAKTANDTSTEYNLLRLTLRGTAFIEELN 1200
QY 1201 RKYEQAKNISQDLEKQAAVHEBAKAGDKAVEIYASVAQLSPLDSETLENEANNIKMEA 1260
DB 1201 RKYEQAKNISQDLEKQAAVHEBAKAGDKAVEIYASVAQLSPLDSETLENEANNIKMEA 1260
QY 1261 ENLEQLIDOKLYEDLREDMRGKELEVNKLLKGTQEQTADQLLARADAAKALAEAAA 1320

Db 1261 ENLEQLIDQKLKDYEDLRDVRGKELEVKNLLEKTEQQTADQLLARADAALAEAA 1320
QY 1321 KKGRDTLQEBANDILNNLKDFDRRVNDNKTAEEALRKIPAINOTITEANEKTRAQQAALG 1380
Db 1321 KKGRDTLQEBANDILNNLKDFDRRVNDNKTAEEALRKIPAINOTITEANEKTRAQQAALG 1380
QY 1381 SAAADATEAKNKAHEAERIASAVQKNATSTKAEAEPTFAEVTDLNNEVNNMLKQLOEAEK 1440
Db 1381 SAAADATEAKNKAHEAERIASAVQKNATSTKAEAEPTFAEVTDLNNEVNNMLKQLOEAEK 1440
QY 1441 ELKRRKQDDADQDMMAGMASQAQAQAEAEINARKAKNSVTSLLSIINDLLEQLQDLTDVLDN 1500
Db 1441 ELKRRKQDDADQDMMAGMASQAQAQAEAEINARKAKNSVTSLLSIINDLLEQLQDLTDVLDN 1500
QY 1501 KLNIEIEGTLNKADEMKSVDLDRKVSVDLENEAKKQAEAAIMDYNRDIEEIMKDIRNLEDIR 1560
Db 1501 KLNIEIEGTLNKADEMKSVDLDRKVSVDLENEAKKQAEAAIMDYNRDIEEIMKDIRNLEDIR 1560

QY 1561 KTLPSGCFNTPTSIKP 1576
Db 1561 KTLPSGCFNTPTSIKP 1576

RESULT 4
AAB19804
ID AAB19804 standard; protein; 1584 AA.
AC AAB19804;

DT 05-MAR-2001 (first entry)
XX Human laminin 2 gamma-1 chain with C-terminal FLAG epitope.
DE Laminin 2; human; nerve regeneration; angiogenic; cell adhesion;
KW degenerative muscle disorder; muscular dystrophy; cell therapy.
KW
XX Homo sapiens.

XX Key Location/Qualifiers
FH Peptide 1. .33
FT /label= Signal_peptide
FT Protein 34. .1609
FT /label= Mature_protein
FT Peptide 1610. .1617
FT /label= FLAG

XX WO2000066730-A2.
PN
XX
PD 09-NOV-2000.
XX 28-APR-2000; 2000WO-US011378.
PF
XX 30-APR-1999; 99US-0131720P.
PR 15-JUN-1999; 99US-0139198P.
PR 12-JUL-1999; 99US-0143289P.
PR 24-SEP-1999; 99US-0155945P.
XX
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
PI Yurchenco P;
XX
DR WPI; 2000-687537/67.
DR N-PSDB; AAA88904.

XX Purified laminin 2 protein, useful for research and therapeutic purposes
PT including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.
XX
PS Claim 5; Page 275-280; 305pp; English.

XX The present sequence is that of the mature gamma-1 chain of human laminin
CC 2, with an additional C-terminal FLAG epitope, resulting from expression
CC in transfected cells from mammalian expression vectors. Laminin 2 is

CC composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1 (100 kDa)
CC chains. It is thought to be specifically required for stabilizing
CC myotubes during skeletal muscle development, and for preventing
CC apoptosis. Genetic defects in its structure or expression are associated
CC with a major type of congenital muscular dystrophy. Laminin 2 is also
CC thought to be important in Schwann cell/basal lamina interactions. The
CC invention provides laminin 2 alpha-2, beta-1 and gamma-1 chain
CC polypeptides (see AAB19791-806) and the polynucleotides encoding them
CC (see AAA8891-906), methods for making recombinant laminin 2, cells that
CC express recombinant laminin 2, and methods for using purified laminin 2
CC for research and therapeutic purposes including peripheral nerve
CC regeneration, treatment of degenerative muscle disorders, angiogenesis
CC regulation, promoting cell attachment and migration, ex vivo cell
CC therapy, improving the take of grafts, improving the biocompatibility of
CC medical devices and preparing improved culture devices and media
XX
SQ Sequence 1584 AA;

Query Match 100.0%; Score 8544; DB 3; Length 1584;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QAAMDECTDEGGRPQRCMPEFNAAFNVTVATNTCGTPEEYCVQGTGVTGTSCHLCD 60
Db 1 QAAMDECTDEGGRPQRCMPEFNAAFNVTVATNTCGTPEEYCVQGTGVTGTSCHLCD 60
QY 61 AGQPHLOHGAFLTDYNNQADTTWQSQOTMLAGVQYPSINLTLLHKGAFDITYVRLKFX 120
Db 61 AGQPHLOHGAFLTDYNNQADTTWQSQOTMLAGVQYPSINLTLLHKGAFDITYVRLKFX 120
QY 121 TSRPESFAIYKRTREDGPWIPQYYSGSCENTYSKANRGFIRTTGGDEQQAALCTDEFSDIS 180
Db 121 TSRPESFAIYKRTREDGPWIPQYYSGSCENTYSKANRGFIRTTGGDEQQAALCTDEFSDIS 180
QY 181 PLTGGNVAFSTLEGRPSAYNFNDSPLVQEWVTATDIRVTLNRLNTFGDEVNDPKVLKSY 240
Db 181 PLTGGNVAFSTLEGRPSAYNFNDSPLVQEWVTATDIRVTLNRLNTFGDEVNDPKVLKSY 240
QY 241 YYAISDEFAVGGRCCKNGHASECMKNEFDKLVNCKHNTYGVDCCKLPFFNDRPWRATA 300
Db 241 YYAISDEFAVGGRCCKNGHASECMKNEFDKLVNCKHNTYGVDCCKLPFFNDRPWRATA 300
QY 301 ESASECLPCDCNGRSQECYFDPPELYRSTGHGGHCTNCQDNTDGAHCRCRENFRLGNNE 360
Db 301 ESASECLPCDCNGRSQECYFDPPELYRSTGHGGHCTNCQDNTDGAHCRCRENFRLGNNE 360
QY 361 ACSSCHCSPVGSLSLSTQCDSYGRCSCKPGWMDKCDRCQPGFHSLTEAGCRPCSCDESGSI 420
Db 361 ACSSCHCSPVGSLSLSTQCDSYGRCSCKPGWMDKCDRCQPGFHSLTEAGCRPCSCDESGSI 420
QY 421 DECNVETGRVCVKDNVEGFNCERCKPGFFNFLESNPRGCTPCFCFGHSSVCTNAVGSYVY 480
Db 421 DECNVETGRVCVKDNVEGFNCERCKPGFFNFLESNPRGCTPCFCFGHSSVCTNAVGSYVY 480
QY 481 SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPFYFIAPAKFLGKQVLSY 540
Db 481 SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPFYFIAPAKFLGKQVLSY 540
QY 541 GQNLFSFRVDRDRDRLSAEDLVLEGAGLRVSVPLIAQGNISYPSSETTVKYVFLHEATDY 600
Db 541 GQNLFSFRVDRDRDRLSAEDLVLEGAGLRVSVPLIAQGNISYPSSETTVKYVFLHEATDY 600
QY 601 PWRPALTPEFQKLLNLTLSIKIRGTYSERSAGYLDVTLASARPGVPATWVESCTCP 660
Db 601 PWRPALTPEFQKLLNLTLSIKIRGTYSERSAGYLDVTLASARPGVPATWVESCTCP 660
QY 661 VGYGGQFCMCLSGYRRRETNPLGYSPCVLCACNGHSETCDPETGVCNCRDNTAGPHCEK 720
Db 661 VGYGGQFCMCLSGYRRRETNPLGYSPCVLCACNGHSETCDPETGVCNCRDNTAGPHCEK 720
QY 721 CSDGYGDSGTAGTSSDCQPCPCPGSSSCAVVPKTKEVVCTNCTGTTGKRCCELDDGYFG 780
Db 721 CSDGYGDSGTAGTSSDCQPCPCPGSSSCAVVPKTKEVVCTNCTGTTGKRCCELDDGYFG 780

QY 781 DPLGRNPVRLCRLCQSDNIDPNAVGNCRNLTGECCKIYNTAGFYCDRCXGDFGPNL 840
Db 781 DPLGRNPVRLCRLCQSDNIDPNAVGNCRNLTGECCKIYNTAGFYCDRCXGDFGPNL 840
QY 841 APNPADKCKACNCPYGTMKQSSCNPNVTGQCECLPHVTGQCGACDPGFYNLQSGQGE 900
Db 841 APNPADKCKACNCPYGTMKQSSCNPNVTGQCECLPHVTGQCGACDPGFYNLQSGQGE 900
QY 901 RCDHALGSTNGQCDIRTGQCECQPGITGQHCEVNHFGFEGEGCKPCDCHPEGSLSL 960
Db 901 RCDHALGSTNGQCDIRTGQCECQPGITGQHCEVNHFGFEGEGCKPCDCHPEGSLSL 960
QY 961 QCKDDGRCEGEGFVGNRCQCEENYFYNRSPGQCECPACRYLVKDKVADHRVKLQELE 1020
Db 961 QCKDDGRCEGEGFVGNRCQCEENYFYNRSPGQCECPACRYLVKDKVADHRVKLQELE 1020
QY 1021 SLIANLGTGDEMVTDOAFEDRLKEAREVMDLLREAOQVDVQDQNLMDRLQVNNLTSSQ 1080
Db 1021 SLIANLGTGDEMVTDOAFEDRLKEAREVMDLLREAOQVDVQDQNLMDRLQVNNLTSSQ 1080
QY 1081 ISRLQINRNTIETGNLAEOARAHVENTERLIEIASRELEKAKVAAANVSVPQESTGDP 1140
Db 1081 ISRLQINRNTIETGNLAEOARAHVENTERLIEIASRELEKAKVAAANVSVPQESTGDP 1140
QY 1141 NMTLLAEARKLAERHKQEAADIVRVAKTANDTSTAYNLLRTLAGENQTAPEIEELN 1200
Db 1141 NMTLLAEARKLAERHKQEAADIVRVAKTANDTSTAYNLLRTLAGENQTAPEIEELN 1200
QY 1201 RYEQAKNTSQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDSETLENEANNIXMEA 1260
Db 1201 RYEQAKNTSQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDSETLENEANNIXMEA 1260
QY 1261 ENLEQLIDOKLYEDLREDMRGKELEVNKLLLEKGTQEQQTADQLLARADAALAEAEA 1320
Db 1261 ENLEQLIDOKLYEDLREDMRGKELEVNKLLLEKGTQEQQTADQLLARADAALAEAEA 1320
QY 1321 KKGRDTLQZANDILNNLKDFRRVNDNKTAAEEALRKIPAINQTIITEANEKTRAQQAALG 1380
Db 1321 KKGRDTLQZANDILNNLKDFRRVNDNKTAAEEALRKIPAINQTIITEANEKTRAQQAALG 1380
QY 1381 SAAADATEAKNKAHEAERIAASAVQKNATSTKAEARTFAEVTDLNNEVNNMLKQLQEA 1440
Db 1381 SAAADATEAKNKAHEAERIAASAVQKNATSTKAEARTFAEVTDLNNEVNNMLKQLQEA 1440
QY 1441 ELKRKQDDADQDMMAGMASQAQAEAEINARKAKNSVTSLLSIINDLLEQLGQDQTDV 1500
Db 1441 ELKRKQDDADQDMMAGMASQAQAEAEINARKAKNSVTSLLSIINDLLEQLGQDQTDV 1500
QY 1501 KLEIEGTILNKADEMKSVDLDRKVSDDLNEAKKQAAIMDYNRDIIEIMKDIRNLEDIR 1560
Db 1501 KLEIEGTILNKADEMKSVDLDRKVSDDLNEAKKQAAIMDYNRDIIEIMKDIRNLEDIR 1560
QY 1561 KTLPSGCNTFPSIEKP 1576
Db 1561 KTLPSGCNTFPSIEKP 1576

RESULT 5
AAB19801
ID AAB19801 standard; protein; 1609 AA.
XX
AC AAB19801;
XX
XX
DT 05-MAR-2001 (first entry)
XX
XX Human laminin 2 gamma-1 chain.
XX
XX Laminin 2; human; nerve regeneration; angiogenic; cell adhesion;
KW degenerative muscle disorder; muscular dystrophy; cell therapy.
KW
XX Homo sapiens.
OS
XX

FH Key Location/Qualifiers
FT Peptide 1..33
FT Protein /label= Signal_peptide
FT /label= Mature_protein
XX WO200066730-A2.
XX 09-NOV-2000.
XX 28-APR-2000; 2000WO-US011378.
XX 30-APR-1999; 99US-0131720P.
PR 15-JUN-1999; 99US-0139198P.
PR 12-JUL-1999; 99US-0143289P.
PR 24-SEP-1999; 99US-0155945P.
XX
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX Yurchenco P;
XX WPI; 2000-687537/67.
DR N-PSDB; AAA88901.
XX
PT Purified laminin 2 protein, useful for research and therapeutic purposes
PT including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.
XX
PS Claim 5; Page 239-244; 305pp; English.
XX
CC The present sequence is that of the gamma-1 chain of human laminin 2.
CC Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1
CC (100 kDa) chains. It is thought to be specifically required for
CC stabilizing myotubes during skeletal muscle development, and for
CC preventing apoptosis. Genetic defects in its structure or expression are
CC associated with a major type of congenital muscular dystrophy. Laminin 2
CC is also thought to be important in Schwann cell/basal lamina
CC interactions. The invention provides laminin 2 alpha-2, beta-1 and gamma-
CC 1 chain polypeptides (see AAB19791-806) and the polynucleotides encoding
CC them (see AAA8891-906), methods for making recombinant laminin 2, cells
CC that express recombinant laminin 2, and methods for using purified
CC laminin 2 for research and therapeutic purposes including peripheral
CC nerve regeneration, treatment of degenerative muscle disorders,
CC angiogenesis regulation, promoting cell attachment and migration, ex vivo
CC cell therapy, improving the take of grafts, improving the
CC biocompatibility of medical devices and preparing improved culture
CC devices and media
XX
SQ Sequence 1609 AA;

Query Match 100.0%; Score 8544; DB 3; Length 1609;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QAAMDECTDEGGRPQRCMPPEFYNAFNVTVATNTCGTPPEEYCVQGTGVTGTSCHLCD 60
Db 34 QAAMDECTDEGGRPQRCMPPEFYNAFNVTVATNTCGTPPEEYCVQGTGVTGTSCHLCD 93
QY 61 AGOPHLQHGAFLTDYNNQADTTWQSQOTMLAGVQYVSSINLTLLHKGAFDITYVRLKFH 120
Db 94 AGOPHLQHGAFLTDYNNQADTTWQSQOTMLAGVQYVSSINLTLLHKGAFDITYVRLKFH 153
QY 121 TSRPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQAALCTDEFSDIS 180
Db 154 TSRPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQAALCTDEFSDIS 213
QY 181 PLTGGNVAFSTLEGRPSAYNFNDSPLVQEWVTATDIRVTNLTNLTGDEVNDPKVLKSY 240
Db 214 PLTGGNVAFSTLEGRPSAYNFNDSPLVQEWVTATDIRVTNLTNLTGDEVNDPKVLKSY 273
QY 241 YYAISDFAVGGRCKNGHASECMKNEFDKLVNCKNTYGVDCCKLCPFFNDRPWRATA 300
Db 274 YYAISDFAVGGRCKNGHASECMKNEFDKLVNCKNTYGVDCCKLCPFFNDRPWRATA 333

QY 301 ESASECLPCDNGRSQCYFDPELYRSTGHGHTNCQDNTDGAHCRCRENFFRLGNNE 360
Db |||||
QY 334 ESASECLPCDNGRSQCYFDPELYRSTGHGHTNCQDNTDGAHCRCRENFFRLGNNE 393
Db |||||
QY 361 ACSSCHCSPVGSLSLSTQCDYGRCSCKPGVMGDKDCRCQPGFHSLTEAGCRPCSCDPSGSI 420
Db |||||
QY 394 ACSSCHCSPVGSLSLSTQCDYGRCSCKPGVMGDKDCRCQPGFHSLTEAGCRPCSCDPSGSI 453
Db |||||
QY 421 DECNVETGRCVCKDNVEGNCERCCKPGFFENLESSNPRGCTPCFCFGHSSVCTNAVGYSVY 480
Db |||||
QY 454 DECNVETGRCVCKDNVEGNCERCCKPGFFENLESSNPRGCTPCFCFGHSSVCTNAVGYSVY 513
Db |||||
QY 481 SISSTFOIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY 540
Db |||||
QY 514 SISSTFOIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY 573
Db |||||
QY 541 GQNLSPSFRVDRDTRLASAEDLVLEGAGLRVSVPVLIAGQNSYPSETTVTKYVPRLHEATDY 600
Db |||||
QY 574 GQNLSPSFRVDRDTRLASAEDLVLEGAGLRVSVPVLIAGQNSYPSETTVTKYVPRLHEATDY 633
Db |||||
QY 601 PWRPALTPFEFQKLLNLTSTIKIRGTYSERSAGYLDVTLASARPGVGPATWVESCTCP 660
Db |||||
QY 634 PWRPALTPFEFQKLLNLTSTIKIRGTYSERSAGYLDVTLASARPGVGPATWVESCTCP 693
Db |||||
QY 661 VGYGGQFCMCLSGYRRRETNLGPYSPCVLCA CNHSETCDPETGVCNCRDNTAGPHCEK 720
Db |||||
QY 694 VGYGGQFCMCLSGYRRRETNLGPYSPCVLCA CNHSETCDPETGVCNCRDNTAGPHCEK 753
Db |||||
QY 721 CSDGYGDSSTAGTSSDCQPCPCGSSCAVVPKTKEVVCTNCPTGTTGKRCELDDGYFG 780
Db |||||
QY 754 CSDGYGDSSTAGTSSDCQPCPCGSSCAVVPKTKEVVCTNCPTGTTGKRCELDDGYFG 813
Db |||||
QY 781 DPLGRNGPVRLCRLCQCSNDIDPNAVGNCNRLTGECCLKIYNTAGFYCDRCCKDGFEGNPL 840
Db |||||
QY 814 DPLGRNGPVRLCRLCQCSNDIDPNAVGNCNRLTGECCLKIYNTAGFYCDRCCKDGFEGNPL 873
Db |||||
QY 841 APNPADKCKACNCNPNYGTMKQOSSCNPVGTQCECLPHVTGQDCGACDPPGFYNLQSGQCE 900
Db |||||
QY 874 APNPADKCKACNCNPNYGTMKQOSSCNPVGTQCECLPHVTGQDCGACDPPGFYNLQSGQCE 933
Db |||||
QY 901 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCHERCCEVNHFGFPEGCKPCDCHPEGSLSL 960
Db |||||
QY 934 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCHERCCEVNHFGFPEGCKPCDCHPEGSLSL 993
Db |||||
QY 961 QCKDDGRCEGREGFVGNRCDQCEENYFYNRSPWPGQCECPACVRLVKDKVADHRVKLQELE 1020
Db |||||
QY 994 QCKDDGRCEGREGFVGNRCDQCEENYFYNRSPWPGQCECPACVRLVKDKVADHRVKLQELE 1053
Db |||||
QY 1021 SLIANLGTGDMVTDQAFEDRLKEAREVMDLLREAQDVVDQNDLMDRLQRVNNTLSSQ 1080
Db |||||
QY 1054 SLIANLGTGDMVTDQAFEDRLKEAREVMDLLREAQDVVDQNDLMDRLQRVNNTLSSQ 1113
Db |||||
QY 1081 ISRLQIRNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1140
Db |||||
QY 1114 ISRLQIRNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1173
Db |||||
QY 1141 NNMTLLEAEARKLAERHKEADDIVRVAKTANDTSTEAYNLLRLTLAGENQTAFEIEELN 1200
Db |||||
QY 1174 NNMTLLEAEARKLAERHKEADDIVRVAKTANDTSTEAYNLLRLTLAGENQTAFEIEELN 1233
Db |||||
QY 1201 RKYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDSETLENEANNIKMEA 1260
Db |||||
QY 1234 RKYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDSETLENEANNIKMEA 1293
Db |||||
QY 1261 ENLEQLIDQKLDYEDLREDMRGKELEVKNLLEKKGTEQQTADQLLARADA AKALAEAA 1320
Db |||||
QY 1294 ENLEQLIDQKLDYEDLREDMRGKELEVKNLLEKKGTEQQTADQLLARADA AKALAEAA 1353
Db |||||
QY 1321 KKGRDTLQEANDILNNLKDFDRRVNDNKTAAEALRKIPAINQTITEANEKTRTAAQALG 1380
Db |||||
QY 1354 KKGRDTLQEANDILNNLKDFDRRVNDNKTAAEALRKIPAINQTITEANEKTRTAAQALG 1413
Db |||||

QY 1381 SAAADATEAKNKAHEAERIAASAVQKNATSTKABAERTFAEVTDLDNVNNMLKQLQEA EK 1440
Db |||||
QY 1414 SAAADATEAKNKAHEAERIAASAVQKNATSTKABAERTFAEVTDLDNVNNMLKQLQEA EK 1473
Db |||||
QY 1441 ELKRKQDDADQDMMAGMASQAAQAEAEINARKAKNSVTSLLSIINDLLEQLQDLTVDLN 1500
Db |||||
QY 1474 ELKRKQDDADQDMMAGMASQAAQAEAEINARKAKNSVTSLLSIINDLLEQLQDLTVDLN 1533
Db |||||
QY 1501 KLNIEGTNLKAKOEMKVSDDLDRKVS DLENEAKKQEAAIMDYNRDIEEIMKD IRLNLEDIR 1560
Db |||||
QY 1534 KLNIEGTNLKAKOEMKVSDDLDRKVS DLENEAKKQEAAIMDYNRDIEEIMKD IRLNLEDIR 1593
Db |||||
QY 1561 KTLPSGCFNTPSIEKP 1576
Db |||||
QY 1594 KTLPSGCFNTPSIEKP 1609
Db |||||
RESULT 6
AAB48452
ID AAB48452 standard; protein; 1609 AA.
XX
AC AAB48452;
XX
DT 02-MAR-2001 (first entry)
XX
DE Human laminin 8 polypeptide, SEQ ID NO: 22.
XX
DE Human; laminin 8; neuroprotective; angiogenic; osteopathic;
KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;
KW vascular tissue injury; neural injury; angiogenesis regulation.
XX
OS Homo sapiens.
XX
PN WO200066732-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US011543.
XX
PR 30-APR-1999; 99US-0131720P.
PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.
PR 11-FEB-2000; 2000US-0182012P.
PA (BIOS-) BIOSTRATUM INC.
XX
XX Kortessmaa J, Tryggvason K;
PI WPI; 2000-687539/67.
XX N-PSDE; AAC83713.
DR
DR Purified laminin 8 protein, useful for research and therapeutic purposes
XX including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.
XX
XX Claim 5; Page 202-207; 245pp; English.
PS
XX The present sequence is a laminin 8 polypeptide chain. Laminins are a
CC family of heterotrimeric glycoproteins that function via binding
CC interactions with neighbouring cell receptors and by forming laminin
CC networks. They are signalling molecules which influence cellular
CC function. Laminin 8 is useful for treating injuries to tissue of
CC mesenchymal origin, such as bone, cartilage, tendon, and ligament,
CC treating injuries to vascular tissue, promoting cell attachment and
CC migration, ex vivo cell therapy, improving the biocompatibility of
CC medical devices, and preparing improved cell culture devices and media.
CC Laminin 8 is also useful for promoting re-endothelialisation at the site
CC of vascular injuries, improving the take of grafts, improving the
CC biocompatibility of medical devices, treating neural injuries (neural
CC regeneration), regulating angiogenesis, and promoting cell attachment and
XX migration
SQ Sequence 1609 AA;

Query Match		100.0%;	Score 8544;	DB 3;	Length 1609;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 1576;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	QAAMDECTDEGGRPQRCMPEFVNAAFNVTVVATNTCGTPPEEYCVQGTGVTKSKCHLCD	60		
Db	34	QAAMDECTDEGGRPQRCMPEFVNAAFNVTVVATNTCGTPPEEYCVQGTGVTKSKCHLCD	93		
QY	61	AGQPHLQHGAAFLTDYNNQADITWQSQTMLAGVQVPSSINLTLLHLGKAFDITYVRLKFH	120		
Db	94	AGQPHLQHGAAFLTDYNNQADITWQSQTMLAGVQVPSSINLTLLHLGKAFDITYVRLKFH	153		
QY	121	TSRPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQALCTDEFSDIS	180		
Db	154	TSRPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQALCTDEFSDIS	213		
QY	181	PLTGGNVAFSTLEGRPSAYNFENSPVLQEWVTATDIRVTLRNTFGDEVNDPKVLKSY	240		
Db	214	PLTGGNVAFSTLEGRPSAYNFENSPVLQEWVTATDIRVTLRNTFGDEVNDPKVLKSY	273		
QY	241	YYAISDFAVGGRCKCNHGHASECMKNEFDKLVNCKNTYGVDCCKLPFFNDRPWRATA	300		
Db	274	YYAISDFAVGGRCKCNHGHASECMKNEFDKLVNCKNTYGVDCCKLPFFNDRPWRATA	333		
QY	301	ESASECLPCDCNRSQECYFDELYRSTGHGGHCTNCQDNTDGAHCERENFFRLGNNE	360		
Db	334	ESASECLPCDCNRSQECYFDELYRSTGHGGHCTNCQDNTDGAHCERENFFRLGNNE	393		
QY	361	ACSSCHSPVGSLSLTCQDSYGRCSCKPGVMGDKDRCPQGFHSLTEAGRPCSCDPSGSI	420		
Db	394	ACSSCHSPVGSLSLTCQDSYGRCSCKPGVMGDKDRCPQGFHSLTEAGRPCSCDPSGSI	453		
QY	421	DECNVETGRVCVKDNVEGFNCFERCKPGFFNLESSNPRGCTPCFCFHHSSVCTNAVGSYV	480		
Db	454	DECNVETGRVCVKDNVEGFNCFERCKPGFFNLESSNPRGCTPCFCFHHSSVCTNAVGSYV	513		
QY	481	SISSTFOIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY	540		
Db	514	SISSTFOIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY	573		
QY	541	GQNLSPFRVDRRLSADLVLGAGLRVSPVLIAGNSYSPSETTVKYVFRLEHATDY	600		
Db	574	GQNLSPFRVDRRLSADLVLGAGLRVSPVLIAGNSYSPSETTVKYVFRLEHATDY	633		
QY	601	PWRPALTPPEFQKLLNNLTSTKIRGTYSERSAGVLDVTLASARPGVGPATWVESCTCP	660		
Db	634	PWRPALTPPEFQKLLNNLTSTKIRGTYSERSAGVLDVTLASARPGVGPATWVESCTCP	693		
QY	661	VGYGGQFCMCLSGYRRETNLGPYSPCVLCACNGHSETCDPETGVCNCRDNTAGPHCEK	720		
Db	694	VGYGGQFCMCLSGYRRETNLGPYSPCVLCACNGHSETCDPETGVCNCRDNTAGPHCEK	753		
QY	721	CSDGYGDSSTAGTSSDCQPCPCPGGSSCAVVPKTEVVCNCPCTGTTGKRCCELCDGDFG	780		
Db	754	CSDGYGDSSTAGTSSDCQPCPCPGGSSCAVVPKTEVVCNCPCTGTTGKRCCELCDGDFG	813		
QY	781	DPLGNGPVRRLCRLCQCSNDIDPNAVGNCRNLTGECCLKIYNTAGFYCDRCKDGFNPL	840		
Db	814	DPLGNGPVRRLCRLCQCSNDIDPNAVGNCRNLTGECCLKIYNTAGFYCDRCKDGFNPL	873		
QY	841	APNPADKCKACNCPYGTWKQSSCNPNVTGQCECLPHVTGQDCGACDPGFYNLQSGQGC	900		
Db	874	APNPADKCKACNCPYGTWKQSSCNPNVTGQCECLPHVTGQDCGACDPGFYNLQSGQGC	933		
QY	901	RCDCHALGSTNGQCDIRTGQCECQPGITGQHCERCEVNHFGFPGPEGCKPCDCHPEGSLSL	960		
Db	934	RCDCHALGSTNGQCDIRTGQCECQPGITGQHCERCEVNHFGFPGPEGCKPCDCHPEGSLSL	993		
QY	961	QCKDDGRCECEGFGVGNRCDCQCEENYFYNRSWPCQCECPACVRLVKDVADHRVKLQELE	1020		
Db	994	QCKDDGRCECEGFGVGNRCDCQCEENYFYNRSWPCQCECPACVRLVKDVADHRVKLQELE	1053		

QY	1021	SLIANLGTGDEMVTQAFEDRLKEAREVMDLLREAQDVKDQVQDNLMRLQRVNNTLSSQ	1080
Db	1054	SLIANLGTGDEMVTQAFEDRLKEAREVMDLLREAQDVKDQVQDNLMRLQRVNNTLSSQ	1113
QY	1081	ISRLQNRNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP	1140
Db	1114	ISRLQNRNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP	1173
QY	1141	NNMTLLAEAEARKLAERHKEADDIVRVAKTANDTSTEAYNLLRTLAGENQTAPEIEELN	1200
Db	1174	NNMTLLAEAEARKLAERHKEADDIVRVAKTANDTSTEAYNLLRTLAGENQTAPEIEELN	1233
QY	1201	RKYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDSETLENEANNIKMEA	1260
Db	1234	RKYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDSETLENEANNIKMEA	1293
QY	1261	ENLEQLIDOKLYEDLREDMRGKELEVKNLLEKGTBOQTADQLLARADAAKALAEAA	1320
Db	1294	ENLEQLIDOKLYEDLREDMRGKELEVKNLLEKGTBOQTADQLLARADAAKALAEAA	1353
QY	1321	KKGRDTLQEANDILNNLKOFDRRVNDNKTAAEEALRKIPAINQITTEANEKTRAAQALG	1380
Db	1354	KKGRDTLQEANDILNNLKOFDRRVNDNKTAAEEALRKIPAINQITTEANEKTRAAQALG	1413
QY	1381	SAAADATEAKNKAHEAERIAASAVQKNATSTKAEAEPTFAEVTDLNEVNNMLKQLEAEK	1440
Db	1414	SAAADATEAKNKAHEAERIAASAVQKNATSTKAEAEPTFAEVTDLNEVNNMLKQLEAEK	1473
QY	1441	ELKRKQDDADQDMMAGMASQAAQAEAEINARKAKNSVTSLLSIINDLLEQLGQDVTVDLN	1500
Db	1474	ELKRKQDDADQDMMAGMASQAAQAEAEINARKAKNSVTSLLSIINDLLEQLGQDVTVDLN	1533
QY	1501	KLNEIEGTLNKAKDEMKSVDLDRKVSQDLENEAKKQEAAIMDYNRDIIEIMKDIRNLEDIR	1560
Db	1534	KLNEIEGTLNKAKDEMKSVDLDRKVSQDLENEAKKQEAAIMDYNRDIIEIMKDIRNLEDIR	1593
QY	1561	KTLPSGCFNTPPSIEKP	1576
Db	1594	KTLPSGCFNTPPSIEKP	1609

RESULT 7

ID	ABB81594	standard; protein; 1609 AA.
XX	ABB81594;	
AC	ABB81594;	
XX	19-SEP-2002	(first entry)
DT	Human laminin 10 third chain protein sequence SEQ ID NO:14.	
XX	Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation; tissue repair development; laminin; healing; vascular tissue; re-endothelialisation; vascular injury; cell attachment; cell stasis; proliferation; migration.	
DE	Homo sapiens.	
XX	Key	Location/Qualifiers
FT	Peptide	1..33
FT	Protein	/label= signal
FT		34..1609
XX		/label= laminin_10_third_chain
PN	WO200250111-A2.	
XX	27-JUN-2002.	
PD	21-DEC-2001; 2001WO-US051035.	
XX	21-DEC-2000; 2000US-0257449P.	
PR	28-MAR-2001; 2001US-0279282P.	
PR	13-NOV-2001; 2001US-00279282.	

XX	(BIOS-) BIOSTRATUM INC.	
PA	Tryggvason K, Doi M, Thyboll J;	
XX	WPI; 2002-557650/59.	
XX	N-PSDB; ABQ72912.	
DR	New human laminin-10 proteins, useful for accelerating the healing of	
XX	vascular tissue, improving the biocompatibility of grafts, or for	
PT	promoting re-endothelialization at the site of vascular injuries.	
PT	Claim 9; Page 165-170; 23:pp; English.	
XX	The present invention describes human laminin alpha 5. Also described is	
XX	an isolated laminin 10. Laminin 10 has vulnerary activity. Laminins are	
CC	useful in maintaining cell/tissue phenotype as well as promoting cell	
CC	growth and differentiation in tissue repair development. Specifically,	
CC	laminin 10 can be used for accelerating the healing injuries of vascular	
CC	tissue, improving the biocompatibility of grafts useful for treating such	
CC	injuries, for promoting re-endothelialisation at the site of vascular	
CC	injuries, and promote cell attachment and subsequent cell stasis,	
CC	proliferation, differentiation, and/or migration. The present sequence	
CC	represents a third chain protein of laminin 10, from the present	
CC	invention	
XX	Sequence 1609 AA;	
SQ	Query Match 100.0%; Score 8544; DB 5; Length 1609;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 QAAMDECTDEGGRPQRCMPPEFVNAAFNVTVATNTCGTPPEEYCVQGTGVTKSCHLCD 60	
DB	34 QAAMDECTDEGGRPQRCMPPEFVNAAFNVTVATNTCGTPPEEYCVQGTGVTKSCHLCD 93	
QY	61 AGQPHLOHGAFLTDYNNQADITWQSQTMLAGVQYPSINLTLLHAKAFDITVYRLKFH 120	
DB	94 AGQPHLOHGAFLTDYNNQADITWQSQTMLAGVQYPSINLTLLHAKAFDITVYRLKFH 153	
QY	121 TSRPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQALCTDFEFSDIS 180	
DB	154 TSRPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQALCTDFEFSDIS 213	
QY	181 PLTGGNVAFSTLEGPRPSAYNFNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSY 240	
DB	214 PLTGGNVAFSTLEGPRPSAYNFNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSY 273	
QY	241 YYAISDFAVGGRCKCNHGHASECMKNEFDKLVCKNCKNTYGVDCCKLPPFFNDRPWRATA 300	
DB	274 YYAISDFAVGGRCKCNHGHASECMKNEFDKLVCKNCKNTYGVDCCKLPPFFNDRPWRATA 333	
QY	301 ESASECLPCDCNGRSQECYFDPPELYRSTGHGGHCTNCQDNTDGAHCRCRENFRLGNNE 360	
DB	334 ESASECLPCDCNGRSQECYFDPPELYRSTGHGGHCTNCQDNTDGAHCRCRENFRLGNNE 393	
QY	361 ACSSCHSPVGSLSLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSDPSGSI 420	
DB	394 ACSSCHSPVGSLSLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSDPSGSI 453	
QY	421 DECNVETGRVCVKONVEGFNCERCKPGFFNFLESSNPRGCTPCFCFGHSSVCTNAVGSYVY 480	
DB	454 DECNVETGRVCVKONVEGFNCERCKPGFFNFLESSNPRGCTPCFCFGHSSVCTNAVGSYVY 513	
QY	481 SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPFRIAPAKFLGKQVLSY 540	
DB	514 SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPFRIAPAKFLGKQVLSY 573	
QY	541 GQNLFSFRVDRDRLTSLAEDLVLEGAGLRVSVPLIAQNSYPSSETTVKYVFRHLHEATDY 600	
DB	574 GQNLFSFRVDRDRLTSLAEDLVLEGAGLRVSVPLIAQNSYPSSETTVKYVFRHLHEATDY 633	
QY	601 PWRPALTPPEFQKLLNNLTISKIRGTYSERSAGYLDVTLASARPGVPATWVESCTCP 660	

DB	634 PWRPALTPPEFQKLLNNLTISKIRGTYSERSAGYLDVTLASARPGVPATWVESCTCP 693	
QY	661 VGYGGQFCMCLSGYRRETFNLGPYSPCVLACNGHSETCDPETGVNCNRDNTAGPHCEK 720	
DB	694 VGYGGQFCMCLSGYRRETFNLGPYSPCVLACNGHSETCDPETGVNCNRDNTAGPHCEK 753	
QY	721 CSDGYGDSTAGTSSDCQPCPCPGSSCAVVPKTKVCTNCPTGTTGKRCCLCDDGYFG 780	
DB	754 CSDGYGDSTAGTSSDCQPCPCPGSSCAVVPKTKVCTNCPTGTTGKRCCLCDDGYFG 813	
QY	781 DPLGRNGPVRRLCRLCQCSNDIDPNAVGNCRNLGTGECLKCIYNTAGFYCDRCCKDGFENPL 840	
DB	814 DPLGRNGPVRRLCRLCQCSNDIDPNAVGNCRNLGTGECLKCIYNTAGFYCDRCCKDGFENPL 873	
QY	841 APNPADKCKACNCNPYGTMKQOSSCNPVGTQCECLPHVTGQDCGACDPGFYNLQSGQCE 900	
DB	874 APNPADKCKACNCNPYGTMKQOSSCNPVGTQCECLPHVTGQDCGACDPGFYNLQSGQCE 933	
QY	901 RDCCHALGSTNGQCDIRTGQCECQPGITGQHCHERCENVHFGFEGPEGCKPCDCHPEGSLSL 960	
DB	934 RDCCHALGSTNGQCDIRTGQCECQPGITGQHCHERCENVHFGFEGPEGCKPCDCHPEGSLSL 993	
QY	961 QCKDDGRCECREGFVGNRCDQCEENYFYNRWPQCECPACRYLVKQVADHRVKLQELE 1020	
DB	994 QCKDDGRCECREGFVGNRCDQCEENYFYNRWPQCECPACRYLVKQVADHRVKLQELE 1053	
QY	1021 SLIANLGTGDEMVTQAFEDRLKEAREVMDLLREADQVDKVDQNLMDRLQRVNNLTSSQ 1080	
DB	1054 SLIANLGTGDEMVTQAFEDRLKEAREVMDLLREADQVDKVDQNLMDRLQRVNNLTSSQ 1113	
QY	1081 ISRLQNIIRNTIETGNLAEQARAVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1140	
DB	1114 ISRLQNIIRNTIETGNLAEQARAVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1173	
QY	1141 NNMTLLAEAEARKLAERHKQEAADDIVRVAKTANDTSTEAYNLLRLTLAGENQTAFAIEELN 1200	
DB	1174 NNMTLLAEAEARKLAERHKQEAADDIVRVAKTANDTSTEAYNLLRLTLAGENQTAFAIEELN 1233	
QY	1201 RKYEQAKNISQDLEKQAAARVHEBAKRGADKAVEIYASVAQLSPDSETLENEANNIKMEA 1260	
DB	1234 RKYEQAKNISQDLEKQAAARVHEBAKRGADKAVEIYASVAQLSPDSETLENEANNIKMEA 1293	
QY	1261 ENLEQLIDQKLKDYEDLREDMRGKELEVKNLLEKKGTEQQTADQLLARADAALAEAEAA 1320	
DB	1294 ENLEQLIDQKLKDYEDLREDMRGKELEVKNLLEKKGTEQQTADQLLARADAALAEAEAA 1353	
QY	1321 KKGRDTLQEAANDILNNLKDFFRVDNKNKTAAEEALRKIPAINQITITEANEKTTREAOQALG 1380	
DB	1354 KKGRDTLQEAANDILNNLKDFFRVDNKNKTAAEEALRKIPAINQITITEANEKTTREAOQALG 1413	
QY	1381 SAAADATEAKNKAHEAERIAASAVQKNATSTKAEAEERTFAEVTDLDNVNNMLKQLQAEK 1440	
DB	1414 SAAADATEAKNKAHEAERIAASAVQKNATSTKAEAEERTFAEVTDLDNVNNMLKQLQAEK 1473	
QY	1441 ELKRKQDDADQDDMMAGMASQAQAEABINARKAKNSVTSLLSIINDLLEQLGQDITVDLN 1500	
DB	1474 ELKRKQDDADQDDMMAGMASQAQAEABINARKAKNSVTSLLSIINDLLEQLGQDITVDLN 1533	
QY	1501 KLNEIEGTILNKADEMKSVDLDRKVSDDLNEAKKQEAALINDYNRDIEEIMKDIRNLEDIR 1560	
DB	1534 KLNEIEGTILNKADEMKSVDLDRKVSDDLNEAKKQEAALINDYNRDIEEIMKDIRNLEDIR 1593	
QY	1561 KTLPSGCFNTPPSIEKP 1576	
DB	1594 KTLPSGCFNTPPSIEKP 1609	

RESULT 8
ADC01887
ID ADC01887 standard; protein; 1609 AA.
XX
AC ADC01887;

XX 18-DEC-2003 (first entry)
DT Human laminin gamma 1 subunit.
XX Cytostatic; human; ds; gene; laminin; tumour; laminin-x; beta3 subunit;
KW gamma1 subunit; alpha4 subunit; angiogenesis.
KW Homo sapiens.
XX OS
XX US2003103975-A1.
XX 05-JUN-2003.
PD 18-NOV-2002; 2002US-00299058.
PF 03-NOV-1999; 99US-0163199P.
XX 03-NOV-2000; 2000US-00706235.
PA (JONE/) JONES J C R.
PA (GONZ/) GONZALES M.
XX Jones JCR, Gonzales M;
PI WPI; 2003-755217/71.
XX N-PSDB; ADC01886.
DR Antigenic fragment of alpha4 laminin, useful for preparing a composition
XX for treating tumor.
PT Disclosure; Page 42-46; 52pp; English.
XX The invention relates to an antigenic fragment of the human alpha4
CC laminin subunit appearing as ADC01881. Also included are a chimaeric
CC and/or fusion protein comprising the antigenic fragment, an antibody to
CC the antigenic fragment, a cell line that produces the antibody, an
CC isolated laminin complex (laminin-x, comprising an alpha4 subunit, a
CC beta3 subunit or gamma1 subunit), modulating angiogenesis and a method of
CC inducing tumours. The antigenic fragment of alpha4 laminin subunit is
CC useful for preparing a composition (e.g. the antibody 2A3) for treating a
CC tumour. The present sequence represents the human gamma 1 laminin
CC subunit.
XX
SQ Sequence 1609 AA;

Query Match 100.0%; Score 8544; DB 7; Length 1609;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QAAMDECTDEGGRPQRCMPFVNAAFNVTVVATNTGTPPEEYCVQGTGVTGKSLCD 60
DB 34 QAAMDECTDEGGRPQRCMPFVNAAFNVTVVATNTGTPPEEYCVQGTGVTGKSLCD 93

QY 61 AGQPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYPPSSINLTLLHGKAFDITYVRLKFH 120
DB 94 AGQPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYPPSSINLTLLHGKAFDITYVRLKFH 153

QY 121 TSRPESFAIKRTREDGPMIPYQYSGSCENTYTSKANRGFIRTGDEQQAALCTDEFSDIS 180
DB 154 TSRPESFAIKRTREDGPMIPYQYSGSCENTYTSKANRGFIRTGDEQQAALCTDEFSDIS 213

QY 181 PLTGNVAFSTLEGRPSAYNFDNSPVLQEWVATDIRVTLNRLNTFGDEVFNDPKVLKSY 240
DB 214 PLTGNVAFSTLEGRPSAYNFDNSPVLQEWVATDIRVTLNRLNTFGDEVFNDPKVLKSY 273

QY 241 YYAISDFAVGGRCKNGHASECMKNEFDKLVCKNGHNTYGVDCCKLPFFNDRPWRRATA 300
DB 274 YYAISDFAVGGRCKNGHASECMKNEFDKLVCKNGHNTYGVDCCKLPFFNDRPWRRATA 333

QY 301 ESASECLPCDCNGRSQECYFDPPELYRSTGHGCHTNCQDNTDGAHCRCRNFERRLGNNE 360
DB 334 ESASECLPCDCNGRSQECYFDPPELYRSTGHGCHTNCQDNTDGAHCRCRNFERRLGNNE 393

QY 361 ACSSCHCSPVGSLSLSTQCDSDYGRCSCKPGVMGDKDCRCQPGFHSILTEAGCRPCSCDPGSGI 420
DB 394 ACSSCHCSPVGSLSLSTQCDSDYGRCSCKPGVMGDKDCRCQPGFHSILTEAGCRPCSCDPGSGI 453

QY 421 DECNVETGRCVCKDNVEGFNCERCCKPGFNFENLESSNPRGCTPCFCFGHSSVCTNAVGSYVY 480
DB 454 DECNVETGRCVCKDNVEGFNCERCCKPGFNFENLESSNPRGCTPCFCFGHSSVCTNAVGSYVY 513

QY 481 SISSTFQIDEDGWAEQORDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY 540
DB 514 SISSTFQIDEDGWAEQORDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY 573

QY 541 GQNLFSFRVDRDRRLSAEDLVLEGAGLRVSVPLIAQGNYSVPSETTVKYVFLRHEATDY 600
DB 574 GQNLFSFRVDRDRRLSAEDLVLEGAGLRVSVPLIAQGNYSVPSETTVKYVFLRHEATDY 633

QY 601 PWRPALTPFEFQKLLNNLTISIKIRGYTSERSAGYLDVTLASARPGGVPATWVESCTCP 660
DB 634 PWRPALTPFEFQKLLNNLTISIKIRGYTSERSAGYLDVTLASARPGGVPATWVESCTCP 693

QY 661 VGYGGQFCMCLSGYRRETPLNGPYSPCVLCAACNGHSETCDPBTGVNCNRDNTAGPHCEK 720
DB 694 VGYGGQFCMCLSGYRRETPLNGPYSPCVLCAACNGHSETCDPBTGVNCNRDNTAGPHCEK 753

QY 721 CSDGYGDSSTAGTSSDCQPCPCPGSSCAVWPKTKEVVTNCPTGTTGKRCCLCDDGYFG 780
DB 754 CSDGYGDSSTAGTSSDCQPCPCPGSSCAVWPKTKEVVTNCPTGTTGKRCCLCDDGYFG 813

QY 781 DPLGRNGPVRLCRLCQCSNIDPNAVGNCRNLTGECIKCIYNTAGFYCDRCCKDGFPGNPL 840
DB 814 DPLGRNGPVRLCRLCQCSNIDPNAVGNCRNLTGECIKCIYNTAGFYCDRCCKDGFPGNPL 873

QY 841 APNPADKCKACNCNPGYTMKQSSCNPVVTGQCECLPHVTGQDCGACDPGFYNLQSGQGE 900
DB 874 APNPADKCKACNCNPGYTMKQSSCNPVVTGQCECLPHVTGQDCGACDPGFYNLQSGQGE 933

QY 901 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCERCEVNHFGFEGCKPCDCHPEGSLSL 960
DB 934 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCERCEVNHFGFEGCKPCDCHPEGSLSL 993

QY 961 QCKDDGRCEGREGFVGNRCDCQCBENYFYNRSPWGCQECAPYRLVKDVADHRVKLQELE 1020
DB 994 QCKDDGRCEGREGFVGNRCDCQCBENYFYNRSPWGCQECAPYRLVKDVADHRVKLQELE 1053

QY 1021 SLIANLGTGDEMVTQAFEDRLKEAREVMDLLREAOVDKVDQNLMDRLQVNNLTSSQ 1080
DB 1054 SLIANLGTGDEMVTQAFEDRLKEAREVMDLLREAOVDKVDQNLMDRLQVNNLTSSQ 1113

QY 1081 ISRLQINRNTIETGNLAEOARAHVENTERLIEIASRELEKAKAAANVSVPQESTGDP 1140
DB 1114 ISRLQINRNTIETGNLAEOARAHVENTERLIEIASRELEKAKAAANVSVPQESTGDP 1173

QY 1141 NMTLLAEAEARKLAERHKQEAADDIVRVAKTANDTSTEAYNLLRLTLAGENQTAPEIEELN 1200
DB 1174 NMTLLAEAEARKLAERHKQEAADDIVRVAKTANDTSTEAYNLLRLTLAGENQTAPEIEELN 1233

QY 1201 RKEYQAKNISQDLEKQAAARVHEAKRAGDKAVEIYASVAQLSPDLSETLENEANNIKMEA 1260
DB 1234 RKEYQAKNISQDLEKQAAARVHEAKRAGDKAVEIYASVAQLSPDLSETLENEANNIKMEA 1293

QY 1261 ENLEQLIDQKLDKDYEDLREDNRGKELEVNKLLKQKTEQQTADQLLARADAALAEAAA 1320
DB 1294 ENLEQLIDQKLDKDYEDLREDNRGKELEVNKLLKQKTEQQTADQLLARADAALAEAAA 1353

QY 1321 KKGRDTLQEAANDILNNLKDPRRRVNDNKTAAEEALRKIPAINQTIITEANKEKTREAQOALG 1380
DB 1354 KKGRDTLQEAANDILNNLKDPRRRVNDNKTAAEEALRKIPAINQTIITEANKEKTREAQOALG 1413

QY 1381 SAAADATEAKNKAHEAERIAASAVQKNATSTKAEABRTFAEVTDLNEVNNMLKQLQEAKE 1440
DB 1414 SAAADATEAKNKAHEAERIAASAVQKNATSTKAEABRTFAEVTDLNEVNNMLKQLQEAKE 1473

QY 1441 ELKRQDDADQDMMAGMASQAAQAEINARKAKNSVTSLSIIINDLLEQLGQDQDVTDLN 1500

Db 1474 ELKRQDDADQDMAGMASQAQAEINARKAKNSVTSLLSIINDLLEQLQGLDVTDLN 1533
QY 1501 KLNIEIGTLNKADEMKSVDLRKVSVDLENEAKKQEAAMDNRYNRIIEIMKDINLEDIR 1560
Db 1534 KLNIEIGTLNKADEMKSVDLRKVSVDLENEAKKQEAAMDNRYNRIIEIMKDINLEDIR 1593
QY 1561 KTLPSGCFNTPSIEKP 1576
Db 1594 KTLPSGCFNTPSIEKP 1609

RESULT 9
AAB19803
ID AAB19803 standard; protein; 1617 AA.
XX
AC AAB19803;
XX 05-MAR-2001 (first entry)
XX Human laminin 2 gamma-1 chain with C-terminal FLAG epitope.
DE
XX Laminin 2; human; nerve regeneration; angiogenic; cell adhesion;
KW degenerative muscle disorder; muscular dystrophy; cell therapy.
XX
OS Homo sapiens.

XX Key Location/Qualifiers
FH Peptide 1..33
FT /label= Signal_peptide
FT Protein 34..1609
FT /label= Mature_protein
FT Peptide 1610..1617
FT /label= FLAG

XX W0200066730-A2.
PN
XX 09-NOV-2000.
XX 28-APR-2000; 2000WO-US011378.
XX 30-APR-1999; 99US-0131720P.
PR 15-JUN-1999; 99US-0139198P.
PR 12-JUL-1999; 99US-0143289P.
PR 24-SEP-1999; 99US-0155945P.
XX
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
XX Yurchenco P;

DR WPI; 2000-687537/67.
XX N-PSDB; AAA88903.
PT Purified laminin 2 protein, useful for research and therapeutic purposes
PT including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.
XX
PS Claim 5; Page 263-268; 305pp; English.

XX The present sequence is that of the gamma-1 chain of human laminin 2,
CC with an additional C-terminal FLAG epitope, resulting from expression in
CC transfected cells from mammalian expression vectors. Laminin 2 is
CC composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1 (100 kDa)
CC chains. It is thought to be specifically required for stabilizing
CC myotubes during skeletal muscle development, and for preventing
CC apoptosis. Genetic defects in its structure or expression are associated
CC with a major type of congenital muscular dystrophy. Laminin 2 is also
CC thought to be important in Schwann cell/basal lamina interactions. The
CC invention provides laminin 2 alpha-2, beta-1 and gamma-1 chain
CC polypeptides (see AAB19791-806) and the polynucleotides encoding them
CC (see AAA88891-906), methods for making recombinant laminin 2, cells that
CC express recombinant laminin 2, and methods for using purified laminin 2
CC for research and therapeutic purposes including peripheral nerve

CC regeneration, treatment of degenerative muscle disorders, angiogenesis
CC regulation, promoting cell attachment and migration, ex vivo cell
CC therapy, improving the take of grafts, improving the biocompatibility of
CC medical devices and preparing improved culture devices and media

XX
SQ Sequence 1617 AA;

Query Match 100.0%; Score 8544; DB 3; Length 1617;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QAAMDECTDEGGRPORCMPEFVNAAFNVTVATNTCGTPPEEYCVQVTGVTGKSchLCD 60
Db 34 QAAMDECTDEGGRPORCMPEFVNAAFNVTVATNTCGTPPEEYCVQVTGVTGKSchLCD 93
QY 61 AGQPHLQHGAFLTDYNNQADITWQSQTMLAGVQYPPSSINLTLLHGAFTDITYVRLKPH 120
Db 94 AGQPHLQHGAFLTDYNNQADITWQSQTMLAGVQYPPSSINLTLLHGAFTDITYVRLKPH 153
QY 121 TSRPESFALYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQAALCTDEFSDIS 180
Db 154 TSRPESFALYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQAALCTDEFSDIS 213
QY 181 PLTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTILNRLNTFGDEVNDPKVLKSY 240
Db 214 PLTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTILNRLNTFGDEVNDPKVLKSY 273
QY 241 YYAISDFAVGGRCKCNHGHASECMKNEFDKLVCKNKHNTYGVDCCKLPFFNDPWRRAATA 300
Db 274 YYAISDFAVGGRCKCNHGHASECMKNEFDKLVCKNKHNTYGVDCCKLPFFNDPWRRAATA 333
QY 301 ESASECLPCDCNGRSQECYFDPPELYRSTGGHCHCTNCDNDGAHCRCRENFRLGNNE 360
Db 334 ESASECLPCDCNGRSQECYFDPPELYRSTGGHCHCTNCDNDGAHCRCRENFRLGNNE 393
QY 361 ACSSCHCSPVGSLSLSTQDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSDPSGSI 420
Db 394 ACSSCHCSPVGSLSLSTQDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSDPSGSI 453
QY 421 DECNVETGRVCVCKDNVEGFNCERCKPFFNLESSNPRGCTPCFCFHHSSVCTNAVGSYVY 480
Db 454 DECNVETGRVCVCKDNVEGFNCERCKPFFNLESSNPRGCTPCFCFHHSSVCTNAVGSYVY 513
QY 481 SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY 540
Db 514 SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY 573
QY 541 GQNLFSFRVDRDRTRLAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYVFRLEHATDY 600
Db 574 GQNLFSFRVDRDRTRLAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYVFRLEHATDY 633
QY 601 PWRPALTPFEFQKLLNLTISKIRGTYSERSAGYLDVTLASARPGVPATWVESCTCP 660
Db 634 PWRPALTPFEFQKLLNLTISKIRGTYSERSAGYLDVTLASARPGVPATWVESCTCP 693
QY 661 VGYGGQFCCEMCLSGYRRETPNLGYPSPCVLCACNGHSETCDPETGVNCRDNTAGPHCEK 720
Db 694 VGYGGQFCCEMCLSGYRRETPNLGYPSPCVLCACNGHSETCDPETGVNCRDNTAGPHCEK 753
QY 721 GSDGYGDDSTAGTSSDCQPCPCPGSSCAVVPKTKEVVCTNCPTGTTGKRCCELDDGYFG 780
Db 754 GSDGYGDDSTAGTSSDCQPCPCPGSSCAVVPKTKEVVCTNCPTGTTGKRCCELDDGYFG 813
QY 781 DPLGRNGPVRLCRLCQCSDNIDPNAVGNCRNLTGECLKCIYNTAGFYCDCKDGFNPL 840
Db 814 DPLGRNGPVRLCRLCQCSDNIDPNAVGNCRNLTGECLKCIYNTAGFYCDCKDGFNPL 873
QY 841 APNPADKCKACNCNPFYGTMTKQSSCNPNVTGQCECLPHVTGQDCGACDPGFYNLQSGQGE 900
Db 874 APNPADKCKACNCNPFYGTMTKQSSCNPNVTGQCECLPHVTGQDCGACDPGFYNLQSGQGE 933
QY 901 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCEVNFHFGFEGPEGCKPCDCHPEGSLSL 960

Db 934 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCHCERCEVNHFGFBEGCKPCDCHPEGSLSL 993

Qy 961 QCKDDGRCECREGFGVGNRCDCQCEENYFYNRSWPGCQCEPCACYRLVKDKVADHRVKLQELE 1020

Db 994 QCKDDGRCECREGFGVGNRCDCQCEENYFYNRSWPGCQCEPCACYRLVKDKVADHRVKLQELE 1053

Qy 1021 SLIANLGTGDEMVTDAQAFEDRLKEAEREVMDLLREAOVDVKVDQNLMDRLQRVNNTLSQ 1080

Db 1054 SLIANLGTGDEMVTDAQAFEDRLKEAEREVMDLLREAOVDVKVDQNLMDRLQRVNNTLSQ 1113

Qy 1081 ISRLQNIIRNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAANVSVTQPESTGDP 1140

Db 1114 ISRLQNIIRNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAANVSVTQPESTGDP 1173

Qy 1141 NMTLLAEERKLAERHKQEAADDIVRVAKTANDTSTEAYNLLRLTAGENQTAFAIEEELN 1200

Db 1174 NMTLLAEERKLAERHKQEAADDIVRVAKTANDTSTEAYNLLRLTAGENQTAFAIEEELN 1233

Qy 1201 RKYEQAKNISQDLEKQAARVHEEAKRAGDKAVEIYASVAQLSPDLSETLENEANNIKMEA 1260

Db 1234 RKYEQAKNISQDLEKQAARVHEEAKRAGDKAVEIYASVAQLSPDLSETLENEANNIKMEA 1293

Qy 1261 ENLEQLIDQKLDVEDLREDMRGKELEVKNLLEKKGTEQQTADQLLARADAAKALAEAEA 1320

Db 1294 ENLEQLIDQKLDVEDLREDMRGKELEVKNLLEKKGTEQQTADQLLARADAAKALAEAEA 1353

Qy 1321 KKGRDTLQEAANDILNLLKDFDRRVNDNKTAAEEALRKIPAINQTTTEANEKTRAQQAALG 1380

Db 1354 KKGRDTLQEAANDILNLLKDFDRRVNDNKTAAEEALRKIPAINQTTTEANEKTRAQQAALG 1413

Qy 1381 SAAADATEAKNKAHEABERIASAVQKNATSTKAEARTFAEVTDLNDEVNMMKQLQEAEEK 1440

Db 1414 SAAADATEAKNKAHEABERIASAVQKNATSTKAEARTFAEVTDLNDEVNMMKQLQEAEEK 1473

Qy 1441 ELKRKQDDADQDMWAGMASQAAQEAENAPKAKNSVTSLLSIINDLLEQLGOLDTVDLN 1500

Db 1474 ELKRKQDDADQDMWAGMASQAAQEAENAPKAKNSVTSLLSIINDLLEQLGOLDTVDLN 1533

Qy 1501 KLNEIEGTLNKADEMKSVDLDRKVSVDLENAKKQEAAIMDYNRDIIEIMKDIRNLEDIR 1560

Db 1534 KLNEIEGTLNKADEMKSVDLDRKVSVDLENAKKQEAAIMDYNRDIIEIMKDIRNLEDIR 1593

Qy 1561 KTLPSGCFNTPSIEKP 1576

Db 1594 KTLPSGCFNTPSIEKP 1609

RESULT 10
AAW50898
ID AAW50898 standard; protein; 1609 AA.
XX
AC AAW50898;
XX

07-DEC-1998 (first entry)
Human laminin G1 chain.

Laminin; human; beta-amyloid; amyloidosis; Alzheimer's disease;
Down's syndrome; hereditary cerebral haemorrhage; inflammation;
malignancy; Familial Mediterranean Fever; multiple myeloma;
type II diabetes; prion disease; Creutzfeldt-Jacob disease; CJD;
Gertsmann-Straussler syndrome; kuru; scrapie; haemodialysis;
carpal tunnel syndrome; senile cardiac amyloid polynuropathy;
Familial Amyloidotic Polynuropathy; thyroid carcinoma; diagnosis;
therapy.

Homo sapiens.
WO9815179-A1.
XX
PN 16-APR-1998.
XX
PD
XX
PF 08-OCT-1997; 97WO-US018145.

XX 08-OCT-1996; 96US-0027981P.
PR (UNIW) UNIV WASHINGTON.
XX Castillo G, Snow AD;
PI WPI; 1998-240534/21.
DR
XX
PT Use of laminin and fragments - for developing products for use in the
diagnosis and treatment of amyloid disease, e.g. Alzheimer's disease or
CJD.
XX
PS Claim 15; Page 106-109; 132pp; English.
XX
CC This is the amino acid sequence of the human laminin G1 chain. The
primary object of the invention is to use laminin, laminin-derived
protein fragments and/or laminin-derived polypeptides as potent
inhibitors of amyloid formation, deposition, accumulation and/or
persistence in Alzheimer's disease and other amyloidoses. The laminin
products (see AAW50888-98) may include mouse or human laminin A or A1
chain, laminin B1 or B2 chain, laminin A2 chain (merosin), laminin G1
chain, the globular repeats of the laminin A1 chain and the beta-amyloid
binding domain of the laminin A chain. A claimed method for treating an
amyloid disease comprises administering a polypeptide having a
conformational similarity to a fragment of a laminin protein. A method
for diagnosing an amyloid disease involves determining levels of laminin
in a sample. Production of laminin or its fourth globular repeat in vivo
provides a method for in vivo inhibition of beta-amyloid amyloidosis. The
products and methods can be used for the diagnosis, prognosis, monitoring
and treatment of amyloidoses such as Alzheimer's disease, Down's syndrome
and hereditary cerebral haemorrhage with amyloidosis of the Dutch type
(where the specific amyloid is the beta-amyloid protein), the amyloidosis
associated with chronic inflammation, various forms of malignancy and
Familial Mediterranean Fever (AA amyloid or inflammation-association
amyloidosis), the amyloidosis associated with multiple myeloma and other
B-cell abnormalities (AL amyloid), the amyloidosis associated with type
II diabetes (amylin or islet amyloid), the amyloidosis associated with
prion diseases including Creutzfeldt-Jacob disease, Gertsmann-Straussler
syndrome, kuru and animal scrapie (PrP amyloid), the amyloidosis
associated with long-term haemodialysis and carpal tunnel syndrome (beta
2-microglobulin amyloid), the amyloidosis associated with senile cardiac
amyloid and Familial Amyloidotic Polynuropathy (prealbumin or
transthyretin amyloid), and the amyloidosis associated with endocrine
tumours such as medullary carcinoma of the thyroid (variant of
procalcitonin)

XX SQ Sequence 1609 AA;

Query Match 100.0%; Score 8540; DB 2; Length 1609;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1575; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QAAAMDECTDEGGRPORCMPEFVNAAFNVTVVATNTCGTPPEYCVQGTGVTKSchLCD 60
Db 34 QAAAMDECTDEGGRPORCMPEFVNAAFNVTVVATNTCGTPPEYCVQGTGVTKSchLCD 93

Qy 61 AQPHLQHGAFLTDYNNQADTTWQSQTMLAGVQYPSSINLTLLHLGKAFDITYVRLKFH 120
Db 94 AQPHLQHGAFLTDYNNQADTTWQSQTMLAGVQYPSSINLTLLHLGKAFDITYVRLKFH 153

Qy 121 TSRPESFAIYKRTREDGPWIPYQYYSGSCENTYSKANRGFIRTTGGDEQQAALCTDEFSDIS 180
Db 154 TSRPESFAIYKRTREDGPWIPYQYYSGSCENTYSKANRGFIRTTGGDEQQAALCTDEFSDIS 213

Qy 181 PLTGGNVAFSTLEGRPSAYNFNDSPLVQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSY 240
Db 214 PLTGGNVAFSTLEGRPSAYNFNDSPLVQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSY 273

Qy 241 YYAISDFAVGGRCCKNGHASECMKNEFDKLVCKNGKNTYGVDCCKCLPPFNDPWRDATA 300
Db 274 YYAISDFAVGGRCCKNGHASECMKNEFDKLVCKNGKNTYGVDCCKCLPPFNDPWRDATA 333

QY 301 ESASECLPCDCNGRSQECYFDPELYRSTGHGGCTNCQDNTDGAHCERCRENTEFRLGNNE 360
Db 334 ESASECLPCDCNGRSQECYFDPELYRSTGHGGCTNCQDNTDGAHCERCRENTEFRLGNNE 393
QY 361 ACSCHCSPVGSLSSTQCDSDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSI 420
Db 394 ACSCHCSPVGSLSSTQCDSDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSI 453
QY 421 DECNVETGRVCVKONVEGFNCERCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGYSVY 480
Db 454 DECNVETGRVCVKONVEGFNCERCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGYSVY 513
QY 481 SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY 540
Db 514 SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY 573
QY 541 GQNLSPSFRVDRDRLRLSAEDLVLEGAGLRVSVPLIAQNSYPSETTVKYVFRLHEATDY 600
Db 574 GQNLSPSFRVDRDRLRLSAEDLVLEGAGLRVSVPLIAQNSYPSETTVKYVFRLHEATDY 633
QY 601 PWRPALTPFEFQKLLNNLTSIKIRGTYSERSAGYLDVTLASARPGPGVPATWVESCTCP 660
Db 634 PWRPALTPFEFQKLLNNLTSIKIRGTYSERSAGYLDVTLASARPGPGVPATWVESCTCP 693
QY 661 VGYGGQCEMCLSGYRRETPLNGPYSPCVLCAACNGHSETCDPETGVNCNRDNTAGPHCEK 720
Db 694 VGYGGQCEMCLSGYRRETPLNGPYSPCVLCAACNGHSETCDPETGVNCNRDNTAGPHCEK 753
QY 721 CSDGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKEVVCTNCPTGTTGKRCELCDGDFYFG 780
Db 754 CSDGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKEVVCTNCPTGTTGKRCELCDGDFYFG 813
QY 781 DPLGRNGPVRRLCRLCQCSNDIDPNAVGNCRNLTGCECLKIYNTAGFYCDRCCKDGFNGNPL 840
Db 814 DPLGRNGPVRRLCRLCQCSNDIDPNAVGNCRNLTGCECLKIYNTAGFYCDRCCKDGFNGNPL 873
QY 841 APNPADKCKACNCNPYGTMKQQSSCNPVTGQCECLPHVTGDCGACDPGFYNLQSGQGCE 900
Db 874 APNPADKCKACNCNPYGTMKQQSSCNPVTGQCECLPHVTGDCGACDPGFYNLQSGQGCE 933
QY 901 RCDCHALGSTNGQCDIRTGQCECOPGITGQHCHERCEVNHFGFPEGCKPCDCHPEGSLSL 960
Db 934 RCDCHALGSTNGQCDIRTGQCECOPGITGQHCHERCEVNHFGFPEGCKPCDCHPEGSLSL 993
QY 961 QCKDDGRCECREGFVGNRCDQCEHENYFYNRSPWGCQECPCACYRLVKDKVADHRVKLQELE 1020
Db 994 QCKDDGRCECREGFVGNRCDQCEHENYFYNRSPWGCQECPCACYRLVKDKVADHRVKLQELE 1053
QY 1021 SLIANLGTGDEMVTDOAFEDRLKEAREVMDLLREACQVKDQVNDQNLMDRLQRVNNTLSSQ 1080
Db 1054 SLIANLGTGDEMVTDOAFEDRLKEAREVMDLLREACQVKDQVNDQNLMDRLQRVNNTLSSQ 1113
QY 1081 ISRLQNIQIRNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1140
Db 1114 ISRLQNIQIRNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1173
QY 1141 NNMTLLABEARKLAERHKQAEADDIVRVAKTANDTSTEAVNLLRLTLAGENQTAPEIEELN 1200
Db 1174 NNMTLLABEARKLAERHKQAEADDIVRVAKTANDTSTEAVNLLRLTLAGENQTAPEIEELN 1233
QY 1201 RKYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPLDSETLENEANNIKMEA 1260
Db 1234 RKYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPLDSETLENEANNIKMEA 1293
QY 1261 ENLEQLIDQKLKDYEDLREDMRGKELEVNKLLKKGTEQQTADQLLARADAAKALAEAAA 1320
Db 1294 ENLEQLIDQKLKDYEDLREDMRGKELEVNKLLKKGTEQQTADQLLARADAAKALAEAAA 1353
QY 1321 KKGRDTLQEAANDILNNLKQFDRRVNDNKTAAEEALRKIPAINQITITEANEKTRTAAQALG 1380
Db 1354 KKGRDTLQEAANDILNNLKQFDRRVNDNKTAAEEALRKIPAINQITITEANEKTRTAAQALG 1413
QY 1381 SAAADATEAKNKAHEAERIAASAVQKNATSTKAEARTFAEVTDLDNEVNNMLKQLQEAKE 1440

Db 1414 SAAADATEAKNKAHEAERIAASAVQKNATSTKAEARTFAEVTDLDNEVNNMLKQLQEAKE 1473
QY 1441 ELKXKQDDADQDMMWAGMASQAQAEAEINARKAKNSVTSLLSIINDLLEQLGQDQDVTDLN 1500
Db 1474 ELKXKQDDADQDMMWAGMASQAQAEAEINARKAKNSVTSLLSIINDLLEQLGQDQDVTDLN 1533
QY 1501 KLNEIEGTINKAKDEMKSVDLDRKVSDDLNEAKKQEAALNDYNRDIEEIMKDINLEDIR 1560
Db 1534 KLNEIEGTINKAKDEMKSVDLDRKVSDDLNEAKKQEAALNDYNRDIEEIMKDINLEDIR 1593
QY 1561 KTLPSGCEPTPSIEKP 1576
Db 1594 KTLPSGCEPTPSIEKP 1609
RESULT 11
AAB19805
ID AAB19805 standard; protein; 1605 AA.
XX
AC AAB19805;
XX
DT 05-MAR-2001 (first entry)
XX Mouse laminin 2 gamma-1 chain.
DE Laminin 2; mouse; nerve regeneration; angiogenic; cell adhesion;
XX degenerative muscle disorder; muscular dystrophy; cell therapy.
KW Mus musculus.
XX
OS
XX
FH Key Location/Qualifiers
FT Peptide 1. .33
FT /label= Signal_peptide
FT Protein 34. .1605
FT /label= Mature_protein
XX
XX WO200066730-A2.
PN
XX
PD 09-NOV-2000.
XX
XX 28-APR-2000; 2000WO-US011378.
PF
XX
PR 30-APR-1999; 99US-0131720P.
PR 15-JUN-1999; 99US-0139198P.
PR 12-JUL-1999; 99US-0143289P.
PR 24-SEP-1999; 99US-0155945P.
XX
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
XX Yurchenco P;
PI
XX
DR WPI; 2000-687537/67.
DR N-PSDB; AAA88905.
XX
PT Purified laminin 2 protein, useful for research and therapeutic purposes
PT including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.
XX
PS Claim 5; page 288-294; 305pp; English.
XX
CC The present sequence is that of the gamma-1 chain of mouse laminin 2.
CC Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1
CC (100 kDa) chains. It is thought to be specifically required for
CC stabilizing myotubes during skeletal muscle development, and for
CC preventing apoptosis. Genetic defects in human laminin 2 structure or
CC expression are associated with a major type of congenital muscular
CC dystrophy. Laminin 2 is also thought to be important in Schwann
CC cell/basal lamina interactions. The invention provides laminin 2 alpha-2,
CC beta-1 and gamma-1 chain polypeptides (see AAB19791-806) and the
CC polynucleotides encoding them (see AAA8891-906), methods for making
CC recombinant laminin 2, cells that express recombinant laminin 2, and
CC methods for using purified laminin 2 for research and therapeutic

CC purposes including peripheral nerve regeneration, treatment of
CC degenerative muscle disorders, angiogenesis regulation, promoting cell
CC attachment and migration, ex vivo cell therapy, improving the take of
CC grafts, improving the biocompatibility of medical devices and preparing
CC improved culture devices and media
XX
SQ Sequence 1605 AA;
Query Match 94.1%; Score 8043; DB 3; Length 1605;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 1470; Conservative 57; Mismatches 47; Indels 2; Gaps 2;
QY 1 QAAMDECTDEGGRPORCMPEFVNAAFNVTVATNTCGTPPEEYCVGTGVTKSchLCD 60
Db :
QY 61 AGQHLQHGAFLTDYNNQADTTWQSQTMLAGVQYPSSINLTLLHKGAFDITYVRLKFH 120
Db 92 AGQHLQHGAFLTDYNNQADTTWQSQTMLAGVQYPNSINLTLLHKGAFDITYVRLKFH 151
QY 121 TSRPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQALCTDEFSDis 180
Db 152 TSRPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQALCTDEFSDis 211
QY 181 PLTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSY 240
Db 212 PLTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSY 271
QY 241 YYAISDFAVGGRCKCNGHASECMKNEFFDLVCNCKHNTYGVDCCKCLPFENDRPWRRATA 300
Db 272 YYAISDFAVGGRCKCNGHASECMKNEFFDLVCNCKHNTYGVDCCKCLPFENDRPWRRATA 331
QY 301 ESASECLPCDCNGRSQECYFDPPELYRSTGHGGHCTNCODNTDGAHCERCFRNLGNNE 360
Db 332 ESASECLPCDCNGRSQECYFDPPELYRSTGHGGHCTNCODNTDGAHCERCFRNLGNTE 391
QY 361 ACSSCHCSPVGSLSLTCDSYGRCSCKPGVMGDKCQPGFHSLSLTEAGRPPCSDPSGSI 420
Db 392 ACSPCHCSPVGSLSLTCDSYGRCSCKPGVMGDKCQPGFHSLSLTEAGRPPCSDPSGST 451
QY 421 DECNVETGRVCVKONVEGFNCERCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGYSVY 480
Db 452 DECNVETGRVCVKONVEGFNCERCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGYSVY 511
QY 481 SISSTFQIDEDGWRAEQRDSEASLEWSSERQDIATVISDSYFPRYFIAPAKFLGKQVLSY 540
Db 512 DISSTFQIDEDGWREQRDSEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSY 571
QY 541 GQNLSPFRVDRRLRLSABDLVLEGAGLRVSVPLIAQNSYSEPTTKYVFRLLHEATDY 600
Db 572 GQNLSPFRVDRRLRLSABDLVLEGAGLRVSVPLIAQNSYSEPTTKYIFRLLHEATDY 631
QY 601 PWRPALTPPEFQKLLNLTSTIKIRGTYSERSAGYLDVTLASARPGVPATWVESCTCP 660
Db 632 PWRPALTPPEFQKLLNLTSTIKIRGTYSERSAGYLDVTLQASARPGVPATWVESCTCP 691
QY 661 VGYGQFCMCLSGYRRETNLGPYSPCVLCAACNGHSETCDPETGVNCNRDNTAGPHCEK 720
Db 692 VGYGQFCETCLPGYRRETPSLGPYSPCVLCTCNGHSETCDPETGVCDNRDNTAGPHCEK 751
QY 721 CSDGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKEVVCTNCPTGTTGKRCCLCDDGYFG 780
Db 752 CSDGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKEVVCTHCPTGTAGKRCCLCDDGYFG 811
QY 781 DPLGNPVRRLCRLCQCSNDIDPNAVGNCRNLITGECCLKIYNTAGFYCDRCCKDGFNPL 840
Db 812 DPLGNPVRRLCRLCQCSNDIDPNAVGNCRNLITGECCLKIYNTAGFYCDRCCKDGFNPL 871
QY 841 APNPADCKACNCPYGTMKQSSCNPVVTGQCECLPHVTGQDCGACDPGFVNLQSGQGE 900
Db 872 APNPADCKACACN-YGTVQQSSCNPVVTGQCCLPHVSGRDCGTCDPGYNLQSGQGE 930
QY 901 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCCERCEVNHFGFPGCKPCDCHPEGSLSL 960

Db 931 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCCERCEVNHFGFPGCKPCDCHPEGSLSL 990
QY 961 QCKDDGRCECREGFGVGNRCDQCEENYFYNRSPWPGCQCPACRYRLVKDVKVADHRVKLQELE 1020
Db 991 QCKDDGRCECREGFGVGNRCDQCEENYFYNRSPWPGCQCPACRYRLVKDAAEHRVKLQELE 1050
QY 1021 SLIANLGTGDEMVTDOAFEDRLKEAEREYMDLLREAQDVQKVDQNLMDRLQRVNNTLSSQ 1080
Db 1051 SLIANLGTGDDMTDOAFEDRLKEAEREYMDLLREAQDVQKVDQNLMDRLQRVNNTLSSQ 1110
QY 1081 ISRLQIRNTIIEETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDF 1140
Db 1111 ISRLQIRNTIIEETGILAEARARSRVSTEQLEIASRELEKAKM-AANVSITQPESTGEP 1169
QY 1141 NNMTLLAEAEARKLAERHKEADDIVRVAKTANDTSTAYNLLRLTLAGENQTAPEIEELN 1200
Db 1170 NNMTLLAEAEARKLAERHKEADDIVRVAKTANETSABAYNLLRLTLAGENQTAPEIEELN 1229
QY 1201 RKYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDSEITLNEANNIKMEA 1260
Db 1230 RKYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEA 1289
QY 1261 ENLEQLIDQKLKDYEDLREDMRGKELEVKNLLEKKGTEQQTADQLLARADAALAEAAA 1320
Db 1290 ADLDRLLIDQKLKDYEDLREDMRGKEHEVKNLLEKGAEQQTADQLLARADAALAEAAA 1349
QY 1321 KKGRTDLOEANDILNLLKDFDRRVNDNKTAAEEALRKIPAINQITITEANEKTRQAQALG 1380
Db 1350 KKGRTDLOEANDILNLLKDFDRRVNDNKTAAEEALRRIPAINRTIAEANEKTRQAQALG 1409
QY 1381 SAAADATEAKNKAHEABRIASAVQKNATSTKAAEAERTFAEVTDLDDNEVNNMLKQLEAEK 1440
Db 1410 NAAADATEAKNKAHEABRIASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAEN 1469
QY 1441 ELKRRQDDADQDMMMAGMASQAAQAEAEINARKAKNSVTLLSIINDLLEQLGQDQDVTDLN 1500
Db 1470 ELKRRQDDADQDMMMAGMASQAAQAEAEINARKAKNSVTLLSQNLNLLDQDQDVTDLN 1529
QY 1501 KLNIEIEGTLNKADEMKNVSDLRKVSVDLENAKKQEAAMIDYNRDIEEIMKDIRNLEDIR 1560
Db 1530 KLNIEIEGSLNKADEMKNASDLDRKVSVDLESEARKQEAAMIDYNRDIAEIKDIHNLEDIK 1589
QY 1561 KTLPSGCFNTPSIEKP 1576
Db 1590 KTLPTGCFNTPSIEKP 1605
RESULT 12
AAB48454
ID AAB48454 standard; protein; 1605 AA.
XX
AC AAB48454;
XX
DT 02-MAR-2001 (first entry)
XX
DE Mouse laminin 8 polypeptide, SEQ ID NO: 26.
XX
KW Mouse; laminin 8; neuroprotective; angiogenic; osteopathic;
KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;
KW vascular tissue injury; neural injury; angiogenesis regulation.
XX
OS Mus musculus.
XX
PN WO200066732-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US011543.
XX
PR 30-APR-1999; 99US-0131720P.
PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.

ABB81596
ID ABB81596 standard; protein; 1605 AA.
XX
AC ABB81596;
XX
DT 19-SEP-2002 (first entry)
XX
DE Mouse laminin 10 third chain protein sequence SEQ ID NO:18.
XX
KW Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;
KW tissue repair development; laminin; healing; vascular tissue;
KW re-endothelialisation; vascular injury; cell attachment; cell stasis;
KW proliferation; migration.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Peptide 1..33
FT Protein /label= signal
FT 34..1605
FT /label= laminin_10_third_chain
XX
XX WO200250111-A2.
XX
XX 27-JUN-2002.
XX
XX 21-DEC-2001; 2001WO-US051035.
XX
XX 21-DEC-2000; 2000US-0257449P.
XX
XX 28-MAR-2001; 2001US-0279282P.
XX
XX 13-NOV-2001; 2001US-00279282.
XX
XX (BIOS-) BIOSTRATUM INC.
XX
XX Tryggvason K, Doi M, Thyboll J;
XX
XX WPI; 2002-557650/59.
XX
XX N-PSDB; ABQ72914.
XX
XX New human laminin-10 proteins, useful for accelerating the healing of
XX PT vascular tissue, improving the biocompatibility of grafts, or for
XX PT promoting re-endothelialization at the site of vascular injuries.
XX
XX Claim 9; Page 191-195; 231pp; English.
XX
XX The present invention describes human laminin alpha 5. Also described is
XX CC an isolated laminin 10. Laminin 10 has vulnery activity. Laminins are
XX CC useful in maintaining cell/tissue phenotype as well as promoting cell
XX CC growth and differentiation in tissue repair development. Specifically,
XX CC laminin 10 can be used for accelerating the healing injuries of vascular
XX CC tissue, improving the biocompatibility of grafts useful for treating such
XX CC injuries, for promoting re-endothelialisation at the site of vascular
XX CC injuries, and promote cell attachment and subsequent cell stasis,
XX CC proliferation, differentiation, and/or migration. The present sequence
XX CC represents a third chain protein of laminin 10, from the present
XX CC invention
XX
SQ Sequence 1605 AA;

Query Match 94.1%; Score 8043; DB 5; Length 1605;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 1470; Conservative 57; Mismatches 47; Indels 2; Gaps 2;

QY 1 QAAMDECTDEGRPQRCMPEFVNAAFNVTVATNTCGTPPEEYCVQGTGVTGKSCHLCD 60
Dd :|||||
Dd 32 RAAMDECADEGRPQRCMPEFVNAAFNVTVATNTCGTPPEEYCVQGTGVTGKSCHLCD 91
QY 61 AGQPHLQHGAFLTDYNNQADTTWQSQTMLAGVQYPSSINLTLHLGKAFDITYVRLKPH 120
Dd |||||
Dd 92 AGQHLQHGAFLTDYNNQADTTWQSQTMLAGVQYPNSINLTLHLGKAFDITYVRLKPH 151
QY 121 TSRPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDIS 180
|||

Db 152 TSRPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDIS 211
QY 181 PLTGGNVAFSTLEGRPSAYNFDSNPSVLQEWVTATDIRVTNLRLNTFGDEVNDPKVLKSY 240
Dd |||||
Dd 212 PLTGGNVAFSTLEGRPSAYNFDSNPSVLQEWVTATDIRVTNLRLNTFGDEVNDPKVLKSY 271
QY 241 YYAISDFAVGGRCKCNGHASECMKNEFDKLVNCCKHNTYGVDCCKLPPFNDRPWRATA 300
Dd |||||
Dd 272 YYAISDFAVGGRCKCNGHASECMKNEFDKLVNCCKHNTYGVDCCKLPPFNDRPWRATA 331
QY 301 ESASECLPCDCNGRSQECYFDPPELYRSTGHGCHTCNQDNTDGAHCRCRENFRLGNNE 360
Dd |||||
Dd 332 ESASECLPCDCNGRSQECYFDPPELYRSTGHGCHTCNQDNTDGAHCRCRENFRLGNTE 391
QY 361 ACSSCHCSPVGSLSLSTQCDYGRCSCKPGWMDKCDRCQPGFHSLTEAGCRPCSCDPSGI 420
Dd |||||
Dd 392 ACSPCHCSPVGSLSLSTQCDYGRCSCKPGWMDKCDRCQPGFHSLTEAGCRPCSCDPSGST 451
QY 421 DECNVETGRVCVKONVEGFNCERCXPGFFNFLESNPRGCTPCFCFHSVSVCTNAVGSVY 480
Dd |||||
Dd 452 DECNVETGRVCVKONVEGFNCERCXPGFFNFLESNPKGCTPCFCFHSVSVCTNAVGSVY 511
QY 481 SISSTFQIDEDGWAEQRDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY 540
Dd |||||
Dd 512 DISSTFQIDEDGWAEQRDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY 571
QY 541 GONLSFSFRVDRDRLSAEDLVLEGAGLRVSVPVLIAGNSYSPSETTVKYVFRLEHATDY 600
Dd |||||
Dd 572 GONLSFSFRVDRDRLSAEDLVLEGAGLRVSVPVLIAGNSYSPSETTVKYVFRLEHATDY 631
QY 601 PWRPALTPPEFQKLLNLTLSIKIRGTYSERSAGYLDVTLASARPPGVPATWVESCTCP 660
Dd |||||
Dd 632 PWRPALTPPEFQKLLNLTLSIKIRGTYSERSAGYLDVTLASARPPGVPATWVESCTCP 691
QY 661 VGYGGQFCMCLSGYRRETNPGLPSPCVLCAENGHSETCDPETGVNCNRDNTAGPHCEK 720
Dd |||||
Dd 692 VGYGGQFCMCLSGYRRETNPGLPSPCVLCAENGHSETCDPETGVNCNRDNTAGPHCEK 751
QY 721 CSDGYGDSSTAGTSSDQCPQCPGSSSCAVVPKTKVCTNCPTGTTGKRCCLCDDGYFG 780
Dd |||||
Dd 752 CSDGYGDSSTAGTSSDQCPQCPGSSSCAVVPKTKVCTNCPTGTTGKRCCLCDDGYFG 811
QY 781 DPLGRNGPVRLCRLCQSDNIDPNAVGNCRNLTGECCLKIYNTAGFYCDRCCKDGGFNGPL 840
Dd |||||
Dd 812 DPLGSNGPVRLCRLCQSDNIDPNAVGNCRNLTGECCLKIYNTAGFYCDRCCKDGGFNGPL 871
QY 841 APNPADKCKACNPNPYGTMKQSSCNPNVTGQCEBCLPHVTGQDCGACDPPFYNLQSGQGCE 900
Dd |||||
Dd 872 APNPADKCKACACN-YGTVQQSSCNPNVTGQCEBCLPHVTGQDCGACDPPFYNLQSGQGCE 930
QY 901 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCHERCEVNHFGFEGEGCKPCDCHPEGSLSL 960
Dd |||||
Dd 931 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCHERCEVNHFGFEGEGCKPCDCHPEGSLSL 990
QY 961 QCKODGRCECEGFGVGNRCDOCEENYFNRSWPGCQCPACVRLVKDKVADHRVKLQLELE 1020
Dd |||||
Dd 991 QCKODGRCECEGFGVGNRCDOCEENYFNRSWPGCQCPACVRLVKDKVADHRVKLQLELE 1050
QY 1021 SLIANLGTGDEMVTDOAFEDRLKEAREVMDLLREAOVDVQDQNLMDRLQRVNNTLSSQ 1080
Dd |||||
Dd 1051 SLIANLGTGDEMVTDOAFEDRLKEAREVMDLLREAOVDVQDQNLMDRLQRVNNTLSSQ 1110
QY 1081 ISRLQNIIRNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSITQPESTGDP 1140
Dd |||||
Dd 1111 ISRLQNIIRNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSITQPESTGDP 1169
QY 1141 NMNTLLAEAREKLAERHKEADDIRVAKTANDTSTAYNLLRTLAGENQTAFEIEELN 1200
Dd |||||
Dd 1170 NMNTLLAEAREKLAERHKEADDIRVAKTANDTSTAYNLLRTLAGENQTAFEIEELN 1229
QY 1201 RKYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDSETLENEANNIKMEA 1260
Dd |||||
Dd 1230 RKYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDSETLENEANNIKMEA 1289

Db 632 PWRPALSPEFFQKLLNLTSLIKIRGTYSERTAGYLDVTLQASRPFGVPATWVESCTCP 691
QY VYGGQFCCEMCLSGYRRTPNLPYSPCVLCAAGHSETCDPETGVNCRDNTAGPHCEK 720
Db 692 VYGGQFCETCLPGYRRTPSLPGYSPCVLCTCNHSETCDPETGVCDNRDNTAGPHCEK 751
QY 721 CSDGYGDSGTAGTSSDCQPCPCPGSSCAVVPKTKWCTNCPTGTGKRCCLCDDGYFG 780
Db 752 CSDGYGDSLTGTSSDCQPCPCPGSSCAVVPKTKWCTNCPTGTGKRCCLCDDGYFG 811
QY 781 DPLGRNGPVLRLCRLCQSDNIDPNAVGNCRNLTGECCLKIYNTAGFYCDRCCKDGFNGPL 840
Db 812 DPLGNGPVLRLCRLCQSDNIDPNAVGNCRNLTGECCLKIYNTAGFYCDRCCKDGFNGPL 871
QY 841 APNPADKCKACNCPYGTMKQSSCNPVGTGCECLPHVTGQDCGACDPGFYNLQSGQCE 900
Db 872 APNPADKCKACNCPYGTMKQSSCNPVGTGCECLPHVTGQDCGACDPGFYNLQSGQCE 931
QY 901 RCDCHALGSTNGQCDIRGTQCECQPGITGHCERCEVNHFGFEGCKPCDCHPEGSLSL 960
Db 932 RCDCHALGSTNGQCDIRGTQCECQPGITGHCERCEVNHFGFEGCKPCDCHPEGSLSL 991
QY 961 QCKDDGRCECREGFGVNRCDQCEENYFYNRSPWPGQCECPACVRLVKDKVADHRVKLOELE 1020
Db 992 QCKDDGRCECREGFGVNRCDQCEENYFYNRSPWPGQCECPACVRLVKDKVADHRVKLOELE 1051
QY 1021 SLIANLGTGDEMVTDOAFEDRLKEAREVMDLLREAOQDVQDQVNDLMDRLQVRNNTLSQ 1080
Db 1052 SLIANLGTGDEMVTDOAFEDRLKEAREVMDLLREAOQDVQDQVNDLMDRLQVRNNTLSQ 1111
QY 1081 ISRLQNRITIEETGNLAQARAHVNTERTLIEIASRELEKAKVAAANVSITQESTGDP 1140
Db 1112 ISRLQNRITIEETGNLAQARAHVNTERTLIEIASRELEKAKVAAANVSITQESTGDP 1171
QY 1141 NNMTLLAEARKLAERHKEADDDIVRVAKTANDTSTEAYNLLRLTAGENQTAFTIEELN 1200
Db 1172 NNMTLLAEARKLAERHKEADDDIVRVAKTANDTSTEAYNLLRLTAGENQTAFTIEELN 1231
QY 1201 RYEQAKNISQDLEKQAAVHEEAKRAGDKAVEIYASVAQLSPDLSETLENNKIKWEA 1260
Db 1232 RYEQAKNISQDLEKQAAVHEEAKRAGDKAVEIYASVAQLSPDLSETLENNKIKWEA 1291
QY 1261 ENLEQLIDQKLKDYEDLREDMRGKEVKNLLEKKGTEQQTADQLLARADAALAEAEA 1320
Db 1292 ADLRLIDQKLKDYEDLREDMRGKEVKNLLEKKGTEQQTADQLLARADAALAEAEA 1351
QY 1321 KKGRTDLOEANDILNNLKDFRRVNDNKTAAEALRKIPAINQTITEANEKTRPAAQALG 1380
Db 1352 KKGRTDLOEANDILNNLKDFRRVNDNKTAAEALRKIPAINQTITEANEKTRPAAQALG 1411
QY 1381 SAAADATEAKNKAHEAERIAASAVQKNATSTKAEARTFAEVTDLDDNEVNNMLKQLEAEK 1440
Db 1412 SAAADATEAKNKAHEAERIAASAVQKNATSTKAEARTFAEVTDLDDNEVNNMLKQLEAEK 1471
QY 1441 ELKRKQDDADQDMMAGMASQAAQAEABINARKAKNSVTSLSIINDLLEQLGQDQDVTDLN 1500
Db 1472 ELKRKQDDADQDMMAGMASQAAQAEABINARKAKNSVTSLSIINDLLEQLGQDQDVTDLN 1531
QY 1501 KLNEIEGTLNKADEMKSVDLDRKVSDDLNEAKQAEAAIMDYNRDIIEIMKDIRNLEDIR 1560
Db 1532 KLNEIEGTLNKADEMKSVDLDRKVSDDLNEAKQAEAAIMDYNRDIIEIMKDIRNLEDIR 1591
QY 1561 KTLPSGCFNTPSIEKP 1576
Db 1592 KTLPSGCFNTPSIEKP 1607

RESULT 15
AAB19806
ID AAB19806 standard; protein; 1572 AA.
XX
AC AAB19806;

XX
DT 05-MAR-2001 (first entry)
XX Mouse laminin 2 mature gamma-1 chain.
DE Laminin 2; mouse; nerve regeneration; angiogenic; cell adhesion;
XX degenerative muscle disorder; muscular dystrophy; cell therapy.
KW Mus musculus.
XX WO2000066730-A2.
OS 09-NOV-2000.
PN 28-APR-2000; 2000WO-US011378.
XX 30-APR-1999; 99US-0131720P.
PR 15-JUN-1999; 99US-0139198P.
PR 12-JUL-1999; 99US-0143289P.
PR 24-SEP-1999; 99US-0155945P.
XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX Yurchenco P;
PI WPI; 2000-687537/67.
XX N-PSDB; AAA88906.
DR Purified laminin 2 protein, useful for research and therapeutic purposes
XX including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.
PT Claim 5; Page 302-306; 305pp; English.
XX The present sequence is that of mouse laminin 2 gamma-1 chain mature
CC protein. Laminin-2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and
CC gamma-1 (100 kDa) chains. It is thought to be specifically required for
CC stabilizing myotubes during skeletal muscle development, and for
CC preventing apoptosis. Genetic defects in human laminin 2 structure or
CC expression are associated with a major type of congenital muscular
CC dystrophy. Laminin 2 is also thought to be important in Schwann
CC cell/basal lamina interactions. The invention provides laminin 2 alpha-2,
CC beta-1 and gamma-1 chain polypeptides (see AAB19791-806) and the
CC polynucleotides encoding them (see AAA8891-906), methods for making
CC recombinant laminin 2, cells that express recombinant laminin 2, and
CC methods for using purified laminin 2 for research and therapeutic
CC purposes including peripheral nerve regeneration, treatment of
CC degenerative muscle disorders, angiogenesis regulation, promoting cell
CC attachment and migration, ex vivo cell therapy, improving the take of
CC grafts, improving the biocompatibility of medical devices and preparing
CC improved culture devices and media
XX Sequence 1572 AA;

Query Match 94.1%; Score 8038; DB 3; Length 1572;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;
QY 3 AMDECTDEGRPQRCMPEFVNAAFNVTVATNTCGTPPEEYCVQGTGVTGKSCHLCDAG 62
Db 1 AMDECADEGRPQRCMPEFVNAAFNVTVATNTCGTPPEEYCVQGTGVTGKSCHLCDAG 60
QY 63 QPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYPPSSINLTLLHGLKAFDITYVRLKPHTS 122
Db 61 QPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYPPSSINLTLLHGLKAFDITYVRLKPHTS 120
QY 123 RPESFAIYKRTREDGFWIPYQYYSGCENTYSKANRGFIRTCGDEQQAALCTDFSDISPL 182
Db 121 RPESFAIYKRTREDGFWIPYQYYSGCENTYSKANRGFIRTCGDEQQAALCTDFSDISPL 180
QY 183 TCGNVAFTLEGRPSAYNFDNSPVQLQEWVTATDIRVTLNRLNTFGDEVNDPKVLKSYYY 242
Db 181 TCGNVAFTLEGRPSAYNFDNSPVQLQEWVTATDIRVTLNRLNTFGDEVNDPKVLKSYYY 240

QY 243 AISDFAVGRCKNGHASECMKNEFDKLVNCKNHTYGVDCBKCLPFFNDPWRRTAES 302
Db 241 AISDFAVGRCKNGHASECVKNEFDKLVNCKNHTYGVDCBKCLPFFNDPWRRTAES 300
QY 303 ASECLPCDCNGRSQECYFDPPELYRSTGHGCHCTNCDNTDGAHCRCRENFRLGNNEAC 362
Db 301 ASECLPCDCNGRSQECYFDPPELYRSTGHGCHCTNCDNTDGAHCRCRENFRLGNTEAC 360
QY 363 SSCHCSPVGSLSSTQSDSYGRCSCKPGVNGDKCDRCQPGFHSLTEAGCRPCSCDPSGIDE 422
Db 361 SPCHCSPVGSLSSTQSDSYGRCSCKPGVNGDKCDRCQPGFHSLTEAGCRPCSCDPSGSTDE 420
QY 423 CNVETGRVCVKDNVEGFNCRCRCKPGFFNJBSSNPRGCTPCFCFEGHSSVCTNAVGYYSI 482
Db 421 CNVETGRVCVKDNVEGFNCRCRCKPGFFNJBSSNPRGCTPCFCFEGHSSVCTNAVGYYSYDI 480
QY 483 SSTFOIDEDGWRAEQRDGEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSYGO 542
Db 481 SSTFOIDEDGWRAEQRDGEASLEWSSERQDIAVISDSYFPRYFIAPKFLGNQVLSYGO 540
QY 543 NLSFSFRVDRDRTRLSAEDLVLEGAGLRVSVPVLIAGNSYPSSETTVKYVFRLHEATDYPW 602
Db 541 NLSFSFRVDRDRTRLSAEDLVLEGAGLRVSVPVLIAGNSYPSSETTVKYVFRLHEATDYPW 600
QY 603 RPALTPFEFQKLLNLTISIKIRGTYSERSAGYLDVTLASARPGPGVPATWVESCTCPVG 662
Db 601 RPALSPFEFQKLLNLTISIKIRGTYSERSAGYLDVTLASARPGPGVPATWVESCTCPVG 660
QY 663 YGGQFCMCLSGYRRETPLNLPYSPCVLCAENGHSETCDPETGVNCRDNTAGHCEKCS 722
Db 661 YGGQFCETCLPGYRRETPLNLPYSPCVLCTCNHSETCDPETGVNCRDNTAGHCEKCS 720
QY 723 DGYGDSSTAGTSSDCQPCPCPGGSSCAVVPKTKVCTNCTGTGKRCCELDDGYFGDP 782
Db 721 DGYGDSSTAGTSSDCQPCPCPGGSSCAVVPKTKVCTNCTGTGKRCCELDDGYFGDP 780
QY 783 LGRNGPVRLCRLCQSDNIDPNAVGNCRNLTGECLKCIYNTAGFYCDRCCKDGFNPLAP 842
Db 781 LGSNGPVRLCRLCQSDNIDPNAVGNCRNLTGECLKCIYNTAGFYCDRCCKDGFNPLAP 840
QY 843 NPADKCKACNCPYGTMKQSSCNPVTCQCECLPHVTGQDCGACDPGFYNLQSGQCERC 902
Db 841 NPADKCKACACN-YGTVQQSSCNPVTCQCECLPHVGRDCTCDPGYINLQSGQCERC 899
QY 903 DCHALGSTNGQCDIRTGQCECQPGITGQHCECERCEVNHFGPEGCKPCDCHHEGSLSLQC 962
Db 900 DCHALGSTNGQCDIRTGQCECQPGITGQHCECERCEVNHFGPEGCKPCDCHHEGSLSLQC 959
QY 963 KDDGRCECREGFVGNRCQDCEENYFYNRSPWPGCECPACVRLVKDKVADHRVKLQELLES 1022
Db 960 KDDGRCECREGFVGNRCQDCEENYFYNRSPWPGCECPACVRLVKDKAAEHRVKLQELLES 1019
QY 1023 IANLGTGDEMVTDOAFEDRLKEAEREVMDLLREAOVDVQDQNLMDRLQRYNNTLSSQIS 1082
Db 1020 IANLGTGDEMVTDOAFEDRLKEAEREVMDLLREAOVDVQDQNLMDRLQRYNNTLSSQIS 1079
QY 1083 RLQNIIRNTIETCNLAERHAEQAHVNTERTLIEIASRELEKAKAAANVSVTQPESTGDPNN 1142
Db 1080 RLQNIIRNTIETCNLAERHAEQAHVNTERTLIEIASRELEKAKM-AANVSITQPESTGEPNN 1138
QY 1143 MTLAEEARKLAERHAEQAHVNTERTLIEIASRELEKAKM-AANVSITQPESTGEPNN 1138
Db 1139 MTLAEEARKLAERHAEQAHVNTERTLIEIASRELEKAKM-AANVSITQPESTGEPNN 1138
QY 1203 YEQAKNISQDLEKQAARVHEBAKRAKDAVEIYASVAQLSPDLSETLENEANNIKMEAE 1262
Db 1199 YEQAKNISQDLEKQAARVHEBAKRAKDAVEIYASVAQLTPVDSEALENEANNIKKEAAD 1258
QY 1263 LEQLIDQKLDYEDLREDMRGKELEVKNLLEKKGTEQQTADQQLARADAAKAALAEAAK 1322
Db 1259 LDRLIDQKLDYEDLREDMRGKELEVKNLLEKKGTEQQTADQQLARADAAKAALAEAAK 1318

QY 1323 GRDTLQEBANDILNLLKDFDRVNDNKTAAEEALRKIPAINQITITEANEKTRQAQALGSA 1382
Db 1319 GRSTLQEBANDILNLLKDFDRVNDNKTAAEEALRRIPAINRTIAEANEKTRQAQALGNA 1378
QY 1383 AADATEAKNKAHEAERIAASAVQKNATSTKAAEABRTFAEVTDLDNVNNMLKQLEAEKEL 1442
Db 1379 AADATEAKNKAHEAERIAASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAENEL 1438
QY 1443 KRKQDDADQDMMAGMASOAAQEAFAINARKAKNSVTSLLSIIINDLLEQLGQDQDVTDLNKL 1502
Db 1439 KRKQDDADQDMMAGMASOAAQEAFAELNARKAKNSVSSLLSQLNNLLDQGLDQDVTDLNKL 1498
QY 1503 NEIEGTINKAKDEMKSVDLDRKVSVDLENEAKKQEAAMDYNRDIEEIMKDIRNLEDIRKT 1562
Db 1499 NEIEGTINKAKDEMKSVDLDRKVSVDLESEARKQEAAMDYNRDIAEIIKDIHNLEDIKKT 1558
QY 1563 LPSGCFNTPSIEKP 1576
Db 1559 LPTGCFNTPSIEKP 1572

Search completed: May 18, 2004, 14:42:25
Job time : 48.8526 secs

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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:30:58 ; Search time 11.9221 Seconds
(without alignments)
6824.493 Million cell updates/sec

Title: US-10-037-182-16
Perfect score: 8544
Sequence: 1 QAAMDECTDEGGRPQRCMPE.....EDIRKTLPSGCFNTPSIEKP 1576

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8544	100.0	1576	4	US-09-562-702A-24
2	8544	100.0	1576	4	US-09-561-818A-24
3	8544	100.0	1584	4	US-09-562-702A-28
4	8544	100.0	1609	4	US-09-562-702A-22
5	8544	100.0	1609	4	US-09-561-818A-22
6	8544	100.0	1617	4	US-09-562-702A-26
7	8043	94.1	1605	4	US-09-562-702A-30
8	8043	94.1	1605	4	US-09-561-818A-26
9	8038	94.1	1572	4	US-09-562-702A-32
10	8038	94.1	1572	4	US-09-561-818A-28
11	3600	42.1	1587	4	US-09-845-583A-10
12	3600	42.1	1587	4	US-09-561-709B-3
13	2637	30.9	1193	1	US-08-317-450B-13
14	2637	30.9	1193	3	US-08-800-593-13
15	2516.5	29.5	1111	1	US-08-317-450B-15
16	2516.5	29.5	1111	3	US-08-800-593-15
17	2355.5	27.6	1171	1	US-08-445-135-1
18	1776	20.8	3088	4	US-09-562-702A-8
19	1776	20.8	3089	4	US-09-562-702A-4
20	1776	20.8	3110	4	US-09-562-702A-2
21	1776	20.8	3110	4	US-09-562-702A-6
22	1776	20.8	3110	4	US-09-561-709B-7
23	1775.5	20.8	3111	2	US-08-460-309-4
24	1775.5	20.8	3111	2	US-08-125-077-4
25	1774.5	20.8	3106	4	US-09-562-702A-10
26	1768.5	20.7	3084	4	US-09-562-702A-12
27	1704	19.9	3075	2	US-08-460-309-5

28	1704	19.9	3075	2	US-08-125-077-5	Sequence 5, Appli
29	1673	19.6	1765	4	US-09-562-702A-16	Sequence 16, Appl
30	1673	19.6	1765	4	US-09-561-818A-16	Sequence 16, Appl
31	1673	19.6	1786	4	US-09-562-702A-14	Sequence 14, Appl
32	1673	19.6	1786	4	US-09-561-818A-14	Sequence 14, Appl
33	1673	19.6	1786	4	US-09-561-709B-9	Sequence 9, Appli
34	1652	19.3	1761	4	US-09-561-709B-1	Sequence 1, Appli
35	1643	19.2	1786	4	US-09-562-702A-18	Sequence 18, Appl
36	1643	19.2	1786	4	US-09-561-818A-18	Sequence 18, Appl
37	1622.5	19.0	1725	4	US-09-562-702A-20	Sequence 20, Appl
38	1622.5	19.0	1725	4	US-09-561-818A-20	Sequence 20, Appl
39	1554	18.2	1799	4	US-09-845-583A-6	Sequence 6, Appli
40	1494	17.5	1798	4	US-09-561-709B-11	Sequence 11, Appl
41	1492	17.5	1798	4	US-09-845-583A-8	Sequence 8, Appli
42	1371	16.0	252	2	US-08-460-309-12	Sequence 12, Appl
43	1371	16.0	252	2	US-08-125-077-12	Sequence 12, Appl
44	1367	16.0	252	1	US-08-152-019A-38	Sequence 38, Appl
45	1346	15.8	251	1	US-08-152-019A-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1
US-09-562-702A-24
; Sequence 24, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 1576
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-24

Query Match 100.0%; Score 8544; DB 4; Length 1576;
Best local Similarity 100.0%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	61	AGQPHLQHGAFLTDYNNQADTTWQSQTMLAGVQYPPSSINLTHLGKAFDITYYRLKXH	120
QY	121	TSRPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQAALCTDEFSDIS	180
Db	121	TSRPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQAALCTDEFSDIS	180
QY	181	PLTGGNVAFSTLEGGRPSAYNFDNSPVLQEWVTATDIRVTNLNRLNTFGDEVNDPKVLKSY	240
Db	181	PLTGGNVAFSTLEGGRPSAYNFDNSPVLQEWVTATDIRVTNLNRLNTFGDEVNDPKVLKSY	240
QY	241	YYAISDFAVGGRCKCNHSHASECMKNEFDKLCVCKHNTYGVDCCKLCLFFNDRPWRATA	300
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Db 301 ESASECLPCDCNCRSQECYFDPPELYRSTGHGGHCTNCQDNTDGAHCRCRENFFRLGNNE 360
QY 361 ACSSCHCSPVGSLSLSTQCDSDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSI 420
Db 361 ACSSCHCSPVGSLSLSTQCDSDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSI 420
QY 421 DECNVETGRCVCKDNVEGFNCERCCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGSYVY 480
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QY 481 SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPFYPIAPAKFLGKQVLSY 540
Db 481 SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPFYPIAPAKFLGKQVLSY 540
QY 541 GQNLFSFRVDRDRTRLSAEDLVLEGAGLRVSVPLIAQGNSSYPSETTVKYVFRLEHATDY 600
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Db 601 PWRPALTPFEFQKLLNNLTISKIRGTYSERSAGYLDVTLASARPGVPATWVESCTCP 660
QY 661 VYGGQFCCEMCLSGYRRETPNLGYPSPCVLCACNGHSETCDPETGVCNCRDNTAGPHCEK 720
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QY 721 CSDGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTEVCTNCPTGTGKRCCELDDGYFG 780
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QY 781 DPLGRNGPVRRLCRQCSDNIDPNAVGNCNELTGECLKCIYNTAGFYCDRCKDGFNGNPL 840
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QY 841 APNPADKCKACNCNPGYTMKQOSSCNPTVGTQCECLPHVTGQDCGACDPPGFYNLQSGQGCE 900
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Db 1381 SAAADATEAKNKAHEAERIA SAVQKNATSTKAEARTFAEVTDL DNEVNNMLKQLQEA EK 1440
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Db 1441 ELKRKODDADQDMMAGMASQAAQAEINARKAKNSVTSLLSIINDLLEQLGQLDTVDLN 1500
QY 1501 KLNEIEGTLNKADEMKSVDLDRKVS DLENEAKKQEAAIMDYNRDIHEIMKDIRNLEDIR 1560
Db 1501 KLNEIEGTLNKADEMKSVDLDRKVS DLENEAKKQEAAIMDYNRDIHEIMKDIRNLEDIR 1560
QY 1561 KTLPSGCFNTPSIEKP 1576
Db 1561 KTLPSGCFNTPSIEKP 1576

RESULT 2
US-09-561-818A-24
; Sequence 24, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortessmaa, Jariiko
; APPLICANT: Tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 1576
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-818A-24

Query Match 100.0%; Score 8544; DB 4; Length 1576;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 PLTGGNVAFSTLEGRPSAYNFDNSPVLOEWMVTATDIRVTNLRLNTFGDEVFNDPKVLKSY 240
Db 181 PLTGGNVAFSTLEGRPSAYNFDNSPVLOEWMVTATDIRVTNLRLNTFGDEVFNDPKVLKSY 240
QY 241 YYAISDFAVGGRCCKNGHASECMKNEFDKLVCKNKHNTYGVDCCKLPFFNDRPWRATA 300
Db 241 YYAISDFAVGGRCCKNGHASECMKNEFDKLVCKNKHNTYGVDCCKLPFFNDRPWRATA 300
QY 301 ESASECLPCDCNCRSQECYFDPPELYRSTGHGGHCTNCQDNTDGAHCRCRENFFRLGNNE 360
Db 301 ESASECLPCDCNCRSQECYFDPPELYRSTGHGGHCTNCQDNTDGAHCRCRENFFRLGNNE 360
QY 361 ACSSCHCSPVGSLSLSTQCDSDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSI 420
Db 361 ACSSCHCSPVGSLSLSTQCDSDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSI 420
QY 421 DECNVETGRCVCKDNVEGFNCERCCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGSYVY 480
Db 421 DECNVETGRCVCKDNVEGFNCERCCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGSYVY 480
QY 481 SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPFYPIAPAKFLGKQVLSY 540

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Db 541 GQNLFSFSFRVDRDRTRLASAEDLVLEGAGLRVSVELIAQGNYSYPSETTVKYVFRLEHATDY 600

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Db 601 PWRPALTPFEFQKLLNNLTSIKIRGTYSERSAGYLDVDTLASARPGPGVPATWVESCTCP 660

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Db 721 CSDGYGDDSTAGTSSDQPCPCPGSSCAVVPKTEVVCTNCPTGTTGKRCCELCDGDFG 780

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Db 841 APNPADKCKACNCPYGTMTKQSSCNVPTGQCECLPHVTDGDCGACDPGFYNLQSGQGCE 900

QY 901 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCBCEVNHFGFEGPEGKPCDCHPEGSLSL 960

Db 901 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCBCEVNHFGFEGPEGKPCDCHPEGSLSL 960

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Db 1021 SLIANLGTGDEMVTDOAFEDRLKEAEREVMDLLREAAQDVKDQDQNLMDRLQRVNNTLSSQ 1080

QY 1081 ISRLQIRNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1140

Db 1081 ISRLQIRNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1140

QY 1141 NNMTLAAEARKLAERHKEQADDIVRVAKTANDTSTEAYNLLRLTLAGENQTAFAIEELN 1200

Db 1141 NNMTLAAEARKLAERHKEQADDIVRVAKTANDTSTEAYNLLRLTLAGENQTAFAIEELN 1200

QY 1201 RKYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDSETLNEANNIKMEA 1260

Db 1201 RKYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDSETLNEANNIKMEA 1260

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Db 1321 KKGRDTLQEAANDILNLLKDFDRRVNDNKTAAEEALRKIPAINQTITEANEXTREAAQALG 1380

QY 1381 SAAADATEAKNKAHEAERIAAVQKNATSTKABEAERTFAEVTDLNEVNNMLKQLOEAEK 1440

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QY 1441 ELKRKQDDADQDMMAGMASQAQAEAEINARKAKNSVTSLLSIINDLLEQLGLDQDVTDLN 1500

Db 1441 ELKRKQDDADQDMMAGMASQAQAEAEINARKAKNSVTSLLSIINDLLEQLGLDQDVTDLN 1500

QY 1501 KLNEIEGTNLKAKDEMKSDDLDRKVSLENEAKKQEAAMIDYNRDIIEIMKDIRNLEDIR 1560

Db 1501 KLNEIEGTNLKAKDEMKSDDLDRKVSLENEAKKQEAAMIDYNRDIIEIMKDIRNLEDIR 1560

QY 1561 KTLPSGCFNTPSIEKP 1576

Db 1561 KTLPSGCFNTPSIEKP 1576

RESULT 3

US-09-562-702A-28

; Sequence 28, Application US/09562702A

; Patent No. 6632790

; GENERAL INFORMATION:

; APPLICANT: Yurchenco, Peter

; TITLE OF INVENTION: Laminin 2 and Methods for Its Use

; FILE REFERENCE: 99-274-B

; CURRENT APPLICATION NUMBER: US/09/562,702A

; CURRENT FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: 60/155,945

; PRIOR FILING DATE: 1999-09-24

; PRIOR APPLICATION NUMBER: 60/143,289

; PRIOR FILING DATE: 1999-07-12

; PRIOR APPLICATION NUMBER: 60/139,198

; PRIOR FILING DATE: 1999-06-15

; PRIOR APPLICATION NUMBER: 60/131,720

; PRIOR FILING DATE: 1999-04-30

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: Patentin Ver. 2.0.

; SEQ ID NO 28

; LENGTH: 1584

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-562-702A-28

Query Match 100.0%; Score 8544; DB 4; Length 1584;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QAAMDECTDEGGRPQRCWPEFVNAAFNVTVATNTCGTPPEEYCVQGTGVTGVTKSCHLCD 60

Db 1 QAAMDECTDEGGRPQRCWPEFVNAAFNVTVATNTCGTPPEEYCVQGTGVTGVTKSCHLCD 60

QY 61 AQOPHLQHGAFLTDVNNQADTTWQSQTMLAGVQYPPSSINLTLLHLGKAFDITYVRLKFH 120

Db 61 AQOPHLQHGAFLTDVNNQADTTWQSQTMLAGVQYPPSSINLTLLHLGKAFDITYVRLKFH 120

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Db 121 TSRPESFAIYKRTREDGPWIPYQYYSGSCENTYSKANRGFIRTTGGDEQALCTDEFSDIS 180

QY 181 PLTGGNVAFTLEGPRSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVNDPKVLKSY 240

Db 181 PLTGGNVAFTLEGPRSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVNDPKVLKSY 240

QY 241 YYAISDFAVGGRCCKNGHASECMKNEFDKLVNCCKHNTYGVDCCKCLPFENDRPWRRATA 300

Db 241 YYAISDFAVGGRCCKNGHASECMKNEFDKLVNCCKHNTYGVDCCKCLPFENDRPWRRATA 300

QY 301 ESASECLPCDCNGRSQECYFDPPELYRSTGGHCTNCQDNTDGAHCRCRENFRLGNNE 360

Db 301 ESASECLPCDCNGRSQECYFDPPELYRSTGGHCTNCQDNTDGAHCRCRENFRLGNNE 360

QY 361 ACSSCHCSPVGSLSLTCQDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSI 420

Db 361 ACSSCHCSPVGSLSLTCQDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSI 420

QY 421 DECNVETGRCVCKDNVEGFNCERCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGYSVY 480

Db 421 DECNVETGRCVCKDNVEGFNCERCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGYSVY 480

QY 481 SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPRFYFIAPAKFLGKQVLSY 540

Db 481 SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPRFYFIAPAKFLGKQVLSY 540

QY 541 GQNLFSFSFRVDRDRTRLASAEDLVLEGAGLRVSVELIAQGNYSYPSETTVKYVFRLEHATDY 600

Db 541 GQNLFSFSFRVDRDRTRLASAEDLVLEGAGLRVSVELIAQGNYSYPSETTVKYVFRLEHATDY 600

QY 601 PWRPALTPFEFQKLLNNLTSIKIRGTYSERSAGYLDVDTLASARPGPGVPATWVESCTCP 660

Db 601 PWRPALTPFQKLLNNLTISKIRGTYSERSAGYLDVTLASARPGVGPATWVESCTCP 660
Qy 661 VYGGQFCBCLSGYRRETNLGPSPCVLCACNGHSETCDPBTGVNCNRDNTAGHCEK 720
Db 661 VYGGQFCBCLSGYRRETNLGPSPCVLCACNGHSETCDPBTGVNCNRDNTAGHCEK 720
Qy 721 CSDGYGDSGTAGTSSDCQPCPGSSCAVWPKTKEVCTNCTGTGKRCCLCDDGYFG 780
Db 721 CSDGYGDSGTAGTSSDCQPCPGSSCAVWPKTKEVCTNCTGTGKRCCLCDDGYFG 780
Qy 781 DPLGRNGPVRLCRLCQCSNDIDPNAVGNCRNLTGECLKCIYNTAGFYCDRCKDGFNGPL 840
Db 781 DPLGRNGPVRLCRLCQCSNDIDPNAVGNCRNLTGECLKCIYNTAGFYCDRCKDGFNGPL 840
Qy 841 APNPADKCKACNCNPYGTMKQSSCNPVTGQCECLPHVTGDCGACDPGFYNLQSGGCE 900
Db 841 APNPADKCKACNCNPYGTMKQSSCNPVTGQCECLPHVTGDCGACDPGFYNLQSGGCE 900
Qy 901 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCHCERCEVNHFGPEGCKPCDCHPEGSLSL 960
Db 901 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCHCERCEVNHFGPEGCKPCDCHPEGSLSL 960
Qy 961 QCKDDGRCECREGFGVGNRCDQCEENTFYNRSWPGCQCEPCYRLVKDKVADHRVKLQBLE 1020
Db 961 QCKDDGRCECREGFGVGNRCDQCEENTFYNRSWPGCQCEPCYRLVKDKVADHRVKLQBLE 1020
Qy 1021 SLIANLGTDEMVTDOAFEDRLKEAREVMDLLREAOQVQDVQDQNLMDRLQRVNNTLSSQ 1080
Db 1021 SLIANLGTDEMVTDOAFEDRLKEAREVMDLLREAOQVQDVQDQNLMDRLQRVNNTLSSQ 1080
Qy 1081 ISRLQNRNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1140
Db 1081 ISRLQNRNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1140
Qy 1141 NNMTLLEAEARKLAERHKEADDIRVAKTANDTSTEAYNLLRLTLAGENQTAFEIEELN 1200
Db 1141 NNMTLLEAEARKLAERHKEADDIRVAKTANDTSTEAYNLLRLTLAGENQTAFEIEELN 1200
Qy 1201 RKYEQAKNISQDLEKQAARVHEEAKRAGDKAVEIYASVAQLSPLDSETLENEANNIKMEA 1260
Db 1201 RKYEQAKNISQDLEKQAARVHEEAKRAGDKAVEIYASVAQLSPLDSETLENEANNIKMEA 1260
Qy 1261 ENLEQLIDQKLDYEDLREDMRGKELEVKNLLEKGTQQTADQLLARADAAKALABEAA 1320
Db 1261 ENLEQLIDQKLDYEDLREDMRGKELEVKNLLEKGTQQTADQLLARADAAKALABEAA 1320
Qy 1321 KKGRDITLOEANDILNNLKDFDRRVNDNKTAAEEALRKIPAINQTI TEANEKTRTAAQALG 1380
Db 1321 KKGRDITLOEANDILNNLKDFDRRVNDNKTAAEEALRKIPAINQTI TEANEKTRTAAQALG 1380
Qy 1381 SAAADATEAKNKAHEAERIASAVQKNATSTKAAEAERTFAEVTDLDNVNNMLKQLQBAEK 1440
Db 1381 SAAADATEAKNKAHEAERIASAVQKNATSTKAAEAERTFAEVTDLDNVNNMLKQLQBAEK 1440
Qy 1441 ELKXKQDDADQDMMAGMASQAAQAEINARKAKNSVTSLLSIINDLLEQLGQDITVDLN 1500
Db 1441 ELKXKQDDADQDMMAGMASQAAQAEINARKAKNSVTSLLSIINDLLEQLGQDITVDLN 1500
Qy 1501 KLINEIEGTLNKADEMKSVDLDRKVSLENEAKKQEAAIMDYNRDIEEIMKDIRNLEDIR 1560
Db 1501 KLINEIEGTLNKADEMKSVDLDRKVSLENEAKKQEAAIMDYNRDIEEIMKDIRNLEDIR 1560
Qy 1561 KTLPSGCFNTPSIEKP 1576
Db 1561 KTLPSGCFNTPSIEKP 1576

RESULT 4
US-09-562-702A-22
; Sequence 22, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:

; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 1609
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-22

Query Match 100.0%; Score 8544; DB 4; Length 1609;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QAAMDECTDEGGRPQRCMPPEFVNAAFNVTVATNTCGTPPEEYCVQGTGVTGKSCHLCD 60
Db 34 QAAMDECTDEGGRPQRCMPPEFVNAAFNVTVATNTCGTPPEEYCVQGTGVTGKSCHLCD 93
Qy 61 AGOPHLQHGAFLTDYNNQADTTWQSQTMLAGVQYPSINLTLHLGKAFDITYVRLKEH 120
Db 94 AGOPHLQHGAFLTDYNNQADTTWQSQTMLAGVQYPSINLTLHLGKAFDITYVRLKEH 153
Qy 121 TSRPESFAIKRTREDGPWIPYQYISGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDIS 180
Db 154 TSRPESFAIKRTREDGPWIPYQYISGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDIS 213
Qy 181 PLTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVNDPKVLKSY 240
Db 214 PLTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVNDPKVLKSY 273
Qy 241 YYAISDFAVGGRCKCNGHASECMKNEFDKLVCKCKHNTYGVDCCKCLPFFNDRPWRRA 300
Db 274 YYAISDFAVGGRCKCNGHASECMKNEFDKLVCKCKHNTYGVDCCKCLPFFNDRPWRRA 333
Qy 301 ESASECLPCDCNGRSQECYFDPPELYRSTGHGGHCTNQDNTDGAHCERCRCNFFRLGNNE 360
Db 334 ESASECLPCDCNGRSQECYFDPPELYRSTGHGGHCTNQDNTDGAHCERCRCNFFRLGNNE 393
Qy 361 ACSSCHCSPVGSLSSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSI 420
Db 394 ACSSCHCSPVGSLSSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSI 453
Qy 421 DECNVETGRCVKDNVEGFNCERCCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGSYVY 480
Db 454 DECNVETGRCVKDNVEGFNCERCCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGSYVY 513
Qy 481 SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPFYFIAPAKFLGKQVLSY 540
Db 514 SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPFYFIAPAKFLGKQVLSY 573
Qy 541 GQNLFSFRVDRDRTRLSEAEDLVLEGAGLRVSVPPLIAQGNYSYSETTVKYVFRLLHEATDY 600
Db 574 GQNLFSFRVDRDRTRLSEAEDLVLEGAGLRVSVPPLIAQGNYSYSETTVKYVFRLLHEATDY 633
Qy 601 PWRPALTPFEFQKLLNNLTISKIRGTYSERSAGYLDVTLASARPGVGPATWVESCTCP 660
Db 634 PWRPALTPFEFQKLLNNLTISKIRGTYSERSAGYLDVTLASARPGVGPATWVESCTCP 693
Qy 661 VYGGQFCBCLSGYRRETNLGPSPCVLCACNGHSETCDPBTGVNCNRDNTAGHCEK 720
Db 694 VYGGQFCBCLSGYRRETNLGPSPCVLCACNGHSETCDPBTGVNCNRDNTAGHCEK 753

QY 721 CSDGYGDSSTAGTSSDCQPCPCGGSSCAVVPKTKKEVVTNCPTGTTGKRCCELDDGYFG 780
Db 754 CSDGYGDSSTAGTSSDCQPCPCGGSSCAVVPKTKKEVVTNCPTGTTGKRCCELDDGYFG 813
QY 781 DPLGRNGPVRCLRLCQCSDNIDPNAVGNCRNLGTGECIKCIYNTAGFYCDRCCKDGFNPL 840
Db 814 DPLGRNGPVRCLRLCQCSDNIDPNAVGNCRNLGTGECIKCIYNTAGFYCDRCCKDGFNPL 873
QY 841 APNPADCKACNCNPGYGTMKQSSCNFVTGQCECLPHVTGQDCGACDPGFYNLQSGQGCE 900
Db 874 APNPADCKACNCNPGYGTMKQSSCNFVTGQCECLPHVTGQDCGACDPGFYNLQSGQGCE 933
QY 901 RCDCHALGSTNGQCDIRTGQCECQGITGQHCHERCCEVNHFGFEGCKPCDCHPEGSLSL 960
Db 934 RCDCHALGSTNGQCDIRTGQCECQGITGQHCHERCCEVNHFGFEGCKPCDCHPEGSLSL 993
QY 961 QCKDDGRCECREGFGVGNRCDCQCEENFYNRSWPGCQCEPCYRLVKDKVADHRVKLQELE 1020
Db 994 QCKDDGRCECREGFGVGNRCDCQCEENFYNRSWPGCQCEPCYRLVKDKVADHRVKLQELE 1053
QY 1021 SLIANLGTGDEMVTDOAFEDRLKEAREVMDLLREAOQVDQVQDQNLMDRLQRVNNTLSSQ 1080
Db 1054 SLIANLGTGDEMVTDOAFEDRLKEAREVMDLLREAOQVDQVQDQNLMDRLQRVNNTLSSQ 1113
QY 1081 ISRLQNTIRNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1140
Db 1114 ISRLQNTIRNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1173
QY 1141 NNMNTLLAEARKLAERHKEADDIIVRAKTANDTSTEAYNLLRTLAGENQTAFEIIEELN 1200
Db 1174 NNMNTLLAEARKLAERHKEADDIIVRAKTANDTSTEAYNLLRTLAGENQTAFEIIEELN 1233
QY 1201 RKYEQAKNTSQDLEKQARVHEEAKGADKAVEIYASVAQISPLDSETLENEANNKMEA 1260
Db 1234 RKYEQAKNTSQDLEKQARVHEEAKGADKAVEIYASVAQISPLDSETLENEANNKMEA 1293
QY 1261 ENLEQLIDQKLDYEDLREDMRGKELEVKNLLEKKGTEQQTADQLLARADAAKALAEHAA 1320
Db 1294 ENLEQLIDQKLDYEDLREDMRGKELEVKNLLEKKGTEQQTADQLLARADAAKALAEHAA 1353
QY 1321 KKGRDTLOEANDILNLLKDFDRRVNDNKTAAEEALRKIPAINQTIIEANEKTRAEQAQALG 1380
Db 1354 KKGRDTLOEANDILNLLKDFDRRVNDNKTAAEEALRKIPAINQTIIEANEKTRAEQAQALG 1413
QY 1381 SAAADATEAKNAHEAERIAASAVQKATSTKABAERTFAEVTDLDDNEVNNMLKQLQEAEX 1440
Db 1414 SAAADATEAKNAHEAERIAASAVQKATSTKABAERTFAEVTDLDDNEVNNMLKQLQEAEX 1473
QY 1441 ELKRKQDDADQDMMAGMASQAAQEAIEINARKAKNSVTSLLSIINDLLEQLGQDQDVTDLN 1500
Db 1474 ELKRKQDDADQDMMAGMASQAAQEAIEINARKAKNSVTSLLSIINDLLEQLGQDQDVTDLN 1533
QY 1501 KLNEIEGTLNKADEMKSVDLDRKVSLENEAKKQEAAIMDYNRDIEEIMKDIRNLEDIR 1560
Db 1534 KLNEIEGTLNKADEMKSVDLDRKVSLENEAKKQEAAIMDYNRDIEEIMKDIRNLEDIR 1593
QY 1561 KTLPSGCFNTPSIEKP 1576
Db 1594 KTLPSGCFNTPSIEKP 1609

RESULT 5
US-09-561-818A-22
; Sequence 22, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortessmaa, Jarkko
; APPLICANT: Tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 1609
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-818A-22

Query Match 100.0%; Score 8544; DB 4; Length 1609;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QAAMDECTDEGGRPQRCMPFVNAAFNVTVATNTCGTPPEEYCVQGTGVTGVTKSCHLCD 60
Db 34 QAAMDECTDEGGRPQRCMPFVNAAFNVTVATNTCGTPPEEYCVQGTGVTGVTKSCHLCD 93
QY 61 AGQPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYPSINLTLLHLGKAFDITYVRLKFH 120
Db 94 AGQPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYPSINLTLLHLGKAFDITYVRLKFH 153
QY 121 TSRPESFAIYKRTREDGPWIPYQYISGSCENTYSKANRGFIRTTGGDEQALCTDEFSDIS 180
Db 154 TSRPESFAIYKRTREDGPWIPYQYISGSCENTYSKANRGFIRTTGGDEQALCTDEFSDIS 213
QY 181 PLTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLSY 240
Db 214 PLTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLSY 273
QY 241 YYAISDFAVGGRCKNGHASECMKNEFDKLVNCCKGNTYGVDCCKLPFFNDRPWRATA 300
Db 274 YYAISDFAVGGRCKNGHASECMKNEFDKLVNCCKGNTYGVDCCKLPFFNDRPWRATA 333
QY 301 ESASECLPCDCNCRSQCEYFDPPELYRSTGHGCHCTNCQDNTDGAHCERCRENFFRLGNE 360
Db 334 ESASECLPCDCNCRSQCEYFDPPELYRSTGHGCHCTNCQDNTDGAHCERCRENFFRLGNE 393
QY 361 ACSSCHCSPVGSLSLSTQCDSYGRCSCKPGVMGDKDCRCQPGFHSLTEAGCRPCSCDPSGSI 420
Db 394 ACSSCHCSPVGSLSLSTQCDSYGRCSCKPGVMGDKDCRCQPGFHSLTEAGCRPCSCDPSGSI 453
QY 421 DECNVETGRCVKDNVEGFNCERCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGSYV 480
Db 454 DECNVETGRCVKDNVEGFNCERCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGSYV 513
QY 481 SISSTFOIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY 540
Db 514 SISSTFOIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY 573
QY 541 GQNLFSFRVDRDRTRLRLSAEDLVLEGAGLRVSVPLIAQNSYSPSEITVKYVFRLEHATDY 600
Db 574 GQNLFSFRVDRDRTRLRLSAEDLVLEGAGLRVSVPLIAQNSYSPSEITVKYVFRLEHATDY 633
QY 601 PWRPALTPFEFQKLLNNLTSIKIRGTYSERSAGYLDVTLASARPGGVPATWVESCTCP 660
Db 634 PWRPALTPFEFQKLLNNLTSIKIRGTYSERSAGYLDVTLASARPGGVPATWVESCTCP 693
QY 661 VGYGGQFCMCLSGYRRETPLNLPYSPCVLCAACNGHSETCDPETGVCNCRDNTAGPHCEK 720
Db 694 VGYGGQFCMCLSGYRRETPLNLPYSPCVLCAACNGHSETCDPETGVCNCRDNTAGPHCEK 753
QY 721 CSDGYGDSSTAGTSSDCQPCPCGGSSCAVVPKTKKEVVTNCPTGTTGKRCCELDDGYFG 780
Db 754 CSDGYGDSSTAGTSSDCQPCPCGGSSCAVVPKTKKEVVTNCPTGTTGKRCCELDDGYFG 813
QY 781 DPLGRNGPVRCLRLCQCSDNIDPNAVGNCRNLGTGECIKCIYNTAGFYCDRCCKDGFNPL 840
Db 814 DPLGRNGPVRCLRLCQCSDNIDPNAVGNCRNLGTGECIKCIYNTAGFYCDRCCKDGFNPL 873
QY 841 APNPADCKACNCNPGYGTMKQSSCNFVTGQCECLPHVTGQDCGACDPGFYNLQSGQGCE 900
Db 874 APNPADCKACNCNPGYGTMKQSSCNFVTGQCECLPHVTGQDCGACDPGFYNLQSGQGCE 933
QY 901 RCDCHALGSTNGQCDIRTGQCECQGITGQHCHERCCEVNHFGFEGCKPCDCHPEGSLSL 960

Db 934 RCDHALGSTNGQCDINTGQCECQPGITGQHCHERCEVNHFGPBGCKPCDCHPEGSLSL 993
Qy 961 QCKDDGRCECREGFGVGNRCDCQCEENFYFNRSWPGCCQCEPCACRYLVKDKVADHRVKLQELE 1020
Db 994 QCKDDGRCECREGFGVGNRCDCQCEENFYFNRSWPGCCQCEPCACRYLVKDKVADHRVKLQELE 1053
Qy 1021 SLIANLGTGDEMVTDOAFEDRLKEAEREVMDLLREAOQDVKDQNDLMDRLQVNNLSSQ 1080
Db 1054 SLIANLGTGDEMVTDOAFEDRLKEAEREVMDLLREAOQDVKDQNDLMDRLQVNNLSSQ 1113
Qy 1081 ISRLQIRNTIETGNLAEOARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1140
Db 1114 ISRLQIRNTIETGNLAEOARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1173
Qy 1141 NNMVLLAEARKLAERHKEQADDIRVAKTANDTSTAYNLLRLTLAGENQTAPEIEELN 1200
Db 1174 NNMVLLAEARKLAERHKEQADDIRVAKTANDTSTAYNLLRLTLAGENQTAPEIEELN 1233
Qy 1201 RKYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDSETLENEANNIKHEA 1260
Db 1234 RKYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDSETLENEANNIKHEA 1293
Qy 1261 ENLEQLIDQKLKDYEDLREDMRGKELEVKNLLEKGTQEQQTADQJLLARADAALABEAA 1320
Db 1294 ENLEQLIDQKLKDYEDLREDMRGKELEVKNLLEKGTQEQQTADQJLLARADAALABEAA 1353
Qy 1321 KKGRDITLOEANDILNNLKDFDRRVNDNKTAAEEALRKIPAINQITTEANEKTRAQQAALG 1380
Db 1354 KKGRDITLOEANDILNNLKDFDRRVNDNKTAAEEALRKIPAINQITTEANEKTRAQQAALG 1413
Qy 1381 SAAADATEAKNAKHAHEABERIASAVQKNATSTKAEARTFAEVTDLNNEVNNMLKQLOEAEK 1440
Db 1414 SAAADATEAKNAKHAHEABERIASAVQKNATSTKAEARTFAEVTDLNNEVNNMLKQLOEAEK 1473
Qy 1441 ELKRKQDDADQDMMAGMASQAAQAEAEINARKAKNSVTSLLSIINDLLEQLGQDITVDLN 1500
Db 1474 ELKRKQDDADQDMMAGMASQAAQAEAEINARKAKNSVTSLLSIINDLLEQLGQDITVDLN 1533
Qy 1501 KLNEIEGTLNKADEMKSVDLDRKVSULENEAKKQAEAAIMDYNRDIIEIMKDIRNLEDIR 1560
Db 1534 KLNEIEGTLNKADEMKSVDLDRKVSULENEAKKQAEAAIMDYNRDIIEIMKDIRNLEDIR 1593
Qy 1561 KTLPSGCFNTPTSEKP 1576
Db 1594 KTLPSGCFNTPTSEKP 1609

RESULT 6

US-09-562-702A-26
; Sequence 26, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 26
; LENGTH: 1617
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-26

Query Match 100.0%; Score 8544; DB 4; Length 1617;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QAAMDECTDEGGRPQRCMPEFVNAAFNVTVVATNTCGTPPEEYCVQGTGVTGKSCHLCD 60
Db 34 QAAMDECTDEGGRPQRCMPEFVNAAFNVTVVATNTCGTPPEEYCVQGTGVTGKSCHLCD 93
Qy 61 AGQPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYPSINLTLLHLKAFDITYVRLKFX 120
Db 94 AGQPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYPSINLTLLHLKAFDITYVRLKFX 153
Qy 121 TSRESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGDEQQAALCTDEFSDIS 180
Db 154 TSRESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGDEQQAALCTDEFSDIS 213
Qy 181 PLTGNVAFSTLEGRPSAYNFNSPVLQEWVTATDIRVTNRLNTFGDEVFNDPKVLKSY 240
Db 214 PLTGNVAFSTLEGRPSAYNFNSPVLQEWVTATDIRVTNRLNTFGDEVFNDPKVLKSY 273
Qy 241 YVAISDFAVGGRCKCNHGASECMKNEFDKLVNCKKHNTYGVDCCKLPFFNDRPWRATA 300
Db 274 YVAISDFAVGGRCKCNHGASECMKNEFDKLVNCKKHNTYGVDCCKLPFFNDRPWRATA 333
Qy 301 ESASECLPCDCNGRSQECYFDPPELYRSTGHGHCNTCQDNTDGAHCERCRENFFRLGNNE 360
Db 334 ESASECLPCDCNGRSQECYFDPPELYRSTGHGHCNTCQDNTDGAHCERCRENFFRLGNNE 393
Qy 361 ACSSCHCSPVGSLSIQDSDSYGRCSCKPGVWGDKDCRCQPGFHSUTEAGCRPCSCDPSGSI 420
Db 394 ACSSCHCSPVGSLSIQDSDSYGRCSCKPGVWGDKDCRCQPGFHSUTEAGCRPCSCDPSGSI 453
Qy 421 DECNVETGRCVCKNVGEGFNCERCKPGFNLESNNPRGCTPCFCFGHSSVCTNAVGSYVY 480
Db 454 DECNVETGRCVCKNVGEGFNCERCKPGFNLESNNPRGCTPCFCFGHSSVCTNAVGSYVY 513
Qy 481 SISSTFOIDEDGWABEQRDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY 540
Db 514 SISSTFOIDEDGWABEQRDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY 573
Qy 541 GQNLFSFRVDRDRTRLAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYVFRLEHATDY 600
Db 574 GQNLFSFRVDRDRTRLAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYVFRLEHATDY 633
Qy 601 PWRPALTPFEFQKLLNNLTSLIKIRGTYSERSAGYLDVTLASARPPGVPATWVESCTCP 660
Db 634 PWRPALTPFEFQKLLNNLTSLIKIRGTYSERSAGYLDVTLASARPPGVPATWVESCTCP 693
Qy 661 VGYGGQFCMCLSGYRRETPNLGPYSPCVLACNGHSETCDPBTGVNCNRDNTAGPHCEK 720
Db 694 VGYGGQFCMCLSGYRRETPNLGPYSPCVLACNGHSETCDPBTGVNCNRDNTAGPHCEK 753
Qy 721 CSDGYGSDTAGTSSDCQPCPCPGGSSCAVVPKTKEVVCTNCTPTGTTGKRCCELDDGYFG 780
Db 754 CSDGYGSDTAGTSSDCQPCPCPGGSSCAVVPKTKEVVCTNCTPTGTTGKRCCELDDGYFG 813
Qy 781 DPLGRNGPVRLCRLCQCSNIDPNAVGNCRNLTGECCLKIYNTAGFYCDRCCKDGFNPL 840
Db 814 DPLGRNGPVRLCRLCQCSNIDPNAVGNCRNLTGECCLKIYNTAGFYCDRCCKDGFNPL 873
Qy 841 APNPADKCKACNCPYGTMKQOSSCNPTVGTQCECLPHVTGQDCGACDPPGFYNLQSGGCE 900
Db 874 APNPADKCKACNCPYGTMKQOSSCNPTVGTQCECLPHVTGQDCGACDPPGFYNLQSGGCE 933
Qy 901 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCHERCEVNHFGPBGCKPCDCHPEGSLSL 960
Db 934 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCHERCEVNHFGPBGCKPCDCHPEGSLSL 993
Qy 961 QCKDDGRCECREGFGVGNRCDCQCEENFYFNRSWPGCCQCEPCACRYLVKDKVADHRVKLQELE 1020
Db 994 QCKDDGRCECREGFGVGNRCDCQCEENFYFNRSWPGCCQCEPCACRYLVKDKVADHRVKLQELE 1053
Qy 1021 SLIANLGTGDEMVTDOAFEDRLKEAEREVMDLLREAOQDVKDQNDLMDRLQVNNLSSQ 1080

Db 1054 SLIANLGTGDEMVTQAFEDRLKEAREVMDLLREAQDVKDQVNDQNLMDRLQRVNNTLSSQ 1113
Qy 1081 ISRLQNIIRNTIETGTLAEQARAHVENTERLIEIASRELEKAKAAANVSVTQPESTGDP 1140
Db 1114 ISRLQNIIRNTIETGTLAEQARAHVENTERLIEIASRELEKAKAAANVSVTQPESTGDP 1173
Qy 1141 NNMTLLAEARKLAERHKEADDIRVAKTANDTSTEAYNLLRLTLAGENQTAFAIEIELN 1200
Db 1174 NNMTLLAEARKLAERHKEADDIRVAKTANDTSTEAYNLLRLTLAGENQTAFAIEIELN 1233
Qy 1201 RKYEQAKNISQDLKQAAARVHEEAKRAGDKAVEIYASVAQLSPDLSETLENEANNIKMEA 1260
Db 1234 RKYEQAKNISQDLKQAAARVHEEAKRAGDKAVEIYASVAQLSPDLSETLENEANNIKMEA 1293
Qy 1261 ENLEQLIDQKLDYEDLREDMRGKELEVKNLLEKKGTEQQTADQLLARADAAKALAEAEA 1320
Db 1294 ENLEQLIDQKLDYEDLREDMRGKELEVKNLLEKKGTEQQTADQLLARADAAKALAEAEA 1353
Qy 1321 KKGRDTLQEAANDILNNLKDFDRRVNDNKTAAEEALRKIPAINQITTEANEKTRAQQAALG 1380
Db 1354 KKGRDTLQEAANDILNNLKDFDRRVNDNKTAAEEALRKIPAINQITTEANEKTRAQQAALG 1413
Qy 1381 SAAADATEAKNKAHEAERIAASAVQKNATSTKAEARTFAEVTDLNEVNNMLKQLOEAEK 1440
Db 1414 SAAADATEAKNKAHEAERIAASAVQKNATSTKAEARTFAEVTDLNEVNNMLKQLOEAEK 1473
Qy 1441 ELKXKQDDADQDMMAGMASQAAQAEAEINARKAKNSVTSLLSIINDLLEQLGQDQDVTDLN 1500
Db 1474 ELKXKQDDADQDMMAGMASQAAQAEAEINARKAKNSVTSLLSIINDLLEQLGQDQDVTDLN 1533
Qy 1501 KLNIEIETLNAKDEMKVSDLRKVSQDLENEAKKQEAAMDYNRDIEEIMKDORNLEDIR 1560
Db 1534 KLNIEIETLNAKDEMKVSDLRKVSQDLENEAKKQEAAMDYNRDIEEIMKDORNLEDIR 1593
Qy 1561 KTLPSGCFNTPSIEKP 1576
Db 1594 KTLPSGCFNTPSIEKP 1609

RESULT 7

US-09-562-702A-30
; Sequence 30, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 1605
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-562-702A-30

Query Match 94.1%; Score 8043; DB 4; Length 1605;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 1470; Conservative 57; Mismatches 47; Indels 2; Gaps 2;

Qy 1 QAAMDECTDEGGRPQRCMPEFVNAAFNVTVVATNTCGTPPEEYCVQGTGVTGKSKHLCD 60
Db 32 RAAMDECADEGGRPQRCMPEFVNAAFNVTVVATNTCGTPPEEYCVQGTGVTGKSKHLCD 91

Qy 61 AGQPHLQHGAAFLTDYNNQADTTWWSQTMLAGVQYSSINLTUHLGKAFDITYVRLKFH 120
Db 92 AGQHLQHGAAFLTDYNNQADTTWWSQTMLAGVQYNSINLTUHLGKAFDITYVRLKFH 151
Qy 121 TSRPESFAIYKTRREDGPWIPYQYSGSCENTYSKANRGFIRTGDEQQAALCTDEFSDIS 180
Db 152 TSRPESFAIYKTRREDGPWIPYQYSGSCENTYSKANRGFIRTGDEQQAALCTDEFSDIS 211
Qy 181 PLTGGNVAFTLEGRPSAYNFDNSPVLOEWTATDIRVTNLRLNTFGDEVFNDPKVLKSY 240
Db 212 PLTGGNVAFTLEGRPSAYNFDNSPVLOEWTATDIRVTNLRLNTFGDEVFNDPKVLKSY 271
Qy 241 YYAISDFAVGGRCKNGHASECMKNEFDKLVCKNCKHNTYGVDCCKLPCFFNDRPWRRA 300
Db 272 YYAISDFAVGGRCKNGHASECMKNEFDKLVCKNCKHNTYGVDCCKLPCFFNDRPWRRA 331
Qy 301 ESASECLPCDCNGRSQECYFDPPELYRSTGHGCHTNCQDNTDGAHCRCRENFRLGNNE 360
Db 332 ESASECLPCDCNGRSQECYFDPPELYRSTGHGCHTNCQDNTDGAHCRCRENFRLGNTE 391
Qy 361 ACSSCHCSPVGSLSLSTQDSYGRCSCKPGVMGDKDRCPQGFHSLTEAGRCPCSDPSGSI 420
Db 392 ACSPCHCSPVGSLSLSTQDSYGRCSCKPGVMGDKDRCPQGFHSLTEAGRCPCSDPSGST 451
Qy 421 DECNVETGRCVCKNVGFCNCRCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGSVY 480
Db 452 DECNVETGRCVCKNVGFCNCRCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGSVY 511
Qy 481 SISSTFOIDEDGWRABQORDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY 540
Db 512 DISSTFOIDEDGWRBQORDGSEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSY 571
Qy 541 QCNLSFSFRVDRRDLRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYVFRLEHATDY 600
Db 572 QCNLSFSFRVDRRDLRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYVFRLEHATDY 631
Qy 601 PWRPALTPFEFQKLLNLTISIKIRGTYSERSAGYLDVTLASARPGPGVPATWVESCTCP 660
Db 632 PWRPALSPFEFQKLLNLTISIKIRGTYSERSAGYLDVTLQASARPGPGVPATWVESCTCP 691
Qy 661 VGYGGQFCMCLSGYRRETPNLGPYSPCVLCACNGHSETCDPETGVNCRDNTAGPHCEK 720
Db 692 VGYGGQFCETCLPGYRRETPSLGPYSPCVLCTCNGHSETCDPETGVNCRDNTAGPHCEK 751
Qy 721 CSDGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKVWCTNCPTGTTGKRCCLCDDGYFG 780
Db 752 CSDGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKVWCTNCPTGTTGKRCCLCDDGYFG 811
Qy 781 DPLGRNGPVRLCRLCQSDNIDPNAVGNCRNLGTGELKCIYNTAGFYCDCKDGFNPL 840
Db 812 DPLGNGPVRLCRLCQSDNIDPNAVGNCRNLGTGELKCIYNTAGFYCDCKDGFNPL 871
Qy 841 APNPADKCKACACN-YGTVQQSSCNPNVTGQCCQLPHVSGRDCGTCDPGYNLQSGQGE 900
Db 872 APNPADKCKACACN-YGTVQQSSCNPNVTGQCCQLPHVSGRDCGTCDPGYNLQSGQGE 930
Qy 901 RCDHALGSTNGQCDIRTGQCECQPGITGQHCHCEVNHFGGPEGCKPCDCHPEGSLSL 960
Db 931 RCDHALGSTNGQCDIRTGQCECQPGITGQHCHCEVNHFGGPEGCKPCDCHPEGSLSL 990
Qy 961 QCKDDGRCECREGFGVGNRCDOCEENYFYNRSWPGCQECPCYRLVKDKVADHRVKLQELE 1020
Db 991 QCKDDGRCECREGFGVGNRCDOCEENYFYNRSWPGCQECPCYRLVKDKAAEHVVKLQELE 1050
Qy 1021 SLIANLGTGDEMVTQAFEDRLKEAREVMDLLREAAQDVKDQVNDQNLMDRLQRVNNTLSSQ 1080
Db 1051 SLIANLGTGDDMTQAFEDRLKEAREVMDLLREAAQDVKDQVNDQNLMDRLQRVNNTLSSQ 1110
Qy 1081 ISRLQNIIRNTIETGTLAEQARAHVENTERLIEIASRELEKAKAAANVSVTQPESTGDP 1140
Db 1111 ISRLQNIIRNTIETGTLAEARARSVESTEOLEIIEIASRELEKAKM-AANVSITQPESTGEP 1169

QY 1141 NNMTLAEEARKLAERHKQEAADDIVRVAKTANDTSTEAYNLLRLTLAGEQTAFIEEELN 1200
Db 1170 NNMTLAEEARRLAERHKQEAADDIVRVAKTANETSAEAYNLLRLTLAGENQTALEIEELN 1229
QY 1201 RKYEQAKNISODLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDSETEANEANNIKMEA 1260
Db 1230 RKYEQAKNISODLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEA 1289
QY 1261 ENLEQLIDOKLXDYEDLREDMRGKELEVNKLLLEKQTEQQTADQOLLARADAAKALAEAA 1320
Db 1290 ADLDRLLIDOKLXDYEDLREDMRGKEHEVNKLLLEKGAEQQTADQOLLARADAAKALAEAA 1349
QY 1321 KKGRDTLOEANDILNLLKDFDRRVNDNKTAAEEALRKIPAINQITITEANEKTRAQQAALG 1380
Db 1350 KKGRSTLOEANDILNLLKDFDRRVNDNKTAAEEALRRIPAINRTIAEANEKTRAQQAALG 1409
QY 1381 SAAADATEAKNKAHEAERIAASAVQKNATSTKAEABRTFAEVTDLDNENVNMLKQLOEAEK 1440
Db 1410 NAAADATEAKNKAHEAERIAASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAEN 1469
QY 1441 ELKRQDDADQDMMAGMASQAAQEAIEINARKAKNSVTSLLSIINDLLEQLGQDQDQD 1500
Db 1470 ELKRQDDADQDMMAGMASQAAQEAELNARKAKNSVSSLLSQNLNLLDQLGQDQDQD 1529
QY 1501 KLNIEGTLNKADEMKSVDLDRKVSQDLENEAKQEAAIMDYNRDIIEIMKDIRNLEDIR 1560
Db 1530 KLNIEGSLNKADEMKAASDLDRKVSQDLESEARKQEAAIMDYNRDIIEIKDIHNLEDIR 1589
QY 1561 KTLPSGCFNTPSIEKP 1576
Db 1590 KTLPTGCFNTPSIEKP 1605

RESULT 8

US-09-561-818A-26
; Sequence 26, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortessmaa, Jarrko
; APPLICANT: Tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 26
; LENGTH: 1605
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-561-818A-26

Query Match 94.1%; Score 8043; DB 4; Length 1605;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 1470; Conservative 57; Mismatches 47; Indels 2; Gaps 2;

QY 1 QAAMDECTDEGGRPQRCMPFVNAAFNVTVVATNTCGTPPEEYCVQTVGTGKSKHLCD 60
Db 32 RAAMDECADEGGRPQRCMPFVNAAFNVTVVATNTCGTPPEEYCVQTVGTGKSKHLCD 91
QY 61 AGQPHLOHGAAFLTDYNNQADTTWQSQTMLAGVQYPPSSINLTLHLGKAFDITYVRLKFKH 120
Db 92 AGQHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYPPNSINLTLHLGKAFDITYVRLKFKH 151
QY 121 TSRPESFAIYKRTREDGPNTPYQYSGSCENTYSKANRGFIRTTGGDEQQAALCTDEFSDIS 180
Db 152 TSRPESFAIYKRTREDGPNTPYQYSGSCENTYSKANRGFIRTTGGDEQQAALCTDEFSDIS 211
QY 181 PLTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVNDPKVLKSY 240
Db 212 PLTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVNDPKVLKSY 271
QY 241 YYAISDFAVGGRCKNGHASECMKNEFDKLCVCKNCKHNTYGVDCCKCLPFNDPWRATA 300

Db 272 YYAISDFAVGGRCKNGHASECMKNEFDKLCVCKNCKHNTYGVDCCKCLPFNDPWRATA 331
QY 301 ESASECLPCDCNGRSQECYFDPPELYRSTGHGHCTNCQDNTDGAHCERCENFFRLGNNE 360
Db 332 ESASECLPCDCNGRSQECYFDPPELYRSTGHGHCTNCQDNTDGAHCERCENFFRLGNTE 391
QY 361 ACSSCHCSPVGLSLSTQCDSYGRCSCKPGVMGDKDRCPGFHSLTEAGCRPCSCDPSGSI 420
Db 392 ACSFCHCSPVGLSLSTQCDSYGRCSCKPGVMGDKDRCPGFHSLTEAGCRPCSCDPSGST 451
QY 421 DECNVETGRCVKDNVEGFNCERCCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGYSVY 480
Db 452 DECNVETGRCVKDNVEGFNCERCCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGYSVY 511
QY 481 SISSTFQIDEDGWRAEQDGESEASLEWSSERQDIAVISDSYFPRYFIAPAKELGKQVLSY 540
Db 512 DISSTFQIDEDGWRVEQDGESEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSY 571
QY 541 GONLSFSFRVDRRDLRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYVFRLHEATDY 600
Db 572 GONLSFSFRVDRRDLRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYIIFRLEHATDY 631
QY 601 PWRPALTPFEFQKLLNNLTSIKIRGTYSERSAGVDDVTLASARPGPGVPATWVESCTCP 660
Db 632 PWRPALSPFEFQKLLNNLTSIKIRGTYSERSAGVDDVTLQASARPGPGVPATWVESCTCP 691
QY 661 VYGGQFCFCEMCLSGYRRETPNLGPYSPCVLCACNHSETCDPETGVCNCRDNTAGPHCEK 720
Db 692 VYGGQFCFCEMCLSGYRRETPNLGPYSPCVLCACNHSETCDPETGVCNCRDNTAGPHCEK 751
QY 721 CSDGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKWVCTNCPTGTTGKRCCELDDGYFG 780
Db 752 CSDGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKWVCTNCPTGTTGKRCCELDDGYFG 811
QY 781 DPLGRNGPVRLLCRLCQSDNIDPNAVGNCRNLTEGLKCIYNTAGFYCDRCCKDGFNPL 840
Db 812 DPLGNGPVRLLCRLCQSDNIDPNAVGNCRNLTEGLKCIYNTAGFYCDRCCKDGFNPL 871
QY 841 APNPADKCKACNCPYGTMKQSSCNPVITGQCECLPHVTGQDCGACDPGFYNLQSGQGE 900
Db 872 APNPADKCKACACN-YGTVQQSSCNPVITGQCECLPHVTGQDCGACDPGFYNLQSGQGE 930
QY 901 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCEVNVHFGFEGEGKPCDCHPEGSLSL 960
Db 931 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCEVNVHFGFEGEGKPCDCHPEGSLSL 990
QY 961 QCKDDGRCECREGFGVNRCDQCEENYFYNRSMPCQCECPACYRLVKDKVADHRVKLQELE 1020
Db 991 QCKDDGRCECREGFGVNRCDQCEENYFYNRSMPCQCECPACYRLVKDKAABHRVKLQELE 1050
QY 1021 SLIANLGTGDEMVTDOAFEDRLKEAEREVMDLLREAQDVQDQDQDQDQDQDQDQDQDQD 1080
Db 1051 SLIANLGTGDEMVTDOAFEDRLKEAEREVMDLLREAQDVQDQDQDQDQDQDQDQDQDQD 1110
QY 1081 ISRLQIRNTIETGTLAEQARAHVENTERLTIETASRELEKAKVAAANVSVTQPESTGDP 1140
Db 1111 ISRLQIRNTIETGTLAEARARSRVESTEQLEIETASRELEKAKM-AANVSITQPESTGEP 1169
QY 1141 NNMTLAEEARKLAERHKQEAADDIVRVAKTANDTSTEAYNLLRLTLAGENQTAPEIEELN 1200
Db 1170 NNMTLAEEARRLAERHKQEAADDIVRVAKTANETSAEAYNLLRLTLAGENQTAPEIEELN 1229
QY 1201 RKYEQAKNISODLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDSETEANEANNIKMEA 1260
Db 1230 RKYEQAKNISODLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEA 1289
QY 1261 ENLEQLIDOKLXDYEDLREDMRGKELEVNKLLLEKQTEQQTADQOLLARADAAKALAEAA 1320
Db 1290 ADLDRLLIDOKLXDYEDLREDMRGKEHEVNKLLLEKGAEQQTADQOLLARADAAKALAEAA 1349
QY 1321 KKGRDTLOEANDILNLLKDFDRRVNDNKTAAEEALRKIPAINQITITEANEKTRAQQAALG 1380

Db 1350 KKGRSTLQEAANDILNNLKDFFRRVNDNKTAAEEALRRIPAINRTIAEANEKTRQAQLALG 1409
Qy 1381 SAAADATEAKNKAHEAERIAASAVQKNATSTKAEARTFAEVTDLDNVNNMLKQLQEAEK 1440
Db 1410 NAAADATEAKNKAHEAERIAASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAEN 1469
Qy 1441 ELKRKQDDADQDMMAGMASQAAQAEAEINARKAKNSVTSLLSIINDLLEQLGQDITVDLN 1500
Db 1470 ELKRKQDDADQDMMAGMASQAAQAEAEINARKAKNSVSSLLSQLNNLLDQLGQDITVDLN 1529
Qy 1501 KLNEIEGTLNKADEMKSVDLDRKVSULENEAKKQEAAIMDYNRDIEEIMKDIRNLEDIR 1560
Db 1530 KLNEIEGSLNKADEMKAASDLDRKVSULESEARKQEAAIMDYNRDIAEIIKDIHNLEDIK 1589
Qy 1561 KTLPSGCFNTPSIEKP 1576
Db 1590 KTLPTGCFNTPSIEKP 1605

RESULT 9
US-09-562-702A-32
; Sequence 32, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 32
; LENGTH: 1572
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-562-702A-32

Query Match 94.1%; Score 8038; DB 4; Length 1572;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;
Qy 3 AMDECTDEGRRPQRCMPEFVNAAFNVTVVATNTCGTPPEEYCVQGTGVTKSCHLCDAG 62
Db 1 AMDECADEGRRPQRCMPEFVNAAFNVTVVATNTCGTPPEEYCVQGTGVTKSCHLCDAG 60
Qy 63 QPHLQHGAFLTDYNNQADTTWQSQTMLAGVQYPSSINLTLHLGKAFDITYVRLKFHTS 122
Db 61 QQHLQHGAFLTDYNNQADTTWQSQTMLAGVQYPNSINLTLHLGKAFDITYVRLKFHTS 120
Qy 123 RPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDISPL 182
Db 121 RPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDISPL 180
Qy 183 TGGNVAFTLEGRPSAYNFNDSPLVQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSYYY 242
Db 181 TGGNVAFTLEGRPSAYNFNDSPLVQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSYYY 240
Qy 243 AISDFAVGGRCCKNGHASECMKNEFDKLVNCKHNTYGVDCCKLPFFNDRPWRATAES 302
Db 241 AISDFAVGGRCCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPFFNDRPWRATAES 300
Qy 303 ASECLPCDCNRSQECYFDPPELYRSTGHGHCNTCQDNTDGAHCERCENFFRLGNNEAC 362
Db 301 ASECLPCDCNRSQECYFDPPELYRSTGHGHCNTCRDNTDGAKCERCENFFRLGNTEAC 360

Qy 363 SSCHCSPVGSLSLTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGRCPSCDPSGSIDE 422
Db 361 SPCHCSPVGSLSLTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGRCPSCDPSGSTDE 420
Qy 423 CNVETGRCVCKDNVEGFNCERCCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGYSYSI 482
Db 421 CNVETGRCVCKDNVEGFNCERCCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGYSYDI 480
Qy 483 SSTFQIDEDGWRABQORDGSEASLEWSSERQDIAVISDSYFFPRYFIAPAKFLGKQVLSYGQ 542
Db 481 SSTFQIDEDGWRVEQORDGSEASLEWSSDRQYIAVISDSYFFPRYFIAPVKFLGNQVLSYGQ 540
Qy 543 NLSFSFRVDRDRTRLAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYVFRLEHATDYPW 602
Db 541 NLSFSFRVDRDRTRLAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYVFRLEHATDYPW 600
Qy 603 RPALTPFEFQKLLNNLTSIKIRGYTSERSAGYLDVTLASARPGPGVPATWVESCTCPVG 662
Db 601 RPALSPFEFQKLLNNLTSIKIRGYTSERSAGYLDVTLQASARPGPGVPATWVESCTCPVG 660
Qy 663 YGGQFCMEMCLSGYRRETPNLGPYSPCVLCACNGHSETCDPETGVCNCRDNTAGPHCEKCS 722
Db 661 YGGQFCETCLPGYRRETPSLGPYSPCVLCTCNGHSETCDPETGVCDNRDNTAGPHCEKCS 720
Qy 723 DGYGDSSTAGTSSDCQPCPCPGGSSCAVVPKTKEVVCTNCPTGTGKRCCLCDDGYFGDP 782
Db 721 DGYGDSSTLTGTSDDCQPCPCPGGSSCAIVPKTKEVVCTHCPTGTAGKRCCLCDDGYFGDP 780
Qy 783 LGRNGPVRLCRLCQSDNIDPNAVGNCRNLTGECCLKIYNTAGFYCDRCCKDGFNPLAP 842
Db 781 LGSNGPVRLCRPCQCNIDNIDPNAVGNCRNLTGECCLKIYNTAGFYCDRCCKEGFFNPLAP 840
Qy 843 NPADKCKACNCPYGTMKQQSSCNPVTTGQCECLPHVTGQDCGACDPGFYNLQSGQGCERC 902
Db 841 NPADKCKACACN-YGTVQQQSSCNPVTTGQCCQLPHVSGRDCGTCDPGYNLQSGQGCERC 899
Qy 903 DCHALGSTNGQCDIRTGQCECQPGITGQHCECERCEVNHFGFEGPCKPCDCHPEGSLSLQC 962
Db 900 DCHALGSTNGQCDIRTGQCECQPGITGQHCECERCETNHFGFEGPCKPCDCHHEGSLSLQC 959
Qy 963 KDDGRCECREGFGVGNRCDQCEENYFYNRSWPGCQECPCYRLVKDVKADHRVKLQELESL 1022
Db 960 KDDGRCECREGFGVGNRCDQCEENYFYNRSWPGCQECPCYRLVKDKAAEHRVKLQELESL 1019
Qy 1023 IANLGTGDEMVTDOAFEDRLKEAEREVDLLREAOQVQDVQDQNLMDRLQRVNNTLSSQIS 1082
Db 1020 IANLGTGDDMVTDOAFEDRLKEAEREVDLLREAEQVQDVQDQNLMDRLQRVNSSLHSQIS 1079
Qy 1083 RLQNIIRNTIETGNLAEQARAHVENTERLFIASRELEKAKVAAANVSVTQPESTGDPNN 1142
Db 1080 RLQNIIRNTIETGILAEARARSRVESTEQLFIASRELEKAKM-AANVSITQPESTGEPNN 1138
Qy 1143 MTLAEEARKLAERHKEADDIRVAKTANDTSTEAYNLLRLTAGENQTAFEIEELNRK 1202
Db 1139 MTLAEEARRLAERHKEADDIRVAKTANETSAAEAYNLLRLTAGENQTALEIEELNRK 1198
Qy 1203 YEOAKNISQDLEKQAARVHEEAKRAGDKAVEIYASVAQLSPLDSETLEANEANNIKMEAEN 1262
Db 1199 YEOAKNISQDLEKQAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAAD 1258
Qy 1263 LEQLIDQKLKDYEDLREDMRGKELEVKNLLEKKGTEQQQTADQLLARADAAKALAEAAKK 1322
Db 1259 LDRLIDQKLKDYEDLREDMRGKEHEVKNLLEKGAEQQTADQLLARADAAKALAEAAKK 1318
Qy 1323 GRDTLOEANDILNNLKDFFRRVNDNKTAAEEALRKIPAINQTI TEANEKTRQAQALGSA 1382
Db 1319 GRSTLOEANDILNNLKDFFRRVNDNKTAAEEALRRIPAINRTIAEANEKTRQAQALGNA 1378
Qy 1383 AADATEAKNKAHEAERIAASAVQKNATSTKAEARTFAEVTDLDNVNNMLKQLQEAKEKEL 1442
Db 1379 AADATEAKNKAHEAERIAASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAENEL 1438
Qy 1443 KRQDDADQDMMAGNASQAAQEAEEINARKAKNSVTSLLSIINDLLEQLGQDITVDLNKL 1502

Db 1439 KRQDDADQDMMWAGMASQAQAEALNARKAKNSVSSLLSQNNLLDQLGQDVTDLNKL 1498
QY 1503 NEIEGTLNKADEMKSVDLDRKVSLENEAKKQEAAMIDNRPDIIEIMKDINLEDIRKT 1562
Db 1499 NEIEGSLNKADEMKSADLDRKVSLESEARKQEAAMIDNRPDIAEIIKDIHNLEDIRKT 1558
QY 1563 LPSGCFNTPSIEKP 1576
Db 1559 LPTGCFNTPSIEKP 1572

RESULT 10
US-09-561-818A-28
; Sequence 28, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortessmaa, Jarrko
; APPLICANT: Tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 28
; LENGTH: 1572
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-561-818A-28

Query Match 94.1%; Score 8038; DB 4; Length 1572;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;

QY 3 AMDECTDEGGPQRCMPEFVNAAFNVVATNTCGTPPEEYCVQGTGVTGKSKHLCADG 62
Db 1 AMDECADEGGPQRCMPEFVNAAFNVVATNTCGTPPEEYCVQGTGVTGKSKHLCADG 60
QY 63 QPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYPPSSINLTLHLGKAFDITYVRLKFHTS 122
Db 61 QPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYPPSSINLTLHLGKAFDITYVRLKFHTS 120
QY 123 RPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQAALCTDFSDISPL 192
Db 121 RPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQAALCTDFSDISPL 180
QY 183 TGGNVAFSTLEGRPSAYNFDNSPVLQEWVTTATDIRVTLNRLNTFGDEVNDPKVLKSYYY 242
Db 181 TGGNVAFSTLEGRPSAYNFDNSPVLQEWVTTATDIRVTLNRLNTFGDEVNDPKVLKSYYY 240
QY 243 AISDFAVGGRCKNGHASECMKNEFDKLVCKNCKHNTYGVDCCKLPFFNDPWRRTAES 302
Db 241 AISDFAVGGRCKNGHASECMKNEFDKLVCKNCKHNTYGVDCCKLPFFNDPWRRTAES 300
QY 303 ASECLPCDCNRSQECYFDPELYRSTGHGGHCTNCQDNTDGAHCERCERENPFRLGNNEAC 362
Db 301 ASECLPCDCNRSQECYFDPELYRSTGHGGHCTNCQDNTDGAHCERCERENPFRLGNTEAC 360
QY 363 SSCHCSPVGSLSLTCDSYGRCSCKPGVMGDKCDRCQPGFHSLSLTEAGCRPCSDPSGSDIE 422
Db 361 SPCHCSPVGSLSLTCDSYGRCSCKPGVMGDKCDRCQPGFHSLSLTEAGCRPCSDPSGSTDE 420
QY 423 CNVETGRVCVKDNVEGNCERCKPGFENLESNNRPGCTPCFCFGHSSVCTNAGYSVYSI 482
Db 421 CNVETGRVCVKDNVEGNCERCKPGFENLESNNRPGCTPCFCFGHSSVCTNAGYSVYDI 480
QY 483 SSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVTSYEPYFIAPAKFLGKQVLSYGO 542
Db 481 SSTFQIDEDGWRAEQRDGSEASLEWSSDRQYIAVTSYEPYFIAPAKFLGKQVLSYGO 540
QY 543 NLSFSFRVDRDRTRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYVFRLEHATDYPW 602

Db 541 NLSFSFRVDRDRTRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYVFRLEHATDYPW 600
QY 603 RPALTPEEFQKLLNNLTISKIRGTYSERSAGYVDDVTLASARPGPGVPATWVESCTCPVG 662
Db 601 RPALSPFEFQKLLNNLTISKIRGTYSERSAGYVDDVTLQOSARPGPGVPATWVESCTCPVG 660
QY 663 YGQFCFCEMCLSGYRRETPNLGPSPCVLCAHNGHSETCDPETGVNCRDNTAGPHCEKCS 722
Db 661 YGQFCFCEMCLSGYRRETPNLGPSPCVLCAHNGHSETCDPETGVNCRDNTAGPHCEKCS 720
QY 723 DGYGDSSTAGTSSDCQPCPCPGGSSCAVVPKTKVWCTNCTGTGKRCCELDDGYFGDP 782
Db 721 DGYGDSSTAGTSSDCQPCPCPGGSSCAVVPKTKVWCTNCTGTGKRCCELDDGYFGDP 780
QY 783 LGNGPVRLLCRQLCQSDNIDPNAVGNCRNLTGECLKCIYNTAGFYCDCKDGFNPLAP 842
Db 781 LGNGPVRLLCRQLCQSDNIDPNAVGNCRNLTGECLKCIYNTAGFYCDCKDGFNPLAP 840
QY 843 NPADKCKACNCPYGTMKQSSCNPVGTGCECLPHVTGQDCGACDPGFYNLQSGQGCERC 902
Db 841 NPADKCKACNCPYGTMKQSSCNPVGTGCECLPHVTGQDCGACDPGFYNLQSGQGCERC 899
QY 903 DCHALGSTNGQCDIRTGQCECQPGITGQHCERCCEVNHFGFEGCKPCDCHPEGSLQOC 962
Db 900 DCHALGSTNGQCDIRTGQCECQPGITGQHCERCCEVNHFGFEGCKPCDCHPEGSLQOC 959
QY 963 KDDGRCECREGFGVGNRCDQCEENYFYNRSWPGCQECPCYRLVKDKVADHRVKLOELFSL 1022
Db 960 KDDGRCECREGFGVGNRCDQCEENYFYNRSWPGCQECPCYRLVKDKVADHRVKLOELFSL 1019
QY 1023 IANLGTGDEMVTDOAFEDRLKEAREVMDLLREAOQVQDVQDQNLMDRLQRVNNTLSSQIS 1082
Db 1020 IANLGTGDEMVTDOAFEDRLKEAREVMDLLREAOQVQDVQDQNLMDRLQRVNNTLSSQIS 1079
QY 1083 RLQNIIRNTIETGNLAEOQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDPNN 1142
Db 1080 RLQNIIRNTIETGNLAEOQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDPNN 1138
QY 1143 MTLAEEARLAEHKEADDIIVRAKTANTSTEAYNLLRLTLAGENQTAPELNLNRK 1202
Db 1139 MTLAEEARLAEHKEADDIIVRAKTANTSTEAYNLLRLTLAGENQTAPELNLNRK 1198
QY 1203 YEAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQVSPDSETLENEANNIKWEAEN 1262
Db 1199 YEAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQVSPDSETLENEANNIKWEAEN 1258
QY 1263 LEQLIDQKLDYEDLREDMRGKELVKNLLEKGTQEQOQADQLLARADAALAEAAK 1322
Db 1259 LEQLIDQKLDYEDLREDMRGKELVKNLLEKGTQEQOQADQLLARADAALAEAAK 1318
QY 1323 GRDTLQEAANDILNNLKDFRRVNDNKTAAEALRKIPAINQTI TEANEKTRTAAQALGSA 1382
Db 1319 GRDTLQEAANDILNNLKDFRRVNDNKTAAEALRKIPAINQTI TEANEKTRTAAQALGSA 1378
QY 1383 AADATEAKNKAHEAERIAASAVQKNATSTKAAEAERTFAEVTDLNNEVNNMLKQLOAEKEL 1442
Db 1379 AADATEAKNKAHEAERIAASAVQKNATSTKAAEAERTFAEVTDLNNEVNNMLKQLOAEKEL 1438
QY 1443 KRKQDDADQDMMWAGMASQAQAEALNARKAKNSVSSLLSQNNLLDQLGQDVTDLNKL 1502
Db 1439 KRKQDDADQDMMWAGMASQAQAEALNARKAKNSVSSLLSQNNLLDQLGQDVTDLNKL 1498
QY 1503 NEIEGTLNKADEMKSVDLDRKVSLENEAKKQEAAMIDNRPDIIEIMKDINLEDIRKT 1562
Db 1499 NEIEGSLNKADEMKSADLDRKVSLESEARKQEAAMIDNRPDIAEIIKDIHNLEDIRKT 1558
QY 1563 LPSGCFNTPSIEKP 1576
Db 1559 LPTGCFNTPSIEKP 1572

RESULT 11
US-09-845-583A-10

; Sequence 10, Application US/09845583A
; Patent No. 6635616
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Brunken, William Joseph
; APPLICANT: Champlaud, Marie-France
; APPLICANT: Hunter, Dale
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
; FILE REFERENCE: 10287-056001
; CURRENT APPLICATION NUMBER: US/09/845,583A
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/200,863
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1587
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-845-583A-10

Query Match 42.1%; Score 3600; DB 4; Length 1587;
Best Local Similarity 43.5%; Pred. No. 1.4e-200;
Matches 695; Conservative 263; Mismatches 575; Indels 64; Gaps 20;

QY 2 AAMDECTDEGGRPQRCMPEFVNAAFNVTVATNTCGTPPEYCVQGTGVTGKTSCHLCDA 61
Db 20 AGMGACYDAGRPQRCPLVFENAAFGRLAQASHTCGSPPEDFCPHVGAAGAGAHQRCDA 79
QY 62 GOPHLOHGAFLTDYNNQADTTWQSQTMLAGVQYPPSSINLTLHLGKAFDITVYRLKFHT 121
Db 80 ADPQRHNASLYLTDHFSQDSESTWQSPSMAFGVQYPTSVNITLRLGKAYEITVYRLKFHT 139
QY 122 SRPESFAIKRTREDGFWIPYQYVYSGSCENTYSKANRGFIRTTGGDEQALCTDEPDISP 181
Db 140 SRPESFAIKRSRADGPWEYQYFYSASCQKTYGRPEGQYLRPGEDEVAFCSTSEFDISP 199
QY 182 LTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTILNRLNTFGDEVNDPKVLKSY 241
Db 200 LSGGNVAFSTLEGRPSAYNFEESPGIQEWVTSTELLISLRLNTFGDDIFKDPKVLQSY 259
QY 242 YAISDFAVGCRCKCNHASECMKNFEDKLVNCCKHNTYGVDCCKLPEFFNDRPWRRTAE 301
Db 260 YAVSDFSVGCRCKCNHASECGPDVAGQLACRCQHNTTGTDCERCLPFFQDRPWARGTAE 319
QY 302 SASECLPCDCNRSQECYFDPPELYSTGHGHCTNCQDNTDGAHCERCENEFRLGNNEA 361
Db 320 AAHECLPCNCSGRSEECTFDRELFRSTGHGRCHHCRDHTAGPHCERCQENFYHWDPRMP 379
QY 362 CSSCHCSPVGSLSSTQCDYSYGRCSCKPGVMGDKCDRCQOPGFHSLTEAGCRPCSCDPSID 421
Db 380 CQPCDCCSAGSLHLQCDTGTCAKFTVTGWKCDRLPLGFHSLSEGGRPCTCNPAGSLD 439
QY 422 ECNVETGRVCYCKDNVEGFCNRCCKPGFNFLESSNPRGCTPCFCFGHSSVCTNAVGVSY 481
Db 440 TCDPRSGRCPCKENVEGNLDCRCRPGTFNLQPHNPAGCSCFCYGHSKVCACASTAQFQV 499
QY 482 ISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY 541
Db 500 ILSDFHQGAEGWARSVGGSEHSPQWSPN---GVLLSPEDEEELTAPGKFLGDQRF 555
QY 542 QNLSFSFRVDRDTRLAEDLVLEGALRVSVPLIAQGNYSYSETTVKYVFRLLH---EAT 598
Db 556 QPLILTRVPPGDSPLPVQ-LRLEGTGLALS--LRHSSLGPGQDARASQGGRAQVPLQET 612
QY 599 DYPWRPALTPPEFQKLLNNLTSIKIRGTYSERSAG--YLDVTLASARPGVPATWVES 656
Db 613 SEDVAPPLPPHFQRLANLTLRLRVSPGSPAGPVFLTEVRLTSARPLSPPASWVEI 672
QY 657 CTCPVYGGQFCMCLSGYRRETPNLGPYSPCVLCAKNGHSETCDPETGVNCNRDNTAGP 716
Db 673 CSCPTGYTGQFCESCAPGYKREMPQGGPYASCVPCTCNQHG-TCDPNTGICVCSHTEGP 731

QY 717 HCEKCSGDYGYDSTAGTSSDCQPCPCPGSSCAVVPKTKVWCTNCPTGTTGKRCCLCDD 776
Db 732 SCERCLPGFYGNPFAGQADDCQPCPCPGQSACTTIPESGEVVTCHCPGQRRRCEVCDD 791
QY 777 GYFGDPLGRNGPVRRLCRLCQSDNIDPNAVGNCRNLTGECCLKIYNTAGFYCDRCCKDGGFF 836
Db 792 GYFGDPLGLFGHPQPCQCSGNVDPNAVGNCDPLSGHCLRLHNTTGDHCEHCQEGFY 851
QY 837 GNPLAPNPADKCKACNCNPNYGTWKQOSSCNPNVTGQCECLPHVTGQDCGACDPGFYNIQSG 896
Db 852 GSALAPRPADKCMPCSCHPQGSVSEQMPCDPVTGQCSCLPHVTARDCSRCPYGGFFDLQPG 911
QY 897 QGCERCDHALGSTNGQCDIRTGQCECQPGITGQHCHCEVNHFGFEGEGCKPCDCHPEG 956
Db 912 RGCRCCKHPLGSEDQCHPKTGQCTCRPGVTGQACDRCOLGFFGSSIKGCRACRCSPLG 971
QY 957 SLSLQCKDDGRCECREGFVGNRCDQCEENYFYNRSWPGQCECPACRYLVKDKVADHRVKL 1016
Db 972 AASAQCHYNGTVCVRPGFEGYKCDRCHYNFFLTADGTHCQCCPSCYALVKEETAKLKARL 1031
QY 1017 OELESILANLGTGDEMVTQAFEDRLKEAREVMDLLREADQVDQVQDQNLMDRLQRVNNT 1076
Db 1032 TLTEGWLQSDCGSPW---GPLDILLGEAPRG--DVYQGHLLPGAREAFLEQMMGLEGA 1086
QY 1077 LSSQISRLQINRNTIETGNLAERAHVENTERLIEIASRELEKAKAVAAANVSVTQPS 1136
Db 1087 VKAAREQLQRLNKGARCAQAGSQKTCTQLADLEAVLESSEEEILHAAAILASLEIPQ-EG 1145
QY 1137 TGDPNMTLLAEERKLAERHKQEAADDIVRVAKTANDTSTAYNLLRLTLAGENQTAPEI 1196
Db 1146 PSQPTKWSHLAIEARALARSHRDTATKIAATAWRALLASNTSYALLWNLL--EGRVALET 1203
QY 1197 E-ELNRKYEQAKNISQDLEKQAARVHEEAKRAGDKAVEIYASVAQLSPLDSETL----- 1249
Db 1204 QRDLEDRIQEVAQAQKALRTAVAEVLPEAE-----SVLATVQVQVADTAPYLALLASP 1256
QY 1250 -----ENEANNIKMEAEENLEQLIDQKLKDYEDLREDMRGKELEVNLLLEKGTQQT--- 1301
Db 1257 GALPKQSRAEGLKAKALEKTV---ASWQHMMATE-AARTLQTAQAATLRQTEPLTMAR 1311
QY 1302 -----ADOLLARADAAKALAEAAKGRDRTLQEAANDILNNLKDFFFFRNDNKTAAEEA 1354
Db 1312 SRLTATFASQLHQGARAALTQASSSVQAATVTVMGARTLLADLEGMKLQFPRPKDQALQ 1371
QY 1355 LRKIPAINQITAEANEKTREAAQALGSAADAAATEAKNKAHEABERIASAVQKNATSTKAE 1414
Db 1372 RKADSVSDRLADTRKTKQAERMGLNAAPLSSSAKKGREAEVLAKDSAKLAKALLRER 1431
QY 1415 ERTFAEVTDLNEVNNMLKQL-QEAEKELKRQDDADQDMMAGMASQAAQAEAEINARKA 1473
Db 1432 KOAHRRASRLTSQTATLQOASQVLAERARQEEAEAEVAGLS-----EMEQQIRES 1486
QY 1474 KNSVTSLLSIINDLLEQLGQDLDL--VDLNLKNEIEGTLNKAKDEM-KVSDLDKRVSDLEN 1530
Db 1487 RISLEKDIETLSSELLARLGSLDTHQAPQAQALNETQWALERLRLQLGSPGSLQRLSLLEQ 1546
QY 1531 EAKQAEAAIMDYNRDIEEIMKDINLEDIRKTLPSGC 1567
Db 1547 ESQQQELQIQGFESDLAEIRADKQNLKONLEAILHSLPENC 1583

RESULT 12
US-09-561-709B-3
; Sequence 3, Application US/09561709B
; Patent No. 6682911
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Champlaud, Marie-France
; APPLICANT: Olson, Pamela
; APPLICANT: Koch, Manuel
; APPLICANT: Brunken, William
; TITLE OF INVENTION: LAMININS AND USES THEREOF
; FILE REFERENCE: 10287-060001

; CURRENT APPLICATION NUMBER: US/09/561,709B									
; CURRENT FILING DATE: 2000-05-01									
; PRIOR APPLICATION NUMBER: US 09/168,949									
; PRIOR FILING DATE: 1998-10-09									
; PRIOR APPLICATION NUMBER: US 60/061,609									
; PRIOR FILING DATE: 1997-10-10									
; NUMBER OF SEQ ID NOS: 13									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 3									
; LENGTH: 1587									
; TYPE: PR1									
; ORGANISM: Homo sapiens									
; US-09-561-709B-3									
Query Match									
Best Local Similarity 42.1%; Score 3600; DB 4; Length 1587;									
Matches 695; Conservative 263; Mismatches 575; Indels 64; Gaps 20;									
QY	2	AAMDECTDEGGRQRCMPPEFVNAAFNVTVVATNTCGTPPEEYCVQGTGVTGKTSCHLCDA	61						
Db	20	AGMGACYDGAGRPQRCPLPVFENAAFGRLAQASHTCGSPPEDFCPHVGAAGAGAHQCRCDA	79						
QY	62	GQPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYPPSSINLTLLHLCAPDITYVRLKFT	121						
Db	80	ADPQRHNASYLTDFHSQDESTWQSPSMAFGVQYPTSVNITRLKAYEITYVRLKFT	139						
QY	122	SRPESFAIKYRTREDGPWIPYQYYSGCSENTYSKANRGFIRTGDEQALCTDEFSDISP	181						
Db	140	SRPESFAIKYRSRADGPWEYQYFASQKTYGRPEGQYLRPGEDERVAFTSEFSDISP	199						
QY	182	LTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSY	241						
Db	200	LSGGNVAFSTLEGRPSAYNFEESPLQEWVTSTELLISLDRNLNTFGDDIFKDPKVLQSY	259						
QY	242	YAIISDFAVGGRCKNGHASECMKNEFDKLVNCCKHNTYGVDCCKLPFFNDRPWRRTAE	301						
Db	260	YAVSDFSVGGRCKNGHASECGPDVAGQLACRQHNNTGTDCERCCLPFFQDRPWARGTAE	319						
QY	302	SASECLPCDCNGRSQECYFDPPELYRSTGHGHCNTCQDNTDGAHCERENFFRLGNNEA	361						
Db	320	AAHECLPCNCSGRSEECTFDRELFRSTGHGRCHCRDHTAGPHCERCQENFYHWDPRMP	379						
QY	362	CSSCHCSPVGLSTQCDSDYGRCSCKPGVMGDKCDRCQPGFHSLTEAGRCPCSDPSGSID	421						
Db	380	QCPDCQASGSLHLQCDTGTCAKPTVTGKCDRCPLPGFHSLSSEGGCRPCTCNPAGSLD	439						
QY	422	ECNVETGRCVCKDNVEGNCERCCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGSVYS	481						
Db	440	TCDPRSGRCPCKENVEGNLDCRCRPGTFNLQPHNPAGCSCFCYGHSKVCASATAQFQVH	499						
QY	482	ISSTFQIDEDGWRAEQRDSEASLEWSSERQDIAVISDSYFPRFYFIAPAKFLGKQVLSYG	541						
Db	500	ILSDFHQAGAEGWARSVCGSEHSPQWSPN---GVLLSPDEEEELTAPGKFLGDQRFSG	555						
QY	542	QNLSPSFRVDRDRTRLSAEDLVLEGAGLRVSVPLIAQGNYSYPSETTVKYVRLH---EAT	598						
Db	556	QPLILTFRVPPGDSPLPVQ-LRLEGTGLALS--LRHSSLSGPQDARASQGGRAQVPLQET	612						
QY	599	DYPWRPALTPPEFQKLLNLTISKIRGTYSERSAG--YLDDEVTLASARPQGPVATWVES	656						
Db	613	SEDVAPPLPPFHFQRLLANLTSLRLRVSPGSPAGPVFLTEVRLTSARPLSPASWVEI	672						
QY	657	CTCPVYGGQFCMCLSGYRRETPNLGPSPVLCACNGHSETCDPETGVCNCRDNTAGP	716						
Db	673	CSCPTGYTQGFCECAPGYKREMPQGGPYASVCPCTCNQHG-TCDPNTGICVCSHHTGP	731						
QY	717	HCEKSDGYGDSTAGTSSDCQPCPCPGSSCAVPKTKEVVCTNCPTGTGKRCCELDD	776						
Db	732	SCERCLPGFYGNPFAGADDQPCPCPGQSACTTIPESGEVVCTHCPPGQGRRCRCEVDD	791						
QY	777	GYFGDPLGRNGPVRLRLCQSDNIDPNVAGNCNLTGECCLKIYNTAGFYCDRCCKDGF	836						
Db	792	GFFGDBLGLFGHPQPCQCQCSGNVDPNAVGNCDPLSGHCLRLHNTTGDHCEHCQEGFY	851						

RESULT 13
US-08-317-450B-13
; Sequence 13, Application US/08317450B
; Patent No. 5660982
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Kallunki, Pekka
; APPLICANT: Pyke, Charles
; TITLE OF INVENTION: Laminin Chains: Diagnostic and
; TITLE OF INVENTION: Therapeutic Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & ALLEGRETTI, LTD.
; STREET: Ten South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/317,450B
; FILING DATE: 04-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Chao, Mark
; REGISTRATION NUMBER: 37,293
; REFERENCE/DOCKET NUMBER: 94,778
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1193 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-317-450B-13

Query Match          30.9%; Score 2637; DB 1; Length 1193;
Best Local Similarity 39.4%; Pred. No. 7.5e-145;
Matches 515; Conservative 235; Mismatches 418; Indels 138; Gaps 12;

QY 286 CLPFFNDRPWRATAESASECLPCDCNGRSQECYFDEPELYRSTGHGGHCTNCQDNTDGAH 345
DB 9 CLCFSLLLPAARATSRRE---VDCNGKSRQCFIDRELHRQTGNGRFCLNCNNDNTDGIH 64

QY 346 CERCRENFFRLGNNEACSSCHSPVGSLSSTQCDSYGRCSCKPGVMGDKDCRCQPGFHSLT 405
DB 65 CEKCKNGFYRHRERDCLPCNCNSKGSLSARCDNSGRCSCKPGVTGARCDRCLPGFHLT 124

QY 406 EAGC-----RPSCDPSGSIDECNVETGRVCVKDNVEGFNCERCCKPGFFNLESSNPR 457
DB 125 DAGCTQDQRLLDKDCDPAAGIPC--DAGRCVCKPAVTGERCDRCRSGYNLDGNPE 182

QY 458 GCTPCFCFGHSSVCTNAVGYSVISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVI 517
DB 183 GCTQCFCYGHASACRSSAEYSVHKITSTFHQDVGWKAVQRNGSPAXLQWSQRHQDVFS 242

QY 518 SDSYFPRYFIAPAKFLGKQVLSYGQNLFSFRVDRDRTRLSAEDLVLEGAGLRVSVPLIA 577
DB 243 AQRLLDPVYFVAPAKFLGNQVSYGQSLSFDRYVRDGRHPSAHDVILEGAGLRITAPLMP 302

QY 578 QGNSYSPSETTVKIVFRLHEATDYPWRPALTPFEFQKLLNNLTISKIRGYTSERSAGYLD 637
DB 303 LGKTLPCGLTKTYTFRLNEHPSNNWSPQLSYFEYRLLRNLTLALRIRATYGEYSTGYDN 362

QY 638 VTLASARPGPGVPATWVESCTCPVGYGGQFCMCLSGYRRETPNLGPYSPCVLCAKNHGS 697
DB 363 VTLISARPVSGAPAPWVEQCICPVGYKQFCQDCASGYKRD SARLGPFGTCIPCNCQG-G 421

QY 698 ETCDPETGVNCRDNTAGPHCEKCDSDGYGDSGTAGTSSDCQPCPCPGGSSCAVVKTKEV 757
DB 422 GACDPDTGDCYSGDENPDIEACDPIGFYNDPHDRS--CKPCCHNGFSCSVIPETEEV 479

QY 758 VCTNCPTGTTGKRCCLCDDGYFGDPLGRNGPVRLCRLCQCSDNIDPNAVGNMRLTGECL 817
DB 480 VCNNCPGPGVTGARCELCADGYFGDPFGEHGPVRPCQPCQNSNVDPSASGNCDRLTGRCL 539

QY 818 KCIYNTAGFYCDCKDGGFFGNPLAPNPADKCKACNCPYGTMTKQQSSCNPNVTGQCECLPH 877
DB 540 KCIHNTAGIYCDQCKAGYFGDPLAPNPADKCRACNCPMGS----- 580

QY 878 VTGQDCGACDPGFYNLQSGQGCERCDCHALGSTNGQCDIRTGQCECQPGITGQHCERCEV 937
DB 581 ----- 580

QY 938 NHFGFPGEGCKPCDCHPEGSLSLQCKDDGRCECREGFVGNRCQDCEENFYNRSWPGCQE 997
DB ----- 997

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581 -----EPVG-----CRSDGTVCCKPGFGPNCHEH-----GAFS 608
998 CPACYRLVKDKVADHRVKLQELSLIANLGTGDEMVTQDQAFEDRLKEAEREVMDLLREAQ 1057
609 CPACYNQVKIQMDQFMQQLQRMALISKAQGGDGVVPDTELEGRMQQAEALQDILRDAQ 668
1058 DVKDQVQNDMLRQVRNNTLSSQISRLQNIIRNTIETGNLAEQARAHVENTERLIEIASR 1117
669 ISEGASRSLGLQAKVRSQENSQSRLLDDLKMTVERVRALGSQYQNRVDRTHRLITQMQL 728
1118 ELEKAKVAAANVSUTQPESTGDPNNMTLLAEAEARKLAERHKQEAADDIVRVAKTANDTSTE 1177
729 SLAESEASLGNNTNIPASDHYVGPNGFKSLAQEATRLAESHVESASNMQLTRETEDYSKQ 788
1178 AYNLLRLTL-----AGENCOTAFETIEELNRKYEAKNISQBLEKQAARVHEEAKRAGDK 1230
789 ALSVRKALHEGVGSGSPDGAV-VQGLVEKLEKTKSLAQQLTREATQAEIEADRSYQH 847
1231 AVEIYASVAQLSPLDSETLE-NEANNIKWEAENLEQLIDCKLKDYEDLREDMRGKELEVK 1289
848 SLRLDSVSPLOGVSDQSFQVEEAKRIKQKADSLSSLVTRHMDFFKRTQKXNLGNWKEEAQ 907
1290 NLLEKKGTEQQTADQLLARADAAKALAEAEAAKKGRDTLQEAANDILNNLKDFDRRVNDNKT 1349
908 QLLQNGKSGREKSDQLLSRANLAKSRAQEAALSMGNATFYEVESILKNLREFDLQVDNRKA 967
1350 AAEALRKIPAINQTITEANEKTEPAAQALGSAADAAATEAKXNKAHEAERIAASAVQKNATS 1409
968 EAEAMKRLSYISKVSDASDKTQQAERALGSAADAAQRAKNGAGEALEISSEIEQEIGS 1027
1410 TKAEARTFAEVTDLDNVNNMLKQLOEAEKELKRKQDDADQDMMAGMASQAAQAEAIN 1469
1028 LNLEANTADGALAMEKGLASLKSEMREVEGELEKELEFDTNMDAVQMVITEAQKVDTR 1087
1470 ARKAKNSVTSLLSIINDLLEQLGQLDVTDLNKLNEIEGILNKAKDEMKVSDLDLRKVSdle 1529
1088 AKNAGVTIQDTLNTLDGLLHMDQPLSVDEEGLVLLEQKLSRAKTOIN-SQLRPMSELE 1146
1530 NEAKHQEAAIMDYNRDIEEIMKDIRNLEDIRKTLPSGCFNTPSIEK 1575
1147 ERARQORGHLLHLETSIDGILADVKNLENIRDNLPPGCYNTQALEQ 1192

RESULT 14
US-08-800-593-13
; Sequence 13, Application US/08800593
; Patent No. 6143505
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Kallunki, Pekka
; APPLICANT: Pyke, Charles
; TITLE OF INVENTION: Laminin Chains: Diagnostic and
; TITLE OF INVENTION: Therapeutic Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800,593
; FILING DATE: 18-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/317,450
; FILING DATE: 04-OCT-1994

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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Chao, Mark
; REGISTRATION NUMBER: 37,293
; REFERENCE/DOCKET NUMBER: 94,778-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1193 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-800-593-13

Query Match      30.9%; Score 2637; DB 3; Length 1193;
Best Local Similarity 39.4%; Pred. No. 7.5e-145;
Matches 515; Conservative 235; Mismatches 418; Indels 138; Gaps 12;

Qy 286 CLPFFNDPWRRTAESASECLPCDCNCRSGQECYFDPELYRSTGHGHCNTCQDNTDGAH 345
Db 9 CLCFSLLLPAARATSRRE---VCDNCGKSRQCFIDRELHRTQGTNGFRCLNCNDNTDGIH 64
Qy 346 CERCRENFFRLGNNEACSSCHSPVGSLSQDSYGRCSCKPGVMGDKCDRCQPGFHSLT 405
Db 65 CEKCKNGFYRHRERDRCLPCNCNSKGSLSARCDNSGRCSCKPGVTGARCDRCLPGFHMILT 124
Qy 406 EAGC-----RPSCDPSGSIDECNVEVTCRCVCKDNVEGFNCERCKPGFFNLESSNPR 457
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Qy 458 GCTPCFCFGHSSVCTNAVGYSVYSSISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVI 517
Db 183 GCTQCFCYCHSASCRSSAEYSVHKITSTTFHQVDGWMKAVQRNGSPAKLQWSQRHQDVFS 242
Qy 518 SDSYFPRYFIAPAKFLGKQVLSYQNLFSFRVDRDRDTRLAEDLVLEGAGLRVSUPLIA 577
Db 243 AQRLDPVYFVAPAKFLGNQQVSYGQSLSFQYRDRGRHPSAHVDVILEGAGLRITAPLMP 302
Qy 578 QGNSYPSETTVKYVFRLEHATDYPWRPALTPPEFQKLLNLTISIKIRGTYSERSAGYLD 637
Db 303 LGKTLPCGLTKTYTFRLEHPSNNSWSPQSYFEYRLLRNLTLALRIRATYGEYSTGYIDN 362
Qy 638 VTLASARPGPGVPATWVESCTCPVYGGQFCBMLCSGYRRETNLGVPSPCVLACNGHS 697
Db 363 VTLISARPVSGAPAPWVEQICPVYKGFQFCQDCASGYKXDSARLGPFGTCIPCNCG-G 421
Qy 698 ETCDBETGVNCRDNTAGPHCEKCSGDYVYGDSTAGTSSDCQPCPCPGSSCAVVPKTEV 757
Db 422 GACDPDTGDCYSGDENPDIECADCPIGFYNDHPDRS--CKPCPCNGFSCSVIPETEEV 479
Qy 758 VCTNCTGTGTRKCELCDDGYFGDPLGRNGPVRLCRLCQCSNIDPNVAGNCNRLTGECL 817
Db 480 VCNPCPPGVGTGARCELADGYFGDPFGEHGPVPCPCQCNNSVDPASGNCDRLTGRCL 539
Qy 818 KCIYNTAGFYCDRCKDGFNPLAPNPADKCKACNCNPPYGTMKQQSSCNPVGTQCECLPH 877
Db 540 KCIHNTAGIYCDQCKAGYFGDPLAPNPADKCKACNCNPMGS----- 580
Qy 878 VTGQDCGACDPGFYNLQSQGCERCDCALGSTNGQCDIRTGQCECQPGITGQHCEV 937
Db 581 ----- 580
Qy 938 NHFGFPGCKPCDCHPEGSLSLQCKDDGRCECEBGFVGNRCQCEENFYNRSWPGCQE 997
Db 581 -----EPVG-----CRSDGTCTVCKPFGGPNCEH-----GAFS 608
Qy 998 CPACYRLVKDKVADHRVKLQLESLIANLGTGDMVTDQAFEDRLKEAREVMDLLREAQ 1057
Db 609 CPACYNQVKIQMDQFMQQLQRMALISKAQGGDGVVDPDTELEGRMQQAELQDILRDAQ 668
Qy 1058 DVKDVDQNLMDRLQRVNNTLSSQISRLQNIIRNTIETGNLAEQARAHVENTERLIEIASR 1117
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Db 669 ISEGASRSLGLQAKVRSQENSYSQSRLLDLKMTVERVRLGSGYQNRVDRDTHRLITQMQL 728
Qy 1118 ELEKAKVAAANVSVTQPESTGDPNNMTLLAAEEARKLAERHKQEAADDIVRVAKTANDTSTE 1177
Db 729 SLAESEASLGNITNPASDHYVGPNGFKSLAQEAATRLAESHVESASNNELTRETEDYSKQ 788
Qy 1178 AYNLLRLTL-----AGENQTAFEIEELNRYEQAKNISQDLEKQAARVHEEAKRAGDK 1230
Db 789 ALSLRKALHEGVSGSGSPDGAV-VQGLVEKLEKTKSLAQQLTREATQAEIEADRSYQH 847
Qy 1231 AVEIYASVAQLSPDLSETLE-NEANNIKMEABENLEQLIDQKLKDYEDLREDMRGKELEVK 1289
Db 848 SLRLLDVSPLOGVSDQSFQVEEAKRIKQKADSLSSLVTRHMDFFKRTQKNLGNWKEEAQ 907
Qy 1290 NLLEKKGTEQQTADQLLARADAALAEAAKKGDRDTLQEAANDILNNLKDFFRRVNDNKT 1349
Db 908 QLLQNGKSGREKSDQLLSRANLAKSRAQEAALSMGNATFYEVESILKNLREFDLQVDNRKA 967
Qy 1350 AAEEALRKIPAINQITTEANEKTRTAAQALGSAADAATAEKNAKHAHEARIASAVQKNATS 1409
Db 968 EAEEAMKRLSYTSQKVSADSKTQQAERALGSAADAQAKNGAGAELEISSEIEQEIGS 1027
Qy 1410 TKAEAEARTFAEVTDLNNEVNNMLKQLQEAEBELKCRKQDDADQDMMVAGMASQAQAEIN 1469
Db 1028 LNLEANTADGALAMEKGLASLKSEMRVEGELERKELEFDTNMDAVQMVITEAQKVDTR 1087
Qy 1470 ARKAKNSVTSLLSIINDLLEQLGQDVTDLNKLNEIEGTNLKAKDKMKVSDLDLDRKVSLE 1529
Db 1088 AKVAGVTIQDTLTLNLDGLLHMDQPLSVDEEGLVLLEQKLSRAKTQIN-SQLRPMSELE 1146
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RESULT 15
US-08-317-450B-15
; Sequence 15, Application US/08317450B
; Patent No. 5660982
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Kallunki, Pekka
; APPLICANT: Pyke, Charles
; TITLE OF INVENTION: Laminin Chains: Diagnostic and
; TITLE OF INVENTION: Therapeutic Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & ALLEGRETTI, LTD.
; STREET: Ten South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/317,450B
; FILING DATE: 04-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Chao, Mark
; REGISTRATION NUMBER: 37,293
; REFERENCE/DOCKET NUMBER: 94,778
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1111 amino acids
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-317-450B-15

Query Match 29.5%; Score 2516.5; DB 1; Length 1111;
Best Local Similarity 39.7%; Pred. No. 6.7e-138;
Matches 486; Conservative 215; Mismatches 385; Indels 137; Gaps 11;

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Db 9 CLCFSLLLPAARATSRRE---VCDNCGKSRQCIFDRELHRQTGNGFRCLNCNDNTDGIH 64

QY 346 CERCRENFRRLGNNEACSSCHCSPVGSLSLTCDSYGRCSCKPGVMGDKCDRCQCPGFHSLT 405
Db 65 CEKCKNGFYHRERDRCLPCNCNSKGSLSARCDNSGRCSCKPGVTGARCDRCLPGFHLT 124

QY 406 EAGC-----RPCSCDPGSGSIDEENVETGRCVCKDNVEGENCERCKPGFFNLESSNPR 457
Db 125 DAGCTQDQRLDLSKDCDCDPAGIAGPC--DAGRCVCKPAVTGERCDRCRSGYYNLDGGNPE 182

QY 458 GCTPCFCFGHSSVCTNAVGYSVYSISSTFQIDEDGWRAEQRDSEASLEWSSERQDIAVI 517
Db 183 GCTQCFCYGHSAACRSSAEYSVHKITSTFHDQVDGWKAVQRNPSPAKLQWSQRHQDVFS 242

QY 518 SDSYFPRYFTAPAKPLGKQVLSYQNLSPFSFRVDRDRTRLSAEDLVLEGAGLRVSVPLIA 577
Db 243 AQRLDPVYFVAPAKFLGNQOVSYGQSLSPDYRDRGGRHPSAHDVILEGAGLRITAPLMP 302

QY 578 QGNSYFSETTVKYVFRLLHEATDYPWRPALTPPEFQKLLNLTSTIKIRGTYSERSAGYLLDD 637
Db 303 LGKTLPCGLTKTYTFRLLNEHPSNNWSPOLSYFEYRLLRLNLTAIRATYGEYSTGYIDN 362

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QY 698 ETCDPETGVNCNRDNTAGPHCEKCSGDYGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTEV 757
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QY 758 VCTNCPTGTTGKRCCLDDGYFGDPLGRNGPVRLRLCQCSDNIDPNAVGNCRNLTGEC 817
Db 480 VCNNCPGVTGARCELADGYFGDPFGEHGPVRPCQPCQCNNSNVDPSASGNCRLTGRCL 539

QY 818 KCIYNTAGFYCDCKDGFNGNPLAPNPADKCKACNCPYGTMKQOSSCNPNVTGQCECLPH 877
Db 540 KCIHNTAGIYCDQCKAGYFGDPLAPNPADKCRACNCPMGS----- 580

QY 878 VTQDCGACDPGFYNLQSGQCERCDCCHALGSTNGQCDIRTGQCEQCPGITGQHCEV 937
Db 581 ----- 580

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Db 609 CPACYNQVKIQMDQFMQQLORMEALISKAQGGDGVVPDTELEGRMQQAEQALQDILRDAQ 668

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QY 1231 AVEIYASVAQLSPLDSETLE-NEANNIKWEAENLEQLIDQKLXDYEDLREDMRGKELEVK 1289
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QY 1350 AABEALRKIPAINQITITEANEKTRAQOALGSAADATEAKNKAHEAERIAASAVQKNATS 1409
Db 968 EAEEAMKRLSYISQKVSADSKTQQAERALGSAADAQRAKNGAGEALEISSEIEQEIGS 1027

QY 1410 TKAEAERTFAEVTDLDNEVNNMLKQLQBAEKELKRKQDDADQDMMWAGMASQAAQAEIN 1469
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QY 1470 ARKAKNSVTSLLSIINDLLEQLG 1492
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Job time : 18.9221 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:56:24 ; Search time 40.0948 Seconds
(without alignments)
10937.572 Million cell updates/sec

Title: US-10-037-182-16
Perfect score: 8544
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues
Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA:*
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
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 - 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
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 - 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
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 - 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
 - 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	8544	100.0	1576	14 US-10-037-182-16	Sequence 16, Appl
2	8544	100.0	1609	14 US-10-037-182-14	Sequence 14, Appl
3	8544	100.0	1609	14 US-10-299-058-12	Sequence 12, Appl
4	8540	100.0	1609	9 US-09-938-275-11	Sequence 11, Appl
5	8540	100.0	1609	15 US-10-372-683-36	Sequence 36, Appl
6	8056	94.3	1607	9 US-09-938-275-10	Sequence 10, Appl
7	8043	94.1	1605	14 US-10-037-182-18	Sequence 18, Appl
8	8038	94.1	1572	14 US-10-037-182-20	Sequence 20, Appl
9	3600	42.1	1587	9 US-09-845-583-10	Sequence 10, Appl
10	3600	42.1	1587	12 US-10-262-839-210	Sequence 210, App
11	3598	42.1	1575	12 US-10-262-839-212	Sequence 212, App
12	3240	37.9	1557	15 US-10-369-493-6816	Sequence 6816, Ap
13	2637	30.9	1193	9 US-09-756-0718-13	Sequence 13, Appl
14	2637	30.9	1193	12 US-10-392-113-14	Sequence 14, Appl
15	2637	30.9	1193	14 US-10-171-311-115	Sequence 115, App

16	2637	30.9	1193	14	US-10-227-738-13	Sequence 13, Appl
17	2637	30.9	1193	14	US-10-053-662A-31	Sequence 31, Appl
18	2637	30.9	1193	15	US-10-295-027-390	Sequence 390, App
19	2637	30.9	1193	15	US-10-295-027-1269	Sequence 1269, Ap
20	2637	30.9	1193	15	US-10-603-725-26	Sequence 26, Appl
21	2637	30.9	1193	16	US-10-188-832-147	Sequence 147, App
22	2630	30.8	1172	15	US-10-603-725-28	Sequence 28, Appl
23	2629	30.8	1193	15	US-10-603-725-30	Sequence 30, Appl
24	2622	30.7	1172	15	US-10-603-725-32	Sequence 32, Appl
25	2612.5	30.6	1190	14	US-10-053-662A-2	Sequence 2, Appl
26	2516.5	29.5	1111	9	US-09-756-0718-15	Sequence 15, Appl
27	2516.5	29.5	1111	12	US-10-392-113-15	Sequence 15, Appl
28	2516.5	29.5	1111	14	US-10-227-738-15	Sequence 15, Appl
29	2454.5	28.7	1171	15	US-10-603-725-36	Sequence 36, Appl
30	2454.5	28.7	1192	12	US-10-392-113-12	Sequence 12, Appl
31	2454.5	28.7	1192	14	US-10-053-662A-32	Sequence 32, Appl
32	2454.5	28.7	1192	15	US-10-603-725-34	Sequence 34, Appl
33	1782.5	20.9	3084	9	US-09-938-275-4	Sequence 4, Appl
34	1782.5	20.9	3084	14	US-10-262-670-2	Sequence 2, Appl
35	1776	20.8	3070	10	US-09-961-403-7	Sequence 7, Appl
36	1726	20.2	3075	9	US-09-938-275-5	Sequence 5, Appl
37	1673	19.6	1765	14	US-10-037-182-8	Sequence 8, Appl
38	1673	19.6	1786	9	US-09-873-676-113	Sequence 113, App
39	1673	19.6	1786	9	US-09-938-275-6	Sequence 6, Appl
40	1673	19.6	1786	14	US-10-037-182-6	Sequence 6, Appl
41	1643	19.2	1786	9	US-09-938-275-7	Sequence 7, Appl
42	1643	19.2	1786	14	US-10-037-182-10	Sequence 10, Appl
43	1626.5	19.0	2823	15	US-10-369-493-5220	Sequence 5220, Ap
44	1626.5	19.0	2823	15	US-10-369-493-5221	Sequence 5221, Ap
45	1622.5	19.0	1725	14	US-10-037-182-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-10-037-182-16
; Sequence 16, Application US/10037182
; Publication No. US20030044899A1
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Doi, Masayuki
; APPLICANT: Thyboll, Jill
; TITLE OF INVENTION: Recombinant Laminin 10
; FILE REFERENCE: 99-274-F
; CURRENT APPLICATION NUMBER: US/10/037,182
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,449
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/279,282
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 1576
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-037-182-16

Query Match	100.0%;	Score 8544;	DB 14;	Length 1576;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1576;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	QAAMDECTDEGGRPCRCMPEFVNAAFNVVVAINTCGTPPEEYCVQGTGVTGTSCHLCD	60	
Db	1	QAAMDECTDEGGRPCRCMPEFVNAAFNVVVAINTCGTPPEEYCVQGTGVTGTSCHLCD	60	
Qy	61	AGQPHLQHGAAFLTDYNNQADTTWQQTMLAGVQYPPSSINLTLLGKAFDITYVRLKFH	120	
Db	61	AGQPHLQHGAAFLTDYNNQADTTWQQTMLAGVQYPPSSINLTLLGKAFDITYVRLKFH	120	
Qy	121	TSRPESFAIYKTRFDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDIS	180	

Db 121 TSRPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDIS 180
QY 181 PLTGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNRLNLTGDEVENDPKVLKSY 240
Db 181 PLTGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNRLNLTGDEVENDPKVLKSY 240
QY 241 YYAISDFAVGRCCKNGHASECMKNEFDKLVNCNKNTYGVDCCKLCPFFNDPWRATA 300
Db 241 YYAISDFAVGRCCKNGHASECMKNEFDKLVNCNKNTYGVDCCKLCPFFNDPWRATA 300
QY 301 ESASECLPCDNGRSQECYFDPYELYSTGHGHCNTCQDNTDGAHCERCENFRRLGNE 360
Db 301 ESASECLPCDNGRSQECYFDPYELYSTGHGHCNTCQDNTDGAHCERCENFRRLGNE 360
QY 361 ACSSCHCSPVGSLSLSTQDSYGRCSCKPGVMGDKCDRCQPGFHSLSLTAAGCRPCSCDPSGSI 420
Db 361 ACSSCHCSPVGSLSLSTQDSYGRCSCKPGVMGDKCDRCQPGFHSLSLTAAGCRPCSCDPSGSI 420
QY 421 DECNVETGRVCCKDNVEGFNCERCCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGSYVY 480
Db 421 DECNVETGRVCCKDNVEGFNCERCCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGSYVY 480
QY 481 SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY 540
Db 481 SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY 540
QY 541 GQNLFSFRVDRDRTRLAEDLVLEGAGLRVSVPVLIAGNSYSPSETTVKYVFLRHEATDY 600
Db 541 GQNLFSFRVDRDRTRLAEDLVLEGAGLRVSVPVLIAGNSYSPSETTVKYVFLRHEATDY 600
QY 601 PWRPALTPFEFQKLLNLTSLIKINGTYSERSAGYLDVTLASARPGVPGVATWVESCTCP 660
Db 601 PWRPALTPFEFQKLLNLTSLIKINGTYSERSAGYLDVTLASARPGVPGVATWVESCTCP 660
QY 661 VGYGGQFCMCLSGYRRETNPNGSPCVLCAACNGHSETCDPETGVCNCRDNTAGPHCEK 720
Db 661 VGYGGQFCMCLSGYRRETNPNGSPCVLCAACNGHSETCDPETGVCNCRDNTAGPHCEK 720
QY 721 CSDGYGDSFAGTSSDCQPCPCPGSSCAVVPKTKVCTNCPTGTTGKCELCDDGYFG 780
Db 721 CSDGYGDSFAGTSSDCQPCPCPGSSCAVVPKTKVCTNCPTGTTGKCELCDDGYFG 780
QY 781 DPLGRNGPVRCLRLCQCSNDIDNAVGNCRNLTGECCLKIYNTAGFYCDRCCKDGFNPL 840
Db 781 DPLGRNGPVRCLRLCQCSNDIDNAVGNCRNLTGECCLKIYNTAGFYCDRCCKDGFNPL 840
QY 841 APNPADKCKACNCPYGTMKQSSCNPVGTQCECLPHVTGQDCGACDPGFYNLQSGQGE 900
Db 841 APNPADKCKACNCPYGTMKQSSCNPVGTQCECLPHVTGQDCGACDPGFYNLQSGQGE 900
QY 901 RCDHALGSTNGQCDIRTGQCEQPGITGQHCEVNHFGFGEKPCDCHPEGSLSL 960
Db 901 RCDHALGSTNGQCDIRTGQCEQPGITGQHCEVNHFGFGEKPCDCHPEGSLSL 960
QY 961 QCKODGRCEGREGFVGNRCDCQCEENYFYNRSWPGQCECPACYRLVKDVADHRVKLQELE 1020
Db 961 QCKODGRCEGREGFVGNRCDCQCEENYFYNRSWPGQCECPACYRLVKDVADHRVKLQELE 1020
QY 1021 SLIANLGTGDEMVTDOAFEDRLKEAREVMDLLREAQDVQKVDQNLMDRLQRVNTLSSQ 1080
Db 1021 SLIANLGTGDEMVTDOAFEDRLKEAREVMDLLREAQDVQKVDQNLMDRLQRVNTLSSQ 1080
QY 1081 ISRLQNTIRNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1140
Db 1081 ISRLQNTIRNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1140
QY 1141 NNMTLLAEEARKLAERHKQEAADDIVRVAKTANDTSTEAYNLLRLTLAGENQTAFEIEELN 1200
Db 1141 NNMTLLAEEARKLAERHKQEAADDIVRVAKTANDTSTEAYNLLRLTLAGENQTAFEIEELN 1200
QY 1201 RKYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDSETLEANEANNIKMEA 1260
Db 1201 RKYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDSETLEANEANNIKMEA 1260

QY 1261 ENLEQLIDQKLDYEDLREDMRGKELEVKNLLEKKGTEQQTADQLLARADAALAEAEA 1320
Db 1261 ENLEQLIDQKLDYEDLREDMRGKELEVKNLLEKKGTEQQTADQLLARADAALAEAEA 1320
QY 1321 KKGRTDLOEANDILNNLKDFDRRVNDNKTAEEALRKIPAINQITTEANEKTRAQOALG 1380
Db 1321 KKGRTDLOEANDILNNLKDFDRRVNDNKTAEEALRKIPAINQITTEANEKTRAQOALG 1380
QY 1381 SAAADATEAKNKAHEABERIASAVQKNATSTKABAEARTFAEVTDLDNVNNMLKQLOEABK 1440
Db 1381 SAAADATEAKNKAHEABERIASAVQKNATSTKABAEARTFAEVTDLDNVNNMLKQLOEABK 1440
QY 1441 ELKRRKQDDADQDMMAGMASQAAQAEAEINARKAKNSVTSLLSIINDLLEQLGQDVTVDLN 1500
Db 1441 ELKRRKQDDADQDMMAGMASQAAQAEAEINARKAKNSVTSLLSIINDLLEQLGQDVTVDLN 1500
QY 1501 KLNIEIEGTLNKADEMKSVDLDRKVSVDLENEAKKQEAAMINDYNRDIEEIMKDIRNLEDIR 1560
Db 1501 KLNIEIEGTLNKADEMKSVDLDRKVSVDLENEAKKQEAAMINDYNRDIEEIMKDIRNLEDIR 1560
QY 1561 KTLPSGCFNTPSIEKP 1576
Db 1561 KTLPSGCFNTPSIEKP 1576

RESULT 2

US-10-037-182-14
; Sequence 14, Application US/10037182
; Publication No. US20030044899A1
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Doi, Masayuki
; APPLICANT: Thyboll, Jill
; TITLE OF INVENTION: Recombinant Laminin 10
; FILE REFERENCE: 99-274-F
; CURRENT APPLICATION NUMBER: US/10/037,182
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,449
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/279,282
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent in ver. 2.0
; SEQ ID NO 14
; LENGTH: 1609
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-037-182-14

Query Match 100.0%; Score 8544; DB 14; Length 1609;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QAAMDECTDEGRPQRCMPEFVNAAFNVTVATNTCGTPPEEYCVQTVGTGTSCHLCD 60
Db 34 QAAMDECTDEGRPQRCMPEFVNAAFNVTVATNTCGTPPEEYCVQTVGTGTSCHLCD 93
QY 61 AGQPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYPSINLTLLHKGAFDITYVRLKHF 120
Db 94 AGQPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYPSINLTLLHKGAFDITYVRLKHF 153
QY 121 TSRPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDIS 180
Db 154 TSRPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDIS 213
QY 181 PLTGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNRLNLTGDEVFNDPKVLKSY 240
Db 214 PLTGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNRLNLTGDEVFNDPKVLKSY 273
QY 241 YYAISDFAVGRCCKNGHASECMKNEFDKLVNCNKNTYGVDCCKLCPFFNDPWRATA 300
Db 274 YYAISDFAVGRCCKNGHASECMKNEFDKLVNCNKNTYGVDCCKLCPFFNDPWRATA 333

QY 301 ESASECLPCDCNGRSQECYFDPFLYRSTGHGGHCTNCODNTDGAHCRCRENFFRLGNNE 360
DB 334 ESASECLPCDCNGRSQECYFDPFLYRSTGHGGHCTNCODNTDGAHCRCRENFFRLGNNE 393
QY 361 ACSSCHCSPVGSLSLSTQCDYSYGRCSCKPGVMGDKCDRCQCPGFHSLTEAGCRPCSDPSSGI 420
DB 394 ACSSCHCSPVGSLSLSTQCDYSYGRCSCKPGVMGDKCDRCQCPGFHSLTEAGCRPCSDPSSGI 453
QY 421 DECNVETGRVCCKDNVEGFNCERCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGSYVY 480
DB 454 DECNVETGRVCCKDNVEGFNCERCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGSYVY 513
QY 481 SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY 540
DB 514 SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY 573
QY 541 GQNLSPFRVDRDRTRLRLSAEDLVLEGAGLRVSVPLIAQGNSSYPSETTVKYVFRLEHATDY 600
DB 574 GQNLSPFRVDRDRTRLRLSAEDLVLEGAGLRVSVPLIAQGNSSYPSETTVKYVFRLEHATDY 633
QY 601 PWRPALTPFEFQKLLNLTLSIKIRGTYSERSAGYLDVTLASARPGPGVPATWVESCCTCP 660
DB 634 PWRPALTPFEFQKLLNLTLSIKIRGTYSERSAGYLDVTLASARPGPGVPATWVESCCTCP 693
QY 661 VYGGQFCMCLSGYRRETPLNLPYSPCVLCAACNGHSETCDPBTGVNCNRDNTAGHCEK 720
DB 694 VYGGQFCMCLSGYRRETPLNLPYSPCVLCAACNGHSETCDPBTGVNCNRDNTAGHCEK 753
QY 721 CSDGYGDSSTAGTSSDCQPCPGSSCAVVPKTEVVCTNCTGTGKRCCELDDGYFG 780
DB 754 CSDGYGDSSTAGTSSDCQPCPGSSCAVVPKTEVVCTNCTGTGKRCCELDDGYFG 813
QY 781 DPLGRNGPVRCLRCQCSNDIDPNVAGNCNRLTGECLKCIYNTAGFYCDRCCKDGGFFGNPL 840
DB 814 DPLGRNGPVRCLRCQCSNDIDPNVAGNCNRLTGECLKCIYNTAGFYCDRCCKDGGFFGNPL 873
QY 841 APNPADKCKACNCPYGMTKQSSCNPTVGTQCECLPHVTGDCGACDPPGFYNLQSGQSGE 900
DB 874 APNPADKCKACNCPYGMTKQSSCNPTVGTQCECLPHVTGDCGACDPPGFYNLQSGQSGE 933
QY 901 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCHERCEVNHFGFPGCKPCDCHPEGSLSL 960
DB 934 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCHERCEVNHFGFPGCKPCDCHPEGSLSL 993
QY 961 QCKDDGRCECEGFVGNRCDQCEENYFYNRSPWPGCECPACVRLVKDKVADHRVKLQELE 1020
DB 994 QCKDDGRCECEGFVGNRCDQCEENYFYNRSPWPGCECPACVRLVKDKVADHRVKLQELE 1053
QY 1021 SLIANLGTGDMVTDOAFEDRLKEAEREVMDLLREAQDVKDQVNDQMLDRLQRVNNTLSQ 1080
DB 1054 SLIANLGTGDMVTDOAFEDRLKEAEREVMDLLREAQDVKDQVNDQMLDRLQRVNNTLSQ 1113
QY 1081 ISRLQNIIRNTIIBETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1140
DB 1114 ISRLQNIIRNTIIBETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1173
QY 1141 NNMTLLEAEARKLAERHKEADDIIVRVAKTANDTSTEAYNLLRLTLAGENQTAFEIEELN 1200
DB 1174 NNMTLLEAEARKLAERHKEADDIIVRVAKTANDTSTEAYNLLRLTLAGENQTAFEIEELN 1233
QY 1201 RKYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDSETLENEANNIKMEA 1260
DB 1234 RKYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDSETLENEANNIKMEA 1293
QY 1261 ENLEQLIDQKLDYEDLREDMRGKELEVKNLLEKKGKTEQQTADQLLARADAAKALAEAAA 1320
DB 1294 ENLEQLIDQKLDYEDLREDMRGKELEVKNLLEKKGKTEQQTADQLLARADAAKALAEAAA 1353
QY 1321 KKGRDTLQEAANDILNNLKDFDRRVNDNKTAAEALRKIPAINQTTIETANEKTRTAAQALG 1380
DB 1354 KKGRDTLQEAANDILNNLKDFDRRVNDNKTAAEALRKIPAINQTTIETANEKTRTAAQALG 1413

QY 1381 SAAADATEAKNKAHEAERIAASAVQKNATSTKAEARTFAEVTDLNEVNNMLKQLOEAEK 1440
DB 1414 SAAADATEAKNKAHEAERIAASAVQKNATSTKAEARTFAEVTDLNEVNNMLKQLOEAEK 1473
QY 1441 ELKXKQDDADQDMMAGMASQAQAEAEINARKAKNSVTSLLSIINDLLEQLGQDITVDLN 1500
DB 1474 ELKXKQDDADQDMMAGMASQAQAEAEINARKAKNSVTSLLSIINDLLEQLGQDITVDLN 1533
QY 1501 KLNEIEGTLNKADEMKSVDLDRKVSVDLENEAKKQEAAMVNRDIEEIMKDIRNLEDIR 1560
DB 1534 KLNEIEGTLNKADEMKSVDLDRKVSVDLENEAKKQEAAMVNRDIEEIMKDIRNLEDIR 1593
QY 1561 KTLPSGCCFNTPSIEKP 1576
DB 1594 KTLPSGCCFNTPSIEKP 1609

RESULT 3
US-10-299-058-12
; Sequence 12, Application US/10299058
; Publication No. US20030103975A1
; GENERAL INFORMATION:
; APPLICANT: JONES, JONATHAN C.R.
; APPLICANT: GONZALES, MEREDITH
; TITLE OF INVENTION: MODULATION OF ANGIOGENESIS AND ENDOTHELIALIZATION
; FILE REFERENCE: 1720-1-002 CIP
; CURRENT APPLICATION NUMBER: US/10/299,058
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/706,235
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: 60/163,199
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1609
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-299-058-12

Query Match 100.0%; Score 8544; DB 14; Length 1609;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QAAMDECTDEGGRPQRCMPEFVNAAFNVTVATNTCGTPPEEYCVQGTGVTGKSCHLCD 60
DB 34 QAAMDECTDEGGRPQRCMPEFVNAAFNVTVATNTCGTPPEEYCVQGTGVTGKSCHLCD 93
QY 61 AGQPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYPSINLTLHLGKAFDITYVRLKPH 120
DB 94 AGQPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYPSINLTLHLGKAFDITYVRLKPH 153
QY 121 TSRPESFAIYKRTREDGPWIPYQYVYSGSCENTYSKANRGFIRTGDEQQAALCTDEFSDIS 180
DB 154 TSRPESFAIYKRTREDGPWIPYQYVYSGSCENTYSKANRGFIRTGDEQQAALCTDEFSDIS 213
QY 181 PLTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSY 240
DB 214 PLTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSY 273
QY 241 YYAISDFAVGGRCKNGHASECMKNEFDKLVNCKHNTYGVDCCKLPFFNDRPWRRATA 300
DB 274 YYAISDFAVGGRCKNGHASECMKNEFDKLVNCKHNTYGVDCCKLPFFNDRPWRRATA 333
QY 301 ESASECLPCDCNGRSQECYFDPPELYRSTGHGGHCTNCQDNTDGAHCRCRENFFRLGNNE 360
DB 334 ESASECLPCDCNGRSQECYFDPPELYRSTGHGGHCTNCQDNTDGAHCRCRENFFRLGNNE 393
QY 361 ACSSCHCSPVGSLSLSTQCDYSYGRCSCKPGVMGDKCDRCQCPGFHSLTEAGCRPCSDPSSGI 420
DB 394 ACSSCHCSPVGSLSLSTQCDYSYGRCSCKPGVMGDKCDRCQCPGFHSLTEAGCRPCSDPSSGI 453
QY 421 DECNVETGRVCCKDNVEGFNCERCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGSYVY 480

new may 19 10:47:30 2004

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Db      454  DECNVETGRVCCKDNVEGFNCERCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGSYVY 513
QY      481  SISSTFQIDEDGWAEQRDGEASLEWSSERQDIAVISDSYFPFYFIAPAKFLGKQVLSY 540
Db      514  SISSTFQIDEDGWAEQRDGEASLEWSSERQDIAVISDSYFPFYFIAPAKFLGKQVLSY 573
QY      541  GQNLFSFRVDRDTRLASAEDLVLEGAGLRVSVPLIAQGNYSVPSETTVKYVFRLEHATDY 600
Db      574  GQNLFSFRVDRDTRLASAEDLVLEGAGLRVSVPLIAQGNYSVPSETTVKYVFRLEHATDY 633
QY      601  PWRPALTPFEFQKLLNNLTSIKIRGTYSERSAGYLDVTLASARPGPGVPATWVESCTCP 660
Db      634  PWRPALTPFEFQKLLNNLTSIKIRGTYSERSAGYLDVTLASARPGPGVPATWVESCTCP 693
QY      661  VGYGGQFCMCLSGYRRETNPNGPSPCYLCAACNGHSETCDPETGVCNCRDNTAGPHCEK 720
Db      694  VGYGGQFCMCLSGYRRETNPNGPSPCYLCAACNGHSETCDPETGVCNCRDNTAGPHCEK 753
QY      721  CSDGYYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKEVVCTNCPTGTTGRCCELCDGYPG 780
Db      754  CSDGYYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKEVVCTNCPTGTTGRCCELCDGYPG 813
QY      781  DPLGRNGPVRCLRCQCSNDIDPNAVGCNRLTGECLKCIYNTAGFYCDRCKDGFNGNPL 840
Db      814  DPLGRNGPVRCLRCQCSNDIDPNAVGCNRLTGECLKCIYNTAGFYCDRCKDGFNGNPL 873
QY      841  APNPADKCKACNCNPGYGTMTKQSSCNPNVTGQCECLPHVTGQDCGACDPGFYNLQSGQGE 900
Db      874  APNPADKCKACNCNPGYGTMTKQSSCNPNVTGQCECLPHVTGQDCGACDPGFYNLQSGQGE 933
QY      901  RCDCHALGSTNGQCDIRTGQCECQPGITGQHCHERCCEVNHFGFEGCKPCDCHPEGSLSL 960
Db      934  RCDCHALGSTNGQCDIRTGQCECQPGITGQHCHERCCEVNHFGFEGCKPCDCHPEGSLSL 993
QY      961  QCKDDGRCECREGFVGNRCDQCEENYFYNRSPWPGQCECPACRYLVKDKVADHRVKLQELE 1020
Db      994  QCKDDGRCECREGFVGNRCDQCEENYFYNRSPWPGQCECPACRYLVKDKVADHRVKLQELE 1053
QY     1021  SLIANLGTGDEMVTDOAFEDRLKEAREVMDLLREAQDVKDVQDQNLMDRLQRVNNTLSQ 1080
Db     1054  SLIANLGTGDEMVTDOAFEDRLKEAREVMDLLREAQDVKDVQDQNLMDRLQRVNNTLSQ 1113
QY     1081  ISRLQNIIRNTIETGCLNLAEOARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1140
Db     1114  ISRLQNIIRNTIETGCLNLAEOARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1173
QY     1141  NMNTLLAEARKLAERHKQEAADDIVRVAKTANDTSTEAYNLLRLTLAGENQTAFEIEELN 1200
Db     1174  NMNTLLAEARKLAERHKQEAADDIVRVAKTANDTSTEAYNLLRLTLAGENQTAFEIEELN 1233
QY     1201  RKYEQAKNISQDLEKQAARVHEEAKRAGDKAVEIYASVAQLSPLDSETLENEANNIKMEA 1260
Db     1234  RKYEQAKNISQDLEKQAARVHEEAKRAGDKAVEIYASVAQLSPLDSETLENEANNIKMEA 1293
QY     1261  ENLEQLIDQKLKDYEDLREDMRGKELEVKNLLEKKGTEQQTADQLLARADAAKALAEAEA 1320
Db     1294  ENLEQLIDQKLKDYEDLREDMRGKELEVKNLLEKKGTEQQTADQLLARADAAKALAEAEA 1353
QY     1321  KKGRDTLQEAANDILNNLKDFDRRVNDNKTAAEEALRKIPAINQITTEANEKTRTAQQAALG 1380
Db     1354  KKGRDTLQEAANDILNNLKDFDRRVNDNKTAAEEALRKIPAINQITTEANEKTRTAQQAALG 1413
QY     1381  SAAADATEAKNKAHEABERIASAVQKNATSTKAAEAERTFAEVTDLNEVNNMLKQLQEAEK 1440
Db     1414  SAAADATEAKNKAHEABERIASAVQKNATSTKAAEAERTFAEVTDLNEVNNMLKQLQEAEK 1473
QY     1441  ELKRKQDDADQDMVMAGMASQAAQEAENAPKAKNSVTSLLSIINDLLEQLGLDITVDLN 1500
Db     1474  ELKRKQDDADQDMVMAGMASQAAQEAENAPKAKNSVTSLLSIINDLLEQLGLDITVDLN 1533
QY     1501  KLINEIEGTLNKAKDEMKSVDLDRKVSQDLENEAKKQEAAIMDYNRDIIEIMKDIRNLEDIR 1560
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Db      1534  KLINEIEGTLNKAKDEMKSVDLDRKVSQDLENEAKKQEAAIMDYNRDIIEIMKDIRNLEDIR 1593
QY      1561  KTLPSGCFNTPSIEKP 1576
Db      1594  KTLPSGCFNTPSIEKP 1609

RESULT 4
US-09-938-275-11
; Sequence 11, Application US/09938275
; Patent No. US20020111309A1
; GENERAL INFORMATION:
; APPLICANT: Gerardo Castillo
; APPLICANT: Alan Snow
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications
; TITLE OF INVENTION: of Laminin and Laminin-Derived Protein Fragments
; FILE REFERENCE: PROTEO.P03
; CURRENT APPLICATION NUMBER: US/09/938,275
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1609
; TYPE: PRT
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Swissprot P11047
; DATABASE ENTRY DATE: 1991-11-01
US-09-938-275-11
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Query Match      100.0%; Score 8540; DB 9; Length 1609;
Best Local Similarity 99.9%; Pred.No. 0;
Matches 1575; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  QAAMDECTDEGRPQRCMPPEFVNAAFNVTVATNTCGTPPEEYCVQTGVTGKSCHLCD 60
Db      34  QAAMDECTDEGRPQRCMPPEFVNAAFNVTVATNTCGTPPEEYCVQTGVTGKSCHLCD 93
QY      61  AGQPHLQHGAALFTDYNNOADTTWQSQTMLAGVQYPPSSINLTILHLGKAFDITYVRLKFH 120
Db      94  AGQPHLQHGAALFTDYNNOADTTWQSQTMLAGVQYPPSSINLTILHLGKAFDITYVRLKFH 153
QY     121  TSRPESFAIYKRTREDGPWIPYQYYSGSCENTYSKANRGFIRTCGDEQQAALCTDEFSDIS 180
Db     154  TSRPESFAIYKRTREDGPWIPYQYYSGSCENTYSKANRGFIRTCGDEQQAALCTDEFSDIS 213
QY     181  PLTGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSY 240
Db     214  PLTGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSY 273
QY     241  YYAISDFAVGGRCKCNHGHASECMKNEFDKLVNCKHNTYGVDCCKCLPFFNDRPWRRA 300
Db     274  YYAISDFAVGGRCKCNHGHASECMKNEFDKLVNCKHNTYGVDCCKCLPFFNDRPWRRA 333
QY     301  ESASECLPCDCNCRSQECYFDPPELYRSTGHGGHCTNCQDNTDGAHCRCRENFRLGNNE 360
Db     334  ESASECLPCDCNCRSQECYFDPPELYRSTGHGGHCTNCQDNTDGAHCRCRENFRLGNNE 393
QY     361  ACSSCHCSPVGSLSSTQDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSDPSGSI 420
Db     394  ACSSCHCSPVGSLSSTQDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSDPSGSI 453
QY     421  DECNVETGRVCCKDNVEGFNCERCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGSYVY 480
Db     454  DECNVETGRVCCKDNVEGFNCERCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGSYVY 513
QY     481  SISSTFQIDEDGWAEQRDGEASLEWSSERQDIAVISDSYFPFYFIAPAKFLGKQVLSY 540
Db     514  SISSTFQIDEDGWAEQRDGEASLEWSSERQDIAVISDSYFPFYFIAPAKFLGKQVLSY 573
QY     541  GQNLFSFRVDRDTRLASAEDLVLEGAGLRVSVPLIAQGNYSVPSETTVKYVFRLEHATDY 600
Db     574  GQNLFSFRVDRDTRLASAEDLVLEGAGLRVSVPLIAQGNYSVPSETTVKYVFRLEHATDY 633
```


601 PWRPALTPEFQKLLNNLTSIKIRGTYSERSAGYLDVTLASARPGPGVPATWVESCTCP 660
634 PWRPALTPEFQKLLNNLTSIKIRGTYSERSAGYLDVTLASARPGPGVPATWVESCTCP 693
661 VGYGGQFCMCLSGYRRETPNLGYPSPCVLCACNGHSETCDPETGVCNCRDNTAGPHCEK 720
694 VGYGGQFCMCLSGYRRETPNLGYPSPCVLCACNGHSETCDPETGVCNCRDNTAGPHCEK 753
721 CSDGYGDSGTAGTSSDCQPCPCPGSSCAVVPKTKEVVCTNCPTGTTGKRCELCDGYFG 780
754 CSDGYGDSGTAGTSSDCQPCPCPGSSCAVVPKTKEVVCTNCPTGTTGKRCELCDGYFG 813
781 DPLGRNGVRLCRLCQCSNDNIDPNAVGNCRNLTGCECLKCIYNTAGFYCDRCKDGFEGNPL 840
814 DPLGRNGVRLCRLCQCSNDNIDPNAVGNCRNLTGCECLKCIYNTAGFYCDRCKDGFEGNPL 873
841 APNPADKCKACNCNPGYTMKQOSSCNPVVTGQCECLPHVTGQDCGACDPGFYNLQSGGCE 900
874 APNPADKCKACNCNPGYTMKQOSSCNPVVTGQCECLPHVTGQDCGACDPGFYNLQSGGCE 933
901 RCDCHALGSTNGQCDIRTGQCECQPGITGOHCERCEVNHFGFEGCKPCDCHPEGSLSL 960
934 RCDCHALGSTNGQCDIRTGQCECQPGITGOHCERCEVNHFGFEGCKPCDCHPEGSLSL 993
961 QCKDDGRCECREGFGVGNRCDQCEENFYNRSWPGCQCPACVRLVKDVADHRVKLOELE 1020
994 QCKDDGRCECREGFGVGNRCDQCEENFYNRSWPGCQCPACVRLVKDVADHRVKLOELE 1053
1021 SLIANLGTGDEMVTDOAFEDRLKEAREVMDLLREAOQVVDQVQVNDLQRLQVNNLTSSQ 1080
1054 SLIANLGTGDEMVTDOAFEDRLKEAREVMDLLREAOQVVDQVQVNDLQRLQVNNLTSSQ 1113
1081 ISRLQNRNTIETGNLAEOQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1140
1114 ISRLQNRNTIETGNLAEOQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1173
1141 NMTLLAEARKLAERHKQEAADDIVRVAKTANDTSTEAYNLLRLTLAGENQTAFEIEELN 1200
1174 NMTLLAEARKLAERHKQEAADDIVRVAKTANDTSTEAYNLLRLTLAGENQTAFEIEELN 1233
1201 RKYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDSETLENEANNIKMEA 1260
1234 RKYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDSETLENEANNIKMEA 1293
1261 ENLEQLIDOKLDYEDLREDMRGKELEVKNLLEKKGTEQQTADQLLARADAALAEAAA 1320
1294 ENLEQLIDOKLDYEDLREDMRGKELEVKNLLEKKGTEQQTADQLLARADAALAEAAA 1353
1321 KKGRTDLOEANDILNNLKDFDRRVNDNKTAAEEALRKIPAINQTI TEANEKTREAOQALG 1380
1354 KKGRTDLOEANDILNNLKDFDRRVNDNKTAAEEALRKIPAINQTI TEANEKTREAOQALG 1413
1381 SAAADATEAKNKAHEAERIAASAVQKNATSTKAAEAERTFAEVTDL DNEVNNMLKQLOEAEK 1440
1414 SAAADATEAKNKAHEAERIAASAVQKNATSTKAAEAERTFAEVTDL DNEVNNMLKQLOEAEK 1473
1441 ELKRRKQDDADQDMMAGMASQAAQAEAEINARKAKNSVTSLLSIINDLLEQLGQDITVDLN 1500
1474 ELKRRKQDDADQDMMAGMASQAAQAEAEINARKAKNSVTSLLSIINDLLEQLGQDITVDLN 1533
1501 KLNEIEGTLNKAKDEMKSVDLDRKVSDDLNEAKKQEAAMNDYNRDIEEIMKDIRNLEDIR 1560
1534 KLNEIEGTLNKAKDEMKSVDLDRKVSDDLNEAKKQEAAMNDYNRDIEEIMKDIRNLEDIR 1593
1561 KTLPSGCCFNTPSIEKP 1576
1594 KTLPSGCCFNTPSIEKP 1609

RESULT 5

US-10-372-683-36

; Sequence 36, Application US/10372683

; Publication No. US20040009171A1
; GENERAL INFORMATION:
; APPLICANT: GERRITSEN, MARY E.
; APPLICANT: PEALE JR., FRANKLIN V.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA
; FILE REFERENCE: P1928R1P1
; CURRENT APPLICATION NUMBER: US/10/372,683
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 10/271,690
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/344,534
; PRIOR FILING DATE: 2001-10-18
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 36
; LENGTH: 1609
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-372-683-36

Query Match 100.0%; Score 8540; DB 15; Length 1609;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1575; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QAAMDECTDEGGRPQRCMPEFVNAFNVTVATNTCGTPPEEYCVQGTGVTGVTKSCHLCD 60
Db 34 QAAMDECTDEGGRPQRCMPEFVNAFNVTVATNTCGTPPEEYCVQGTGVTGVTKSCHLCD 93
QY 61 AGQPHLQHGAFLTDYNNQADTTWQSTMLAGVQYPSINLTLHLGKAFDITYVRLKFH 120
Db 94 AGQPHLQHGAFLTDYNNQADTTWQSTMLAGVQYPSINLTLHLGKAFDITYVRLKFH 153
QY 121 TSRPESFAIYKRTREDGWPWIPYQYVSGSCENTYSKANRGFIRTTGGDEQALCTDEFSDIS 180
Db 154 TSRPESFAIYKRTREDGWPWIPYQYVSGSCENTYSKANRGFIRTTGGDEQALCTDEFSDIS 213
QY 181 PLTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSY 240
Db 214 PLTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSY 273
QY 241 YYAISDFAVGGRCKCNHASECMKNEFDKLVNCCKHNTYGVDCCKLPFFNDRPWRRATA 300
Db 274 YYAISDFAVGGRCKCNHASECMKNEFDKLVNCCKHNTYGVDCCKLPFFNDRPWRRATA 333
QY 301 ESASECLPCDCNGRSQECYFDPPELYRSTGHGHCNTCQDNTDGAHCRCRENFRLGNNE 360
Db 334 ESASECLPCDCNGRSQECYFDPPELYRSTGHGHCNTCQDNTDGAHCRCRENFRLGNNE 393
QY 361 ACSSCHCSPVGSLSLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSI 420
Db 394 ACSSCHCSPVGSLSLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSI 453
QY 421 DECNVETGRCVCKDNVEGFNCERCCKPFFNLESNPRGCTPCFCFGHSSVCTNAVGSYVY 480
Db 454 DECNVETGRCVCKDNVEGFNCERCCKPFFNLESNPRGCTPCFCFGHSSVCTNAVGSYVY 513
QY 481 SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPFRIAPAKFLGKQVLSY 540
Db 514 SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPFRIAPAKFLGKQVLSY 573
QY 541 GQNLFSFRVDRDRTRLASAEDLVLEGAGLRVSVPLIAQGNYSYSETTVKYVFLRHEATDY 600
Db 574 GQNLFSFRVDRDRTRLASAEDLVLEGAGLRVSVPLIAQGNYSYSETTVKYVFLRHEATDY 633
QY 601 PWRPALTPEFQKLLNNLTSIKIRGTYSERSAGYLDVTLASARPGPGVPATWVESCTCP 660
Db 634 PWRPALTPEFQKLLNNLTSIKIRGTYSERSAGYLDVTLASARPGPGVPATWVESCTCP 693
QY 661 VGYGGQFCMCLSGYRRETPNLGYPSPCVLCACNGHSETCDPETGVCNCRDNTAGPHCEK 720
Db 694 VGYGGQFCMCLSGYRRETPNLGYPSPCVLCACNGHSETCDPETGVCNCRDNTAGPHCEK 753
QY 721 CSDGYGDSGTAGTSSDCQPCPCPGSSCAVVPKTKEVVCTNCPTGTTGKRCELCDGYFG 780

Db 754 CSDGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTEVVCNTCPTGTGKRCCLCDDGYFG 813
Qy 781 DPLGRNPVRLCRLCQSDNIDPNVAVGNCNRLTGECLKCIYNTAGFYCDRCCKDGGFFGNPL 840
Db 814 DPLGRNPVRLCRLCQSDNIDPNVAVGNCNRLTGECLKCIYNTAGFYCDRCCKDGGFFGNPL 873
Qy 841 APNPADKCKACNCPYGTMMKQSSCNPNVTGQCECLPHVTGQDCGACDPGFYNLQSGGCE 900
Db 874 APNPADKCKACNCPYGTMMKQSSCNPNVTGQCECLPHVTGQDCGACDPGFYNLQSGGCE 933
Qy 901 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCERCEVNHFGPEGCKPCDCHPEGSLSL 960
Db 934 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCERCEVNHFGPEGCKPCDCHPEGSLSL 993
Qy 961 QCKDDGRCECREGFGVGNRCQDCEENYFYNRSWPGCQCEPCACVRLVKDKVADHRVKLQELE 1020
Db 994 QCKDDGRCECREGFGVGNRCQDCEENYFYNRSWPGCQCEPCACVRLVKDKVADHRVKLQELE 1053
Qy 1021 SLIANLGTGDEMVTDAQAFEDRLKEAEREVMDLLREAQDVQDVQDQNLMDRLQVNNLTSSQ 1080
Db 1054 SLIANLGTGDEMVTDAQAFEDRLKEAEREVMDLLREAQDVQDVQDQNLMDRLQVNNLTSSQ 1113
Qy 1081 ISRLQIRNTIIEETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSVPSTGDP 1140
Db 1114 ISRLQIRNTIIEETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSVPSTGDP 1173
Qy 1141 NMVTLAEERKLAERHKEADDIIVRAKTANDTSTEAYNLLRLTLAGENOTAFIEELN 1200
Db 1174 NMVTLAEERKLAERHKEADDIIVRAKTANDTSTEAYNLLRLTLAGENOTAFIEELN 1233
Qy 1201 RYEQAKNISQLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDSETLENEANNIKMEA 1260
Db 1234 RYEQAKNISQLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDSETLENEANNIKMEA 1293
Qy 1261 ENLEQLIDQKLKDYEDLREDMRGKELEVNKLLKKGTEQOTADQLLARADAQAALG 1320
Db 1294 ENLEQLIDQKLKDYEDLREDMRGKELEVNKLLKKGTEQOTADQLLARADAQAALG 1353
Qy 1321 KKGRDTLQEAENDILNNLKQFDRRVNDNKTAAEALRKIPAINQITTEANEKTRQAQALG 1380
Db 1354 KKGRDTLQEAENDILNNLKQFDRRVNDNKTAAEALRKIPAINQITTEANEKTRQAQALG 1413
Qy 1381 SAAADATEAKNKAHEAERIAASAVQKNATSTKAEARTFAEVTDLNNEVNNMLKQLQEA 1440
Db 1414 SAAADATEAKNKAHEAERIAASAVQKNATSTKAEARTFAEVTDLNNEVNNMLKQLQEA 1473
Qy 1441 ELKRKQDDADQDMMAGMASQAQAEAINARKAKNSVTSLSIINDLLEQLQDQDVTDLN 1500
Db 1474 ELKRKQDDADQDMMAGMASQAQAEAINARKAKNSVTSLSIINDLLEQLQDQDVTDLN 1533
Qy 1501 KLNEIEGTLNKADEMKSVDLDRKVSVDLENEAKKQEAAIMDYNRDIIEIMKDINLEDIR 1560
Db 1534 KLNEIEGTLNKADEMKSVDLDRKVSVDLENEAKKQEAAIMDYNRDIIEIMKDINLEDIR 1593
Qy 1561 KTLPSGCFNTPSIEKP 1576
Db 1594 KTLPSGCFNTPSIEKP 1609

RESULT 6
US-09-938-275-10
; Sequence 10, Application US/09938275
; Patent No. US2002011309A1
; GENERAL INFORMATION:
; APPLICANT: Gerardo Castillo
; APPLICANT: Alan Snow
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications
; TITLE OF INVENTION: of Laminin and Laminin-Derived Protein Fragments
; FILE REFERENCE: PROTEO.P03
; CURRENT APPLICATION NUMBER: US/09/938,275
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1607
; TYPE: PRT
; ORGANISM: Mus Musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Swissprot P02468
; DATABASE ENTRY DATE: 1989-07-01
US-09-938-275-10

Query Match 94.3%; Score 8056; DB 9; Length 1607;

Best Local Similarity 93.2%; Pred. No. 0;

Matches 1469; Conservative 59; Mismatches 48; Indels 0; Gaps 0;

Qy 1 QAAMDECTDEGGRPCRCMPEFVNAAFNVTVATNTCGTPPEEYCVQGTGVTKSCHLCD 60
Db 32 RAAMDECADEGGRPCRCMPEFVNAAFNVTVATNTCGTPPEEYCVQGTGVTKSCHLCD 91
Qy 61 AQOPHLQHGAFLTDYNNQADTTWQSQTMLAGVQYPPSSINLTLLHKGAFDITYVRLKFH 120
Db 92 AQOHLQHGAFLTDYNNQADTTWQSQTMLAGVQYPPSSINLTLLHKGAFDITYVRLKFH 151
Qy 121 TSRPESFAIYKRTREDGFWIPYQYYSGSCENTYSKANRGFIRTGDEQALCTDEFSDIS 180
Db 152 TSRPESFAIYKRTREDGFWIPYQYYSGSCENTYSKANRGFIRTGDEQALCTDEFSDIS 211
Qy 181 PLTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPWRATA 240
Db 212 PLTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPWRATA 271
Qy 241 YIAISDFAVGGRCKNGHASECMKNEFDKLVCKNCKHNTYGVDCCKCLPFFNDRPWRATA 300
Db 272 YIAISDFAVGGRCKNGHASECMKNEFDKLVCKNCKHNTYGVDCCKCLPFFNDRPWRATA 331
Qy 301 ESASECLPCDCNCRSQECYFDPPELYRSTGHGCHCTNCQDNTDGAHCRCRNFRLGNNE 360
Db 332 ESASECLPCDCNCRSQECYFDPPELYRSTGHGCHCTNCQDNTDGAHCRCRNFRLGNNE 391
Qy 361 ACSSCHCSPVGLSTQCDYSYGRCSCKPGVMGDKCDRCQPGFHSLSLTAAGCRPCSCDPSGSI 420
Db 392 ACSPCHCSPVGLSTQCDYSYGRCSCKPGVMGDKCDRCQPGFHSLSLTAAGCRPCSCDPSGSI 451
Qy 421 DECNVETGRVCCKDNVEGFNCERCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGSYVY 480
Db 452 DECNVETGRVCCKDNVEGFNCERCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGSYVY 511
Qy 481 SISSTFQIDEDGWRABQRDSEASLEWSSERQDIAVISDFPFPYFIAPAKFLGKQVLSY 540
Db 512 DISSTFQIDEDGWRABQRDSEASLEWSSERQDIAVISDFPFPYFIAPAKFLGKQVLSY 571
Qy 541 GQNLFSFRVDRDRDRLSAEDLVLEGAGLRVSVPLIAQNSYPSSETTKYVFRHLHEATDY 600
Db 572 GQNLFSFRVDRDRDRLSAEDLVLEGAGLRVSVPLIAQNSYPSSETTKYVFRHLHEATDY 631
Qy 601 PWRPALTPPEFQKLLNNLTSLIKIRGTYSERSAGYLDVTLASARPGVPATWVESCTCP 660
Db 632 PWRPALTPPEFQKLLNNLTSLIKIRGTYSERSAGYLDVTLASARPGVPATWVESCTCP 691
Qy 661 VGYGGQFCMCLSGYRRETPNLGPIPCVLCACNGHSETCDPETGVNCNRDNTAGPHCEK 720
Db 692 VGYGGQFCMCLSGYRRETPNLGPIPCVLCACNGHSETCDPETGVNCNRDNTAGPHCEK 751
Qy 721 CSDGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTEVVCNTCPTGTGKRCCLCDDGYFG 780
Db 752 CSDGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTEVVCNTCPTGTGKRCCLCDDGYFG 811
Qy 781 DPLGRNGPVRCLCRLCQSDNIDPNVAVGNCNRLTGECLKCIYNTAGFYCDRCCKDGGFFGNPL 840
Db 812 DPLGRNGPVRCLCRLCQSDNIDPNVAVGNCNRLTGECLKCIYNTAGFYCDRCCKDGGFFGNPL 871
Qy 841 APNPADKCKACNCPYGTMMKQSSCNPNVTGQCECLPHVTGQDCGACDPGFYNLQSGGCE 900
Db 872 APNPADKCKACNCPYGTMMKQSSCNPNVTGQCECLPHVTGQDCGACDPGFYNLQSGGCE 931

QY 901 RCDCHALGSTNGQCDIRTTGQCEQPGITGOHCERCEVNHFGFEGCKPCDCHPEGSLSL 960
DB 932 RCDCHALGSTNGQCDIRTTGQCEQPGITGOHCERCEVNHFGFEGCKPCDCHPEGSLSL 991
QY 961 QKDDGRCECREGFGVGNRCDCQCEENFYFNRSWPGCQCEPACRYLVKDKVADHRVKLQELE 1020
DB 992 QKDDGRCECREGFGVGNRCDCQCEENFYFNRSWPGCQCEPACRYLVKDKAAEHRVKLQELE 1051
QY 1021 SLIANLGTGDEMVTDOAFEDRLKEABREVMDDLREACQVDKVDQNLMDRLQRVNNTLSQ 1080
DB 1052 SLIANLGTGDEMVTDOAFEDRLKEABREVTDLLEACQVDKVDQNLMDRLQRVNNTLSQ 1111
QY 1081 ISRLQNRINTIETGNLAEQARAHVENTERLIEIASRELEKAKAAANVSUTQPESTGDP 1140
DB 1112 ISRLQNRINTIETGILAEARARSVESTEQLEIEIASRELEKAKAAANVSITQPESTGEP 1171
QY 1141 NNMTLLABEARKLAERHKQEAADDIVRVAKTANDTSTEAYNLLRLTLAGENQTAFEIIEELN 1200
DB 1172 NNMTLLABEARRLAERHKQEAADDIVRVAKTANETSAAEYNLLRLTLAGENQTALEIIEELN 1231
QY 1201 RKYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDLSETLENEANNIKMEA 1260
DB 1232 RKYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKMEA 1291
QY 1261 ENLEQLIDOKLDYEDLREDMRGKEHEVKNLLEKKGTEQQTADQLLARADAALABEAAA 1320
DB 1292 ADLRLIDOKLDYEDLREDMRGKEHEVKNLLEKGAEQQTADQLLARADAALABEAAA 1351
QY 1321 KKGRDTLQEAANDILNNLKDFDRRVNDNKTAEEALRKIPAINOTITEANEKTRTAAQALG 1380
DB 1352 KKGRSTLQEAANDILNNLKDFDRRVNDNKTAEEALRRIPAINRTIAEANEKTRTAAQALG 1411
QY 1381 SAAADATEAKNAKAEAEERIAASAVQKNATSTKAEAEARTFAEVTDLNEVNNMLKQLEAEK 1440
DB 1412 NAAADATEAKNAKAEAEERIAASAVQKNATSTKADAERTFEVTDLNEVNGMLRQLEEAEN 1471
QY 1441 ELKRKQDDADQDDMMWAGMASQAAQAEALNARKAKNSVSSLLSLLQNLNLLDQLGQDITVDLN 1500
DB 1472 ELKRKQDDADQDDMMWAGMASQAAQAEALNARKAKNSVSSLLSLLQNLNLLDQLGQDITVDLN 1531
QY 1501 KLINEIEGTLNKADEMKSVDLDRKVSLENEAKKQEAAMDVNRDIEEIMKDIRNLEDIR 1560
DB 1532 KLINEIEGSLNKADEMKSASDLDRKVSLESEARKQEAAMDVNRDIAEIIKDIHNLEDIK 1591
QY 1561 KTLPSGCFNTPSIEKP 1576
DB 1592 KTLPTGCFNTPSIEKP 1607

RESULT 7

US-10-037-182-18
; Sequence 18, Application US/10037182
; Publication No. US2003004899A1
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Doi, Masayuki
; APPLICANT: Thyboll, Jill
; TITLE OF INVENTION: Recombinant Laminin 10
; FILE REFERENCE: 99-274-F
; CURRENT APPLICATION NUMBER: US/10/037,182
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,449
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/279,282
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 1605
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-037-182-18

Query Match 94.1%; Score 8043; DB 14; Length 1605;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 1470; Conservative 57; Mismatches 47; Indels 2; Gaps 2;
QY 1 QAAMDECTDEGGRPQRCMPEFVNAAFNVTVATNTCGTPPEYCVQGTGVTGKSHLCD 60
DB 32 RAAMDECADEGGRPQRCMPEFVNAAFNVTVATNTCGTPPEYCVQGTGVTGKSHLCD 91
QY 61 AGQPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYPSINLTLHLGKAFDITYVRLKFH 120
DB 92 AGQPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYPSINLTLHLGKAFDITYVRLKFH 151
QY 121 TSRPESFAIKRTREDGPWIPYQYVSGSCENTYSKANRGFIRTCGDEQQAALCTDEFSDIS 180
DB 152 TSRPESFAIKRTREDGPWIPYQYVSGSCENTYSKANRGFIRTCGDEQQAALCTDEFSDIS 211
QY 181 PLTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTILNRLNFTFGDEVFNDPKVLKSY 240
DB 212 PLTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTILNRLNFTFGDEVFNDPKVLKSY 271
QY 241 YYAISDFAVGGRCKCNHGHASECMKNEFDKLVNCNCKHNTYGVDCCKLPFFENDRPWRRATA 300
DB 272 YYAISDFAVGGRCKCNHGHASECMKNEFDKLVNCNCKHNTYGVDCCKLPFFENDRPWRRATA 331
QY 301 ESASECLPCDCNCRSQECYFDPPELYRSTGHGCHCTNCQDNTDGAHCRCRENFRLGNNE 360
DB 332 ESASECLPCDCNCRSQECYFDPPELYRSTGHGCHCTNCQDNTDGAHCRCRENFRLGNTE 391
QY 361 ACSSCHCSPVGSLSLSTQDSYGRCSCKPGVMGDKCDRCQPGFHSILTEAGCRPCSCDPSGSI 420
DB 392 ACSPCHCSPVGSLSLSTQDSYGRCSCKPGVMGDKCDRCQPGFHSILTEAGCRPCSCDPSGST 451
QY 421 DECNVETGRVCVCKDNVEGFNCERCCKPGFFNLESSNPRGCTPCFCFHHSSVCTNAVGSYVY 480
DB 452 DECNVETGRVCVCKDNVEGFNCERCCKPGFFNLESSNPKGCTPCFCFHHSSVCTNAVGSYVY 511
QY 481 SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY 540
DB 512 DISSTFQIDEDGWRAEQRDGSEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSY 571
QY 541 GQNLFSFRVDRDTRLASAEDLVLEGAGLRVSVPLIAQGNYSFSETTVKYVFRLEHATDY 600
DB 572 GQNLFSFRVDRDTRLASAEDLVLEGAGLRVSVPLIAQGNYSFSETTVKYIFRLEHATDY 631
QY 601 PWRPALTPFEFQKLLNLTISIKIRGYTSERSAGYLDVTLASARPGVPATWVESCTCP 660
DB 632 PWRPALSPFEFQKLLNLTISIKIRGYTSERSAGYLDVTLASARPGVPATWVESCTCP 691
QY 661 VGYGGQFCETCLPGYRRETSLGYPSPCVLCTCNHSETCDPETGVCDRCRDNTAGPHCEK 720
DB 692 VGYGGQFCETCLPGYRRETSLGYPSPCVLCTCNHSETCDPETGVCDRCRDNTAGPHCEK 751
QY 721 CSDGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKVWCTNCPTGTGKRCCELCDGDFYFG 780
DB 752 CSDGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKVWCTNCPTGTGKRCCELCDGDFYFG 811
QY 781 DPLGRNGPVRCLRLCQSDNIDPNAVGNCRNLTGECLKCIYNTAGFYCDRCCKDGFNPL 840
DB 812 DPLGNSGPVRCLRLCQSDNIDPNAVGNCRNLTGECLKCIYNTAGFYCDRCCKDGFNPL 871
QY 841 APNPADKCKACACN-VGTVOQSSCNPNVTGQCECLPHVTGQDCGACDPGFYNLQSGQCE 900
DB 872 APNPADKCKACACN-VGTVOQSSCNPNVTGQCECLPHVTGQDCGACDPGFYNLQSGQCE 930
QY 901 RCDCHALGSTNGQCDIRTTGQCEQPGITGOHCERCEVNHFGFEGCKPCDCHPEGSLSL 960
DB 931 RCDCHALGSTNGQCDIRTTGQCEQPGITGOHCERCEVNHFGFEGCKPCDCHPEGSLSL 990
QY 961 QKDDGRCECREGFGVGNRCDCQCEENFYFNRSWPGCQCEPACRYLVKDKVADHRVKLQELE 1020
DB 991 QKDDGRCECREGFGVGNRCDCQCEENFYFNRSWPGCQCEPACRYLVKDKAAEHRVKLQELE 1050

QY 1021 SLIANLGTGDEMVTQAFEDRLKEAEREVMDDLREAAQDVQKVDQNLMDRLQRVNNTLSQ 1080
DB 1051 SLIANLGTGDDMVTQAFEDRLKEAEREVTDLLREAAQEVQVDQNLMDRLQRVNSSLHSQ 1110
QY 1081 ISRLQNRNTIETGNLAEQARAHVENTERLJIASRELEKAKVAANVSVTQPESTGDP 1140
DB 1111 ISRLQNRNTIETGILAEARARSVESTEQJLIEIASRELEKAKM-AANVSITQPESTGEP 1169
QY 1141 NMMTLLAEARKLAERHKEADDDIVRVAKTANDTSTEAYNLLRTLAGENQTAFEIEELN 1200
DB 1170 NMMTLLAEARRLAERHKEADDDIVRVAKTANETSAAEAYNLLRTLAGENQTALEIEELN 1229
QY 1201 RKYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDSELEANEANNIKMEA 1260
DB 1230 RKYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALEANEANNIKKEA 1289
QY 1261 ENLEQLIDOKLDYEDLREDMRGKELEVNKLLKKGKTEQQTADQQLLARADAAKALAEAAA 1320
DB 1290 ADLDRLLIDOKLDYEDLREDMRGKEHEVNKLLKKGKAEQQTADQQLLARADAAKALAEAAA 1349
QY 1321 KKGRDTLOEANDILNLLKDFDRRVNDNKTAAEEALRKIPAINQITITEANEKTRAAQALG 1380
DB 1350 KKGRSTLOEANDILNLLKDFDRRVNDNKTAAEEALRRIPAINRTIAEANEKTRAAQLALG 1409
QY 1381 SAAADATEAKNKAHEAERIAASAVQKNATSTKAEABERTFAEVTDLDDNEVNNMLKQLOEAEK 1440
DB 1410 NAAADATEAKNKAHEAERIAASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAEN 1469
QY 1441 ELKXKQDDADQDMMAGVASQAAQAEAEINARKAKNSVTSLLSIINDLLEQLGQDQDLDN 1500
DB 1470 ELKXKQDDADQDMMAGVASQAAQAEAEINARKAKNSVSSLLSQNLNLLDQLGQDQDLDN 1529
QY 1501 KLNIEIGTLNKADEMKVSDLDLDRKVSDDLENEAKKQAEAAIMDYNRDIIEIMKDIRNLEDIR 1560
DB 1530 KLNIEGSLNKADEMKASOLDLDRKVSDDLESEARKQAEAAIMDYNRDIAEIIKDIHNLEDIK 1589
QY 1561 KTLPGSCFNTPSIEKP 1576
DB 1590 KTLPGCFNTPSIEKP 1605

RESULT 8

US-10-037-182-20
; Sequence 20, Application US/10037182
; Publication No. US20030044899A1
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Doi, Masayuki
; APPLICANT: Thyboll, Jill
; TITLE OF INVENTION: Recombinant Laminin 10
; FILE REFERENCE: 99-274-F
; CURRENT APPLICATION NUMBER: US/10/037,182
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,449
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/279,282
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 1572
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-037-182-20
Query Match 94.1%; Score 8038; DB 14; Length 1572;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;
QY 3 AMDECTDEGGRPQRCMPEFVNAAFNVTVVATNTCGTPEEYCVQGTGVTGVTKSCHLCDAG 62
DB 1 AMDECADEGGRPQRCMPEFVNAAFNVTVVATNTCGTPEEYCVQGTGVTGVTKSCHLCDAG 60

QY 63 QPHLQHGAFLTDYNNQADTTWQSQTMLAGVQYPPSSINLTLLHLGKAPDITYVRLKFHTS 122
DB 61 QQHLQHGAFLTDYNNQADTTWQSQTMLAGVQYPPSSINLTLLHLGKAPDITYVRLKFHTS 120
QY 123 RPESFAIYKRTREDGPWIPYQYYSGSCENTYSKANRGFIRTTGGDEQQAALCTDEFSDISPL 182
DB 121 RPESFAIYKRTREDGPWIPYQYYSGSCENTYSKANRGFIRTTGGDEQQAALCTDEFSDISPL 180
QY 183 TGGNVAFTLEGRPSAYNFDNSPVLQEWVTATDIRVTNRLNTFGDEVENDPKVLKSYYY 242
DB 181 TGGNVAFTLEGRPSAYNFDNSPVLQEWVTATDIRVTNRLNTFGDEVENDPKVLKSYYY 240
QY 243 AISDFAVGGRCKCNHGHASECMKNEFDKLVNCKHNTYGVDCCKLPPFFNDRPWRRAEAS 302
DB 241 AISDFAVGGRCKCNHGHASECMKNEFDKLVNCKHNTYGVDCCKLPPFFNDRPWRRAEAS 300
QY 303 ASECLPCDCNRSQECYFDPPELYRSTGHGHCTNCQDNTDGAHCERCERENFFRLGNNEAC 362
DB 301 ASECLPCDCNRSQECYFDPPELYRSTGHGHCTNCQDNTDGAHCERCERENFFRLGNTEAC 360
QY 363 SSCHCSPVGLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLSLTAAGCRPCSCDPSGSIDE 422
DB 361 SPCHCSPVGLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLSLTAAGCRPCSCDPSGSTDE 420
QY 423 CNVETGRCVCKONVEGFNCERCKPGFFNLESNPRGCTPCFCFHSSVCTNAVGSYSYI 482
DB 421 CNVETGRCVCKONVEGFNCERCKPGFFNLESNPKGCTPCFCFHSSVCTNAVGSYSYDI 480
QY 483 SSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSYGQ 542
DB 481 SSTFQIDEDGWRVEQRDSEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYGQ 540
QY 543 NLSFSFRVDRRDTRLSAEDLVLEGAGLRVSVPLIAQNSYSETPVTVKVFRLHEATDYPW 602
DB 541 NLSFSFRVDRRDTRLSAEDLVLEGAGLRVSVPLIAQNSYSETPVTVKVFRLHEATDYPW 600
QY 603 RPALTPEFEFQKLLNLTLSIKIRGTYSERSAGYLDVTLASARPGVGPATWVESCTCPVG 662
DB 601 RPALSPFEFQKLLNLTLSIKIRGTYSERSAGYLDVTLASARPGVGPATWVESCTCPVG 660
QY 663 YGQFCETCLPGYRRETPSLGYPSPCVLCTCNHSETCDPETGVCDNRDNTAGPHCEKCS 722
DB 661 YGQFCETCLPGYRRETPSLGYPSPCVLCTCNHSETCDPETGVCDNRDNTAGPHCEKCS 720
QY 723 DGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKXVVCTNCPTGTTGRCCLCDDGYFGDP 782
DB 721 DGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKXVVCTNCPTGTTGRCCLCDDGYFGDP 780
QY 783 LGRNGPVRCLRLCQCSNDIDPNAVGNCRNLTGECILKCIYNTAGFYCDRCCKDGFPGNPLAP 842
DB 781 LGSNGPVRCLRLCQCSNDIDPNAVGNCRNLTGECILKCIYNTAGFYCDRCCKDGFPGNPLAP 840
QY 843 NPADKCKACACNCPYGTMKQSSCNPNVTGQCECLPHVTGQDCGACDPGFYNLQSGQGCERC 902
DB 841 NPADKCKACACN-YGTVQSSCNPNVTGQCCQLPHVSGRDCGTCDPGYVNLQSGQGCERC 899
QY 903 DCHALGSTNGQCDIRTGQCECQPGITGOHCERCERENFFHFGFEGEGCKPCDCHPEGSLSLQC 962
DB 900 DCHALGSTNGQCDIRTGQCECQPGITGOHCERCERENFFHFGFEGEGCKPCDCHPEGSLSLQC 959
QY 963 KDDGRCECREGFGVGNRCDCQCEENYFYNRSWPGCCQECPCYRLVKDKVADHRVKLQJESL 1022
DB 960 KDDGRCECREGFGVGNRCDCQCEENYFYNRSWPGCCQECPCYRLVKDKAAEHRVKLQJESL 1019
QY 1023 IANLGTGDEMVTQAFEDRLKEAEREVMDDLREAAQDVQKVDQNLMDRLQRVNNTLSSQIS 1082
DB 1020 IANLGTGDDMVTQAFEDRLKEAEREVTDLLEAAQEVQKVDQNLMDRLQRVNSSLHSQIS 1079
QY 1083 RLQNRNTIETGNLAEQARAHVENTERLJIASRELEKAKVAANVSVTQPESTGDPNN 1142
DB 1080 RLQNRNTIETGILAEARARSVESTEQJLIEIASRELEKAKM-AANVSITQPESTGEPNN 1138
QY 1143 MTLLEAEARKLAERHKEADDDIVRVAKTANDTSTEAYNLLRTLAGENQTAFEIEELNRK 1202

Db 1139 MTLAEEARRLAERHKEADDDIVRVAKTANETSAEAYNLLRLTAGENQTALEIEELNRK 1198
Qy 1203 YEOAKNISODLEKQAAVHEEAKRAGDKAVEIYASVAQLSPLDSETLEANEANNIKMEAEN 1262
Db 1199 YEOAKNISODLEKQAAVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAAD 1258
Qy 1263 LEQLIDOKLDYEDLRDMRGKELEVKNNLLEKGTQEQTADOLLARADAALAEAAKK 1322
Db 1259 LDRLLDOKLDYEDLRDMRGKEHEVKNNLLEKGAEQQTADOLLARADAALAEAAKK 1318
Qy 1323 GRDTLOEANDIILNNLKDPRRVNDKNKTAEEALPKIPAINOTITEANEKTRQAQALGSA 1382
Db 1319 GRSTLOEANDIILNNLKDPRRVNDKNKTAEEALPRIPAINRTIAEANEKTRQAQALGNA 1378
Qy 1383 AADATEAKNKAHEAERIASAVQKNATSTKAEABRTFAEVTDLDNVNNMLKQLOEAEKEL 1442
Db 1379 AADATEAKNKAHEAERIASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAENEL 1438
Qy 1443 KRKQDDADQDMMAGMASQAQAEAEINARKAKNSVTSLLSIINDLLEQLGQLDTVDLNKL 1502
Db 1439 KRKQDDADQDMMAGMASQAQAEAEINARKAKNSVSSLLSOLNLLDQLGQLDTVDLNKL 1498
Qy 1503 NEIEGTLNKAKDEKMSDLDRKVSLENEAKKQEAAMIDYNRDIEEIMKDIRNLEDIRKT 1562
Db 1499 NEIEGSLNKAKDEKMSDLDRKVSLESEARKQEAAMIDYNRDIAEIIKDIHNLEDIKKT 1558
Qy 1563 LPSCGFNTPSIEKP 1576
Db 1559 LPTGCFNTPSIEKP 1572

RESULT 9
US-09-845-583-10
; Sequence 10, Application US/09845583
; Patent No. US20020142954A1
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Brunken, William Joseph
; APPLICANT: Champliand, Marie-France
; APPLICANT: Hunter, Dale
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
; FILE REFERENCE: 10287-056001
; CURRENT APPLICATION NUMBER: US/09/845,583
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/200,863
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1587
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-845-583-10

Query Match 42.1%; Score 3600; DB 9; Length 1587;
Best Local Similarity 43.5%; Pred. No. 4.9e-196;
Matches 695; Conservative 263; Mismatches 575; Indels 54; Gaps 20;

Qy 2 AAMDECTDEGGRPQRCMPEFVNAAFNVTVVATNTCGTPPEEYCVQTGVTGYSCHLCDA 61
Db 20 AGMGACYDGAGRPQRCPLPVFENAAFGRLAQASHTCGSPPEDFCPHVGAAGAGAHQRCDA 79
Qy 62 GQPHLOHGAAFLTDYNNQADTTWQSQTMLAGVQYPSSINLTLHLGKAFDITYVRLKFHT 121
Db 80 ADPQRHNASYLTDHFSQDESTWQSPSMAFGVQYPTSVNITLRGKAYEITYVRLKFHT 139
Qy 122 SRPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDISP 181
Db 140 SRPESFAIYKRSRADGPWEPIQYFYSASCQKTYGRPEGQYLRPGEDERVAFTSEFSDISP 199
Qy 182 LTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTLNRLNTFGDEVNDPKVLKSYY 241

Db 200 LSGGNVAFSTLEGRPSAYNFEESPGIQEWVTSTELLISLDRLNTFGDDIFKDPKVLQSY 259
Qy 242 YAIISDFAVGGRCKNCNGHASECMKNEFDKLVNCNKHNTYGVDCCKLPPFFNDRPWRATAE 301
Db 260 YAVSDFSFGGRCKNCNGHASECGPDVAGQLACRCQHTTGTDCERCLPFFQDRPWARGTAE 319
Qy 302 SASECLPCDCNGRSQECYDFDPPELYRSTGHGGCHTNCQDNTDGAHCERCENFFRLGNNEA 361
Db 320 AAHECLPCNCSGRSEECTDFRELFRSTGHGGCHHCRDHTAGPHCERCQENFYHWDPRMP 379
Qy 362 CSSCHCSPVGSLSLTCDSYGRCSCKPGVMGDKDCRCQPGFHSLSLTAAGCRPCSCDPPSGSID 421
Db 380 CQPCDCQASGLHLQCDTGTCACTPTVTGWKCDRCLPFGFHSLSSEGGCRPCTCNPAGSLD 439
Qy 422 ECVNVTGRVCVKNDVGEFNCERCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGSVYS 481
Db 440 TCDPRSGRCPCKENVEGNLDCRCRPGTFNLQPHNPAGSCSCFCYGHSHKVCASTAQFQVHH 499
Qy 482 ISSTFQIDEDGWRAEQDRGSEASLEWSSERQDIAVISDSYFPYFIAPAKFLGKQVLSYG 541
Db 500 ILSDPHQGAEGWARSVGGSEHSPQWSPN---GVLLSPDEDEELTAPGKFLGDRQFSYG 555
Qy 542 QNLSFSFRVDRRDLRLSAEDLVLEGAGLRVSVPLIAQNSYPSSETTVKYVFRLLH---EAT 598
Db 556 QPLILTFRVPPGDSPLPVQ-LRLEGTGLALS--LRHSSLSGPDARASQGGRAQVPLQET 612
Qy 599 DYPWRPALTPFEFQKLNLTLSIKIRGTYSERSAG--YLDDVTLASARPGVGPATWVES 656
Db 613 SEDVAPPLPPFHFQRLANLTLRLRVSPGSPAGPVFELTEVRLTSARPGLSPPASWVEI 672
Qy 657 CTCPVGYGGQFCMCLSGYRRETPNLGPYSPCVLCACNGHSETCDPETGVNCNRDNTAGP 716
Db 673 CSCPTGYTGQFCESCAPGYKREMPQGGPYASCVPCTCNQHG-TCDPNTGICVCSHHTGEP 731
Qy 717 HCEKCSGYGSDTAGTSSQPCPCPGSSCAVVPKTEWVCTNCTPTGTTGKRCBELCDD 776
Db 732 SCERCLPGFYGNPFAGQADDCQPCPCPGQSACTTIPESGEVWCTHCPGQRRRCEVCDD 791
Qy 777 GYFGDPLGRNGPVRRLCRLCOCSDNIDPNAVGNCRNLTGECCLKIYNTAGFYCDCKDGEFF 836
Db 792 GFFGDPLGLFGHPQPCQCCSGNVDPNAVGNCDPLSGHCLRLHNTTGDHCEHCQEGFY 851
Qy 837 GNPLAPNPADKCKACNCPYGTMKQOSSCNPVVTGQCECLPHVTGQDCGACDPGFYNLQSG 896
Db 852 GSALAPRPADKCMPCSCHPQSVSEQMPCDPVTGQCSCLPHVTARDCSRCPYGFEDLQPG 911
Qy 897 QGCRCDCHALGSTNGQCDIRTGQCECQPGITGQCHCERCEVNHFGFPGPEGCKPCDCHPEG 956
Db 912 RGRSCKCHPLGSOEDQCHPKTGQCTCRPGVTGQACDRQCLGFFGSSIKGRACRCSPLG 971
Qy 957 SLSLQCKDDGRCECREGFGVGNRCDQCEENFYFNRSWPGQCECPACYRLVKDKVADHRVKL 1016
Db 972 AASAOCHYNGTVCVRPGFEGYKCDRCHYNFFLTADGTHCQCCPSCYALVKEETAKLAKRL 1031
Qy 1017 QELESLIANLGTGDEMVTDOAFEDRLKEAEREVMDLLREAOQDVQDQNLMDRLQRVNNT 1076
Db 1032 TLTEGWLQGSDCGSPW---GPLDILLGEAPRG--DVYQGHLLLPGAREAFLEQMMGLEGA 1086
Qy 1077 LSSQISRLQNIRNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSVTQPE 1136
Db 1087 VKAAREQLQRLNKGARCAQAGSQKCTCTQLADLEAVLESSEEEILHAAAILASLEIPQ-EG 1145
Qy 1137 TGDNNMTLLAEEARKLAERHKEQEAADDIVRVAKTANDTSTEAYNLLRLTAGENQTAPEI 1196
Db 1146 PSQPTKWSHLAIEARALARASHRDTATKIAATAWRALLASNTSYALLWNL--EGRVALET 1203
Qy 1197 E-ELNRYEQAKNISQDLEKQAARVHEEAKRAGDKAVEIYASVAQLSPLDSETL----- 1249
Db 1204 ORLDREYQEVQAAQKALRTAVALPEAE-----SVLATVQQVGADTAPYALLASP 1256
Qy 1250 -----ENEANNIKMEAEENLEQLIDQKLKDYEDLRDMRGKELEVKNNLLEKGTQEQT--- 1301
Db 1257 GALPQKSRRAEDLGLKAKALEKTV---ASWQHIMATE-AARTLQTAQAQATLRQTEPLTMAR 1311

QY 1302 -----ADQLARADAALAEAAKKGRTDLQEANDILNKLDFRRVNDNKTAEEA 1354
Db 1312 SRLTATFASQLHQGARAALTQASSSVQAATVTWVGARTLLADLEGMKLQFPRPKDQAALQ 1371
QY 1355 LRKIPAINQTITEANEKTRQAQALGSAADATEAKNKAHEAERIAAVQKNATSTKAEA 1414
Db 1372 RKADSVSDRLADTRKTKQAERMLGNAAPLSSSAKKKGREAEVLAKDSAKLAKALLRER 1431
QY 1415 ERTFAEVTDLNNEVNMMLKQL-QEAEKELKRQDDADQDMMAGMASQAQAEINARKA 1473
Db 1432 KQAHRRASRLTSQTQATLQASQVVLASEARREQLAEAEVAGLS-----EMEQQIRES 1486
QY 1474 KNSVTSLLSIINDLLEQLGQDLD--VDLNLKLINEIEGTLNKAKDEM-KVSDLDLDRKXVSDLEN 1530
Db 1487 RISLEKDIETLSSELLARLSLDTHQAPAAQALNETQWALERLRLOLGSFPGSLQKLSLLEQ 1546
QY 1531 EAKKQEAAMIDYNRDIIEIMKDIRNLEDIRKTLPSGC 1567
Db 1547 ESQQQLQIQGFESDLAEIRADKQNLKONLEAILHSLPENC 1583

RESULT 10

US-10-262-839-210

Sequence 210, Application US/10262839

Publication No. US20040038877A1

GENERAL INFORMATION:

APPLICANT: Alsobrook, John,

APPLICANT: Anderson, David W.,

APPLICANT: Boldog, Ferenc,

APPLICANT: Burgess, Catherine,

APPLICANT: Catterton, Elina,

APPLICANT: Edinger, Shlomit,

APPLICANT: Ellerman, Karen,

APPLICANT: Gerlach, Valerie,

APPLICANT: Gorman, Linda,

APPLICANT: Guo, Xiaojia,

APPLICANT: Ji, Weizhen,

APPLICANT: Kekuda, Ramesh,

APPLICANT: Leach, Martin,

APPLICANT: Li, Li,

APPLICANT: Miller, Charles,

APPLICANT: Patturajan, Meera,

APPLICANT: Reiger, Daniel,

APPLICANT: Rothenberg, Mark,

APPLICANT: Shimkets, Richard,

APPLICANT: Smithson, Glennda,

APPLICANT: Spytek, Kimberly,

APPLICANT: Taupier, Raymond, jr.,

APPLICANT: Vernet, Corine,

APPLICANT: Voss, Edward,

APPLICANT: Zerhusen, Brian,

APPLICANT: Zhong, Mei

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

FILE REFERENCE: 21402-462A

CURRENT APPLICATION NUMBER: US/10/262,839

PRIOR FILING DATE: 2002-10-01

PRIOR APPLICATION NUMBER: 60/326,483

PRIOR FILING DATE: 2001-10-02

PRIOR APPLICATION NUMBER: 60/327,917

PRIOR FILING DATE: 2001-10-09

PRIOR APPLICATION NUMBER: 60/328,029

PRIOR FILING DATE: 2001-10-09

PRIOR APPLICATION NUMBER: 60/328,056

PRIOR FILING DATE: 2001-10-09

PRIOR APPLICATION NUMBER: 60/381,101

PRIOR FILING DATE: 2002-05-16

PRIOR APPLICATION NUMBER: 60/371,972

PRIOR FILING DATE: 2002-04-12

PRIOR APPLICATION NUMBER: 60/327,342

PRIOR FILING DATE: 2001-10-05

PRIOR APPLICATION NUMBER: 60/328,044

PRIOR FILING DATE: 2001-10-09

; PRIOR APPLICATION NUMBER: 60/328,849
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/374,738
; PRIOR FILING DATE: 2002-04-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 367
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 210
; LENGTH: 1587
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-839-210

Query Match 42.1%; Score 3600; DB 12; Length 1587;
Best Local Similarity 43.5%; Pred. No. 4.9e-196;
Matches 695; Conservative 263; Mismatches 575; Indels 64; Gaps 20;

QY 2 AAMDECTDEGGRPQRCMPEFVNAFNVTVATNTCGTPPEEYCVQGTGVTGVTKSCHLCDA 61
Db 20 AGMGACYDAGRPQRCPLPVFENAAFGRLAQASHTCGSPPEDFCPHVGAAGAGAHQCRCDA 79
QY 62 GPHLQHGAFLTDYNNQADTTWQSQTMLAGVQYPSSINLTLLHKGAFDITYVRLKFHT 121
Db 80 ADPQRHNASYLTDFHSQDESTWQSPSMAGVQYPTSVNITRLGKAYEITYVRLKFHT 139
QY 122 SRPESFAIYKRTREDGPWIPYOYYSGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDISP 181
Db 140 SRPESFAIYKRSRADGPWEPIQFYSASCQKTYGRPEGQYLRPGEDEVAFCTSEFSDISP 199
QY 182 LTGGNVAFSTLEGPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVENDPKVLKSY 241
Db 200 LSGGNVAFSTLEGPSAYNFEESPLQEWVTSTELLISLDRNLNTFGDDIFKDPKVLQSY 259
QY 242 YAISDFAVGGRCKKNGHASECMKNEFDKLVNCKHNTYGVDCCKLFPFNDRPWRRTAE 301
Db 260 YAVSDFSVGGRCKKNGHASECGPDVAGQLACRCHQNTTGTDCERCCLFPFQDRPWARGTAE 319
QY 302 SASACLPCDCNGRQECYFDPELYRSTGHGHCCTNCQDNTDGAHCERCENFFRLGNEA 361
Db 320 AAHECLPCNCSGRSEECTFDRELFRSTGHGGRCHHCRDHTAGPHCERCQENFYHWDPRMP 379
QY 362 CSSCHCSPVGSLSLTCQDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGRCPCSDPSGSD 421
Db 380 CQPCDCQSAGSLHLQCDTGTCAKPTVTGWKCDRCLPGFHSLSSEGGCRPCTCNPAGSLD 439
QY 422 ECVETGRCVCKDNVEGFNCERCKPGFFNLBSSNPRGCTPCFCFGHSSVCTNAVGVSVYS 481
Db 440 TCDPRSGRCPCKENVEGNLDCRCPGTNLPQHPNAGCSCFCYGHSKVCASTAQFQVHH 499
QY 482 ISSTFQIDEDGWAEQORDGSEASLEWSSERQDIAVISDSYFPRYFTIAPAKFLGKQVLSYG 541
Db 500 ILSDFHQGAEGWARSVGGSEHSPQWSPN----GVLLSPEDEBELTAPGKFLGDQRFSG 555
QY 542 QNLSFSFRVDRRDLRLSAEDLVLEGAGLRVSVPLIAQGNISYPSETTVKXVFRLLH---EAT 598
Db 556 QPLILTRVPPGDSPLPVQ-LRLEGTGLALS--LRHSSLGSPQDARASQGGRAQVPLQET 612
QY 599 DYPWRPALTPFEFQKLLNLTSLKIRGTYSERSAG--YLDVDTLASARPGVGPATWVES 656
Db 613 SEDVAPPLPPFFHQRLLANLTSLRLRVSPGSPAGVPVLTETVRLTSARPLSPPASWVEI 672
QY 657 CTCPVGYGGQFCMCLSGYRRETNPNGPSPCVLCACNHSETCDPETGVCNCRDNTAGP 716
Db 673 CSCPTGYTGQFCESCAPGYKREMPQGGPYASCVPCTCNQHG-TCDPNTGICVCSHHTGP 731
QY 717 HCEKCSGYGDSYTAGTSSDCQPCPCPGGSSCAVVPKTKVCTNCPTGTTGKRCCELCD 776
Db 732 SCERCLPGFYGNPFAGQADDCCQPCPCPGQSACTTIPESGEVCTHCPGQGRRCRCEVCDD 791
QY 777 GYFGDPLGRNGPVRCLRLCQCSNDIDPNVAGNCLRTGELKCIYNTAGYCDRCCKDGF 836
Db 792 GFEGDPLGLFGHPQCHQCQCSGNVDPNVAGNCDPLSGHCLRLCHNTTGDHCEHCQEGFY 851

Db 380 CQPCDCQAGSLHLQCDTGTCAKPTVTGWKCDRLCPGFHSLSEGGCRPCTCNPAAGSLD 439
QY 422 ECVETGRVCVCKDNVEGFNCERCKPGFFNFLESSNPRGTCFCFGHSSVCTNAVGSVYS 481
Db 440 TCDPRSGRCPCKENVEGNLCDCRPGTFNLQPHNPAGGSCFCYGHSKVCASTAQFQVHH 499
QY 482 ISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIASISYFPPRYFIAPAKFLCKQVLSYG 541
Db 500 ILSDFHQAGWARSVGGSEHSPQSPN---GVLLSPDEDEELTAPGKFLGDQRFSGY 555
QY 542 QNLFSFRVDRDRTRLSAEDLVLEGALRVSVPLIAQNSYSPSETTVKYVFRLLH---EAT 598
Db 556 QPLILTRVFPDPSLPVQ-LRLEGTGLALS--LRHSSLSGPDARASQGGRAQVPLQET 612
QY 599 DYPWRPALTPFEFQKLLNNLTSIKIRGTYSERSAG--YLDVDTLASARPFGVPATWVES 656
Db 613 SEDVAPPLPFFHFORLLANLTSRLRVSPGSPAGPVLTEVRLTSARPGLSPPASWVEI 672
QY 657 CTCVPGYGGFCCEMCLSGYRRETNLGYPSPCVLACNCHSETCDPETGVNCRDNTAGP 716
Db 673 CSCPTGYTGFCESCAPGYKREMPQGGPYASCVPCTCNQHG-TCDPNTGICVCSHTEGP 731
QY 717 HCEKCSGYYGDSSTAGTSSDCQPCPCPGGSSCAVVPKTEVCTNCPTGTGKRCCELDD 776
Db 732 SCERCLPGFYGNPFAGQADDCQPCPCPGQSACTTIPSGEVVCTHCPGPGRRCEVCDD 791
QY 777 GYFGDPLGRNGPVRCLRLCQCSNIDPNVAGNCRNLTEGLCKCIYNTAGPYCDRCKDGF 836
Db 792 GFFGDPLGLFGHPQPCQCHQCCSGNVDPNAVGNCDPLSGHCLRLNHTTGDHCEHCQEGFY 851
QY 837 GNPLAPNPADKCKACNCPYGMKQSSCNPVVTGQCECLPHVTGQDCGACDPPGFYNLQSG 896
Db 852 GSALAPRPADKCMPCSCHPQGSVSEQMPDPTVTGQCSCLPHVTARDCSRCPYGFDFLQPG 911
QY 897 QGCERCDCHALGSTNGQCDIRTGQCECQPGITGQHCHERCEVNHFGFGBEGCKPCDCHPEG 956
Db 912 RGCRCCKHPLGSOEDQCHPKTQCTCRPGVTGQACDRCOLGFFGSSIKGCRACRCSPLG 971
QY 957 SLSLOCKDGRCECREGFGVGNRCQCEENFYFNRSWPGCQCECPACRYLVKDKVADHRVKL 1016
Db 972 AASAOCHVNGTCVCRPGFEGYKCDRCHYNFFLTADGTHCQCPSCYALVKEETAKLKL 1031
QY 1017 QELESILANLGTGDEMVTDAQFEDRLKEAEREVMDDLREAOQVQKVDQNDLMDRLQRVNNT 1076
Db 1032 TLTEGWLQSDCGSPW--GFLDILLGEAPRG--DVYQGHLLPGAREAPLEQMMGLEGA 1086
QY 1077 LSSQISRLQNIIRNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSUTQPS 1136
Db 1087 VKAAREQLQRLNKGARCAQAGSQKTCQTLADLEAVLESSESEIILHAAAILASLEIPQ-EG 1145
QY 1137 TGDPNMTLLAEARKLAERHKEQADDIRVAKTANDTSTAYNLLRLTLAGENQTAFEI 1196
Db 1146 PSQPTKWSHLAIEARALARSHRDTATKIAATAWPAALLASNTSYALLWNLL--EGRVALET 1203
QY 1197 E-ELNPKYEQAKNISQDLEKQAARVHEEAKRAGDKAVEIYASVAQSLPDLSETL----- 1249
Db 1204 QRDLEDRYQEVQAAQKALEKTAVAEVLPEAE-----SVLATVQVQADTAPYLALLASP 1256
QY 1250 -----ENEANNIKMEAEENLEQLIDQKLKDYEDLREDMRGKELEVKNLLEKGTQQTADQ 1304
Db 1257 GALPQKSRAEDLGLKAKALEKTV---ASWQHMAE-AARTLQTAQAATLRQTEPLT--K 1309
QY 1305 LLARADAALKALAEAAKGRDRTLQEAANDILNLLKDFRRVNDNKNKAEEALRKIPAINQT 1364
Db 1310 LHQARAALTQASSSVQAAATVVMGARTLLADLEGMKLFPPRPKQAAALQKADSVSDRL 1369
QY 1365 ITEANEKTRAAQALGSAADATEAKNKAHEARLIASAVQKNATSTKAEARTFAEVTDL 1424
Db 1370 LADTKTKQAERMLGNAAPLSSSSAKKKGREAEVLAKDSAKLAKALLRERKQARRASRL 1429
QY 1425 DNEVNMLKQL-QEAEKELKRRKQDDADQDMMAGMASQAQAEAEINARKAKNSVTLSLI 1483

Db 1430 TSQTQATLQASQVLAASEARRQEEAERVGAGLS-----EMEQIRESRISLEKDIET 1484
QY 1484 INDLLEQLGQDGT--VDLNKLNEIEGILNKAKDEM-KVSDLDKVDSDLENEAKKQEAATM 1540
Db 1485 LSELLARGLSLDTHQAPAAQALNETQWALERLRLQLGSPGLQRLKLSLLEQESQQQLQIQ 1544
QY 1541 DYNRDIEEIMKDIRNLEDIRKTLPSGC 1567
Db 1545 GFESDLAEIRADKQNLAILHSLPENC 1571

RESULT 12
US-10-369-493-6816
; Sequence 6816, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6816
; LENGTH: 1557
; TYPE: PR1
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6816

Query Match 37.9%; Score 3240; DB 15; Length 1557;
Best Local Similarity 39.0%; Pred. No. 1.4e-175;
Matches 636; Conservative 289; Mismatches 541; Indels 166; Gaps 32;

QY 7 CTDEGR-PQRCMPFVNAFNVVATNTCGTP-PBEYCVQGTGVTGSKCHLCDAGQP 64
Db 25 CYDRATRQPCRCVPDFVNAFNVVATNTCGTKRPTKFCVQSGHTGORSVCETCDDRHE 84
QY 65 HLQGAFLTDYNNQADTTWQSQTMLAGVQYSSINLTLLHKGAFDITVRLKFTSRP 124
Db 85 GFSHPAKYLTDFNVGNNTWQSDTMQEQYPTTNTLTLVLGKSFDTIYVRLKFI SPRP 144
QY 125 ESFAIYKTRTREDGPWIPYQYVSGSCENTYSKANRGFI RTGGDEQQAALCTDDEFSDISPLTG 184
Db 145 ESFTIYKTHTDSEWEPWQYVSGSCENTYSKANRGFI RTGGDEQQAALCTDDEFSDISPLTG 203
QY 185 GNVAFSTLEGRPSAYNPDNSPVLOEWVATDIRVTLNRLNTFGDEVFNDPKVLKSYIYAI 244
Db 204 GNIAFSTLEGRPSAHAFEESEVLQKVVTAIRISLNRMTTFGDEVFNDPKVLKSYIYAI 263
QY 245 SDFAVGGRCKNGHASECMKNEF---DKLVNCKHNTYGVDCCKLPFFNDRPWRRA 300
Db 264 SDFAVGGRCKNGHASECMKNEF---DKLVNCKHNTYGVDCCKLPFFNDRPWRRA 323
QY 301 ESASECLPCDCNRSQCEYDPPELYRSTGHGHCNTCQDNTDGAHCERENFFRLGNNE 360
Db 324 VEANECIACNCSQLSNRCYFDQQLFEETGHGHCIDCQNTQGVHCEQCIANHWRRPGEN 383
QY 361 ACSSCHCSPVGSLSLSTQCDSDYGRCSCKPGVMGDKCDRCQPFHSLTEAGCPSCDPSGI 420
Db 384 YCVACGCGNEIGSLSTQCDSDYGRCSCKPGVMGDKCDRCQPFHSLTEAGCPSCDPSGI 443
QY 421 D---ECNVETGRVCCKDNVEGFNCERCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVG 477
Db 444 NNQPRCDSSSGSCSKLNVGRCQCKKPGYFDLSTENQFGCTPCFCFGHSSVCTNAVG 503
QY 478 SVYSISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIASISYFPPRYFIAPAKFLGKQV 537

Db 504 FAMNVSSVFDQDKQWAGQNRIGLQ-DTQWAEALDKAVAVSDTDNSPVYFVAPEQFLGDQR 562

Qy 538 LSYGQNLFSFRVDRDRLSAEDLVLEGAGLR-VSVPLIAQGNSSYPSETTVKYVFLRHE 596

Db 563 SSYNQDLVFTLKVAKHVTNQDVKDIIVGADROQLSTSIQAQGNPFPTTEAQTFRFVHA 622

Qy 597 ATDYPWRPALTPFEFQKLLNNLTSIKIRGTYSERSAGYLDVTLASARPGGV----PAT 652

Db 623 DPYFGWYPRINELDFIGILSNITAIKIRGTYSYKIDIGYLSNVNLGTAGVAPSAANPKQAT 682

Qy 653 WYESCTCPVGYGGQFCMCLSGYRRETNPGLPSPCVLCAACNGHSETCDPETGVCNCRDN 712

Db 683 WIEHCECLPGFVGQFCESGFRRETKEFGPFNHCIKDCDCHNSNSCEAEGSCICEHN 742

Qy 713 TAGPHCEKCSGGYGDSTAGTSSDCQPCPCPGSSCAVVPKTKEVVCTNCPTGTGKRCE 772

Db 743 TAGDTCERCARGYGDALQGTEDCQKPCPNDGPC-ILHADGDVICTECPNGYTGRRCD 801

Qy 773 LCDDGYFGDPLGRNGPVRRLCRLCQCSNDIDPNAVGNCRNLTGECCLKCIYNTAGFYCDRCK 832

Db 802 ECSDGYFGNP--KDGTE--CVECACSGNTDPNSIGNCDKITGECKKCIFNTHFGNCENCK 857

Qy 833 DGFFGNPLAPNPADKCKACNCPYGTMKQOS-----SCNPVTGQCECLPHVTGQDCGACD 887

Db 858 PGYWGDA LI-EPKGNQCSCGFAAGTRPNNNDYTLLECNQDQDCLPNIIGIQCDQCA 916

Qy 888 PGFVNLQSGQCERCDCCHALGSTNGQCDIRTGQCECOPGITGOHCERCEVNHFGFPEGC 947

Db 917 HGFYNTITSLGLGCQECNCDPLGSEGNWCDVNTGQCCQCKPGVTGQRCDCRACADYHFGSANGC 976

Qy 948 KPCDCHPEGSLSLQCK-DDGRCECREGFGVGNRCDCQCEENFYNRSWPGCQCECPACRYLVK 1006

Db 977 QPCDCEYIGSENQCCDVNSGQCLCKENVEGRRCCDQCAENRY--GITQGCLPCDDCYTLIQ 1034

Qy 1007 DKVADHRVKLQLESLIANLGTGDEMVTDOAFEDRLKBAER--EVMDLLREAQDVKDVD 1063

Db 1035 SRVNVFREKVKSLDNTLQEIITENPAPVNDTKFDEKVKETSRAASEVWEAVK--OKTKEGG 1092

Qy 1064 QNLMDRLQRVNTLSSQISRLQNRNTIETGNLAEQARAHVENTERLIEIASREL---- 1119

Db 1093 GTIKTKSKAIKDEIVAALKESLTSIDESVAQAKVGADAEADMKRWELIENARREIENVL 1152

Qy 1120 -----EKAKVAAANVSVTPESTGDPNNMTLLAEARKLAERHKEADDIVRVAKTA 1171

Db 1153 HYLETEGEERAQI-AYNASQKYGEQS---KRMSELASGTREAEKHLKQASEIQLSEQA 1208

Qy 1172 NDTSTBAYNLLRLTAGENQTAFFIEELNRKYEQ-AKNISQDLEKQAARVHEEAKRAGDK 1230

Db 1209 IANATOANKEASDAIYGGEIQISQIAELKEKQNLNESIHRITLD-----LAEQKKSAD 1263

Qy 1231 AVEIYA-----SVAQLSPLDSETLENEANNIKMEAELENLEQLIDQKLKD---YEDLREDM 1281

Db 1264 ANNLAASVLTNVEAVKIPSVDPKBLRNDVAGVLESEN--LVDSSVKENSANDELDFEV 1320

Qy 1282 RGKELEVKNLLEKQKTEQQTADQLLARADAAKALAEAAKKGRTDLOEANDILNNLKDFD 1341

Db 1321 NRSVADARNELQSSQDQQRVSDQLMLELEKSRERIVDSVSTADTKLKDAEAAALQVLEFFG 1380

Qy 1342 RRVNDNKTAAEEALRKIPAINQ---TITEANEKTREA---QQAALGSAADATEAKNKAH 1394

Db 1381 AKIEKSRNDAAVAEFAGVEGINQRLDDIIDAQDKRNSLPIDKQFVIDYRKSAADVLLNETH 1440

Qy 1395 E-AERIASAVQKNA-TSTKAAERTFAEVTDLNEVNNMLKQLQEAELKRLKQDDADQD 1452

Db 1441 ALADRYKDIHSDVDTRDSTEA-----VQYDIEQLMEELTDSNENLQYKKQAEED 1491

Qy 1453 MTMAGMASQ-----AAQEAETNARKAKNSVTLSLSIINDLLEQLGLQDITVDNLKLN 1503

Db 1492 QMATEAVRKQLLPRILPSKQMLPFSLRKMKSRKSSILWVL----- 1532

Qy 1504 EIEGTLNKADEMKVSDLRKVSLENEAKKQEAAMDVYNDIEEIMKDIRNLEDIRKTL 1563

Db 1533 -----NLEEIRDNL 1541

Qy 1564 PSGCFNTPPSIEK 1575

Db 1542 PTRCFNVINLEQ 1553

RESULT 13

US-09-756-071B-13

; Sequence 13, Application US/09756071B

; Patent No. US20020052307A1

; GENERAL INFORMATION:

; APPLICANT: Tryggvason, Karl

; Kallunki, Pekka

; Pyke, Charles

; TITLE OF INVENTION: Laminin Chains: Diagnostic Uses

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fay Sharpe Fagan Minnich & McKee

; STREET: 1100 Superior Ave, Suite 700

; CITY: Cleveland

; STATE: Ohio

; COUNTRY: USA

; ZIP: 44114

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/756,071B

; FILING DATE: 08-Jan-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 09/663,147

; FILING DATE: 150-September 2000

; ATTORNEY/AGENT INFORMATION:

; NAME: Minnich, Richard, J.

; REGISTRATION NUMBER: 24,175

; REFERENCE/DOCKET NUMBER: TRV 20014

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 216-861-5582

; TELEFAX: 216-241-1666

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1193 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-756-071B-13

Query Match 30.9%; Score 2637; DB 9; Length 1193;

Best local Similarity 39.4%; Pred. No. 2.1e-141;

Matches 515; Conservative 235; Mismatches 418; Indels 138; Gaps 12;

Qy 286 CLPFFNDPWRRTAESAASECLPCDCNCRSQECYFDPPELYRSTGHGHCNQCNDTDGAH 345

Db 9 CLCFSLLLPAARATSRRE----VDCNCKSRQCFIDRELHQGTNGFRCLNCNDNTDGIH 64

Qy 346 CERCRENFRNLGNNEACSSCHCSFVGSLSLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLT 405

Db 65 CEKCKNGFYHRRERDRCLPCNCSKGSLSARCDNSGRCSCKPGVTGARCDRCLPGFHMILT 124

Qy 406 EAGC-----RPCSDPSSIDECNVETGRVCCKONVEGFNCERCKPGFFNLESSNPR 457

Db 125 DAGCTQDQRLDLSKDCDPCAGIAGPC--DAGRCVCKPAVTGERCDRCRSYYNLDGNGPE 182

Qy 458 GCTPCFCFCGHSSVCTNAVGVSYVSYISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVI 517

Db 183 GCTQCFCYCHSASCSSAEYSVHKITSTFHDQVDGWKAVQRNGSPAKLQWSQRHQDVFS 242

Qy 518 SDSYFPFPRYFIAPAKFLGQVLSYQNLSSFSFRVDRDRTRLAEDLVLEGAGLRVSVPLIA 577


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Db 243 AQRDLPVYFVAPAKFLGNQVSYGSLSFDRVDRGRHPSAHDVILEGAGLRITAPLMP 302
Qy 578 QGNSYPSETTVKYVFRLEHATDYPWRPALTPFEFQKLLNLTISIKIRGYSERSAGYLD 637
Db 303 LGKTLPCGLTKYTFRLNEHPSNNWSPOLSYFEYRLLRLNLALRIRATYGEYSTGYDN 362
Qy 638 VTLASARPGVPATWVESCTCPVYGGOFCMCLSGYRRPRLNLPYSPCVLCAKNGHS 697
Db 363 VTLISARPVSGAPAPWVEQICPVGYKGFQDCASGYKRDARSARLPGFTGTCPCNQG-G 421
Qy 698 ETCDPETGVCNCRDNTAGPHCEKSDGYGDSSTAGTSSDCPCPCPGSSCAVVPKTEV 757
Db 422 GACDPTGDCYSGDENPDIECADCPIGFYNDPHDPRS--CKPCCHNGFSCSVPTETEV 479
Qy 758 VCTNCPGTGTRKCELCDDGYFGDPLGRNGPVRCLRCQSDNIDPNVAGNCNRLTGECL 817
Db 480 VCNNCPGVTGARCELCAADGYFGDFGHPVRPCQPCQNSNVDPSASGNCRLTGRCL 539
Qy 818 KCIYNTAGFYCDRCKDGFNPLAPNADKCKACNCNPGYTMKQSSCNPNVTGQCECLPH 877
Db 540 KCIHNTAGIYCDQCKAGYFGDPLAPNADKCRACNCNPMGS----- 580
Qy 878 VTGQDCGACDPGFYNLQSGQGCERCDCALGSTNGQCDIRTGQCECQPGITGHCERCEV 937
Db 581 ----- 580
Qy 938 NHFGFPEGCKPCDCHREGSLSLQCKDDGRCECREGFGVNRCDQCEENYFYNRSPGQCE 997
Db 581 -----EPVG-----CRSDGTCVCKPGFGGNCHE-----GAFS 608
Qy 998 CPACYRLVKDVADHRVKLOELESILANLGTGDEMVTDOAFEDRLKEAREVMDLLREAQ 1057
Db 609 CPACYNQVKIQMDQFMQQLQRMALISKAQGGDVVPDTELEGRMQAEQALQDILRDAQ 668
Qy 1058 DVKDQDQNLMDRLQVNTLSSQISRLQNRITETETGLAELQARAHVENTERLIEIASR 1117
Db 669 ISEGASRLGLQAKVRSQENSYSQSLDDKMTVERVALGSQYQNRVRDTHRLITQML 728
Qy 1118 ELEKAKVAAANVSVTQPESTGDPNNMTLLAEARKLAERHKEADDIRVAKTANDTSTE 1177
Db 729 SLAESEASLGNINIPASDHVYVGPNGFKSLAQEAATRLAESHVESASNMEOQLTBEDYSKQ 788
Qy 1178 AYNLRLTL-----AGENQTAFTETELNRKYEQAKNISQDLEKQAAARVHEEAKRAGDK 1230
Db 789 ALSVRKALHEGVSGSGSPDGAV-VQGLVEKLEKTSLSLVRHMDEFKRTQKNLGNWKEEAQ 847
Qy 1231 AVEIYASVAQSLPDSLE-NEANNIKWEAENLEQLDQKLKDYEDLREDMRGKELEVK 1289
Db 848 SLRLDVSPLQGVSDQSFQVEEAKRIKQKADSLSLVTRHMDEFKRTQKNLGNWKEEAQ 907
Qy 1290 NLEKKGTEQOTAPQLLARADAKALAEAAKGRDITLQEAANDILNKLDFRRVNDNKT 1349
Db 908 QLLONGKSGREKSDQLLSRANLAKSRAQEAALSMGNATPYEVESILKNLREFDLQVDNRKA 967
Qy 1350 AAEALRKIPAINQTI TEANEKTEAQAALGSAADATEAKNKAHEAERIASAVQKNATS 1409
Db 968 EAEAMKRLSVISQKVSADSKTQAEARALGSAADAAQRAKNGAGEALEISSEIEQEIGS 1027
Qy 1410 TKAEARTFAEVTDLNNEVNNMLKQLEAEKELKRKODDADQDMMAGVAAQAEAIN 1469
Db 1028 LNLEANVTADGALAMEKGLASLSEMREVEGELEKELEFDTNMDAVQMVTEAQKVDTR 1087
Qy 1470 ARKAKNSVTSLSIINDLLEQLGLDITVDLNLKLEIEGTLNKAKDEMKSVDLDRKVSLE 1529
Db 1088 AKNAGVTIQTDLNTLGLHMDPLSVDEGLVLEQLKLSRAKTQIN-SQLRPMMSLE 1146
Qy 1530 NEAKKQEAALNDYNRDIIEIMKDIRNLEDIRKTLPSGCFNTPSIEK 1575
Db 1147 ERARQQRGHLLETSIDGILADVKVLENIRDNLPNGCYNTQALEQ 1192
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RESULT 14
US-10-392-113-14

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; Sequence 14, Application US/10392113
; Publication No. US20030224993A1
; GENERAL INFORMATION:
; APPLICANT: Deleu, Laurent
; TITLE OF INVENTION: COMPOSITIONS THAT INHIBIT PROLIFERATION
; TITLE OF INVENTION: OF CANCER CELLS
; FILE REFERENCE: 21108.000503
; CURRENT APPLICATION NUMBER: US/10/392,113
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: 60/365,078
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: PCT/US01/32127
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/239,705
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1193
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
; OTHER INFORMATION: Synthetic Construct
US-10-392-113-14
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Query Match 30.9%; Score 2637; DB 12; Length 1193;
Best Local Similarity 39.4%; Pred. No. 2.1e-141;
Matches 515; Conservative 237; Mismatches 416; Indels 138; Gaps 12;

Qy 286 CLPFFNDPRWRRTAESAECPLCDNCRSQECYFDPPELYRSTGHGHCNCDNDTGAH 345
Db 9 CLCFSLLLPAARATSRRE----VDCNCKSRQCIFDRELHRTGNGFRCLNCNDNDGIH 64
Qy 346 CERCRENFFRLGNNEACSSCHSCPVGSLSTQCDYSYGRCSCKPVGMDKCDRCQPGHSLT 405
Db 65 CEKCKNGFYRHRERDRCLPCNCSKXGSLARCDNSGRCSCKPVGTVGARCDRCCLPGFHLT 124
Qy 406 EAGC-----RPCSDPSGSDIECNVETGRCVCKDNVEGFNCERCKPGFFNLESSNPR 457
Db 125 DAGCTQDQRLDLSKDCDPAIAGPC--DAGRCVCKPVTGRCRCRSGYNNLDGNGPE 182
Qy 458 GCTPCFCFGHSSVCTNAVGVSYVSYSSSTFQIDEDGWRAEQDGDSEASLEWSSERQDI 517
Db 183 GCTQCFCYGHASACRSAAEYSVHKITSTFHDQVDGWKAVQRNGSPAKLQWSQRHQDVFS 242
Qy 518 SDSYFPYFIAPAKFLGKQVLSYQNLSPFSFRVDRDRRLSAEDLVLEGAGLRVSVPLIA 577
Db 243 AQRDLPVYFVAPAKFLGNQVSYGSLSFDRVDRGRHPSAHDVILEGAGLRITAPLMP 302
Qy 578 QGNSYPSETTVKYVFRLEHATDYPWRPALTPFEFQKLLNLTISIKIRGYSERSAGYLD 637
Db 303 LGKTLPCGLTKYTFRLNEHPSNNWSPOLSYFEYRLLRLNLALRIRATYGEYSTGYDN 362
Qy 638 VTLASARPGVPATWVESCTCPVYGGOFCMCLSGYRRPRLNLPYSPCVLCAKNGHS 697
Db 363 VTLISARPVSGAPAPWVEQICPVGYKGFQDCASGYKRDARSARLPGFTGTCPCNQG-G 421
Qy 698 ETCDPETGVCNCRDNTAGPHCEKSDGYGDSSTAGTSSDCPCPCPGSSCAVVPKTEV 757
Db 422 GACDPTGDCYSGDENPDIECADCPIGFYNDPHDPRS--CKPCCHNGFSCSVPTETEV 479
Qy 758 VCTNCPGTGTRKCELCDDGYFGDPLGRNGPVRCLRCQSDNIDPNVAGNCNRLTGECL 817
Db 480 VCNNCPGVTGARCELCAADGYFGDFGHPVRPCQPCQNSNVDPSASGNCRLTGRCL 539
Qy 818 KCIYNTAGFYCDRCKDGFNPLAPNADKCKACNCNPGYTMKQSSCNPNVTGQCECLPH 877
Db 540 KCIHNTAGIYCDQCKAGYFGDPLAPNADKCRACNCNPMGS----- 580
Qy 878 VTGQDCGACDPGFYNLQSGQGCERCDCALGSTNGQCDIRTGQCECQPGITGHCERCEV 937
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Db 581 ----- 580
Qy 938 NHFGFEGCKPCDCHPEGSLSLQCKDDGRCECREGFGVGNRCDCQCEENYFYNRSWPGCQE 997
Db 581 -----EPVG-----CRSDGTCVCCKPGFGGPNCEH-----GAFS 608
Qy 998 CPACYRLVKDKVADHRVKLQELSLIANLGTGDEMVTDOAFEDRLKEAREVMDLLREAQ 1057
Db 609 CPACYNQVKIQMDQFMQQLQRMALISKAQGGDVVPDTELEGRMQQAQALQDLRDAQ 668
Qy 1058 DVKVDQNLMDRLQVRNNTLSSQISRLQNIIRNTIETGNLAQAARAHVENTERLIEIASR 1117
Db 669 ISEGASRSLGLQAKVRSQENSQSRLLDDLKMTVERVRALGSQYQNRVRDTHRLITQMQL 728
Qy 1118 ELEKAKVAAANVSVTQPESTGDPNNMTLLAEEARKLAERHKQAEADDIVRVAKTANDTSTE 1177
Db 729 SLAESEASLGNTNIPASDHYVVGNGFKSLAQEAATRLAESHVESASNMEQLTRETEDYSKQ 788
Qy 1178 AYNLLRLTL-----AGENQTAFAEIEELNRKYEQAQNTSQDLEKQAARVHEEAKRAGDK 1230
Db 789 ALSVRKALHEGVGSGSGSPDGAU-VQGLVEKLEKTKSLAQQLTREATQAEIEADRSYQH 847
Qy 1231 AVEIVASVAQLSPLDSETLE-NEANNIKMEAEENLEQLIDQKLKDYEDLREDMRKELEVK 1289
Db 848 SLRLDSVSRLLQGVSDQSFQVEEAKRIKQKADSLSTLVTRHMDEFKRTQKNLGNWKEEAQ 907
Qy 1290 NLEKKGTEQQTADQLLARADAKALAEBAKKGRTDLOEANDILNNLKDFDRRVNDNKT 1349
Db 908 QLLONGKSGREKSDQLLSRANLAKSRAQEAALSMGNATFYEVSILKNLREFDLQVDNRKA 967
Qy 1350 AAEEALRKIPAINQITTEANEXTRBAQQALGSAADATEAKNKAHEAERIAASAVQKNATS 1409
Db 968 EAEAMKRLSYISQKVSADSKTQQAERALGSAADAQRAKNGAGEALEISSEIEQEIQS 1027
Qy 1410 TKAEARTFAEVTDLNNEVNNMLKQLQEAELKELKRKQDDADQDMMAGMASQAQAEABIN 1469
Db 1028 LNLEANTADGALAMEKGLASLXSEMREVEGELERKELEFDTNMDAVQMVI TEAQKVDTR 1087
Qy 1470 ARKAKNSVTSLLSIINDLLEQLGQDVTVDLNLKLEIEGTLNKADEMKSVDLRKVSdle 1529
Db 1088 AKNAGVTIQDTLNTLDGLLHMDQPLSVDEGLVLLEQLKSLAKTQIN-SQLRPNMSELE 1146
Qy 1530 NEAKKQEAAMIDYNRDIEEIMKDINLEDIRKTLPSGCFNTPSIEK 1575
Db 1147 ERARQORGHHLHLETSIDGILADVKNLENIRDNLPFGCYNTQALEQ 1192

RESULT 15
US-10-171-311-115
; Sequence 115, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoersh, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF CERVICAL CANCER
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 115
; LENGTH: 1193
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-311-115

Query Match      30.9%; Score 2637; DB 14; Length 1193;
Best Local Similarity 39.4%; Pred.No. 2.1e-141;
Matches 515; Conservative 237; Mismatches 416; Indels 138; Gaps 12;

Qy 286 CLPFFNDRPWRRAATAESAECPLDCDNGRSQECYFDPPELVRSTGHGHCNTCQDNDIDGAH 345
Db 9 CLCFSLLLPAAARATSRRE-----VDCNGKSRQCIFDRELHRTGTNGFRCLNCNDNDIDGIH 64
Qy 346 CERORENFFRLGNNEACSSCHSPVGSLSLSTQDSYGRCSCKPGVMGDKCDRCQPGFHSILT 405
Db 65 CEKCKNGFYRHRERDRCLPCNCNKGSLARSNDNGRCSCKPGVTGARCDRCLPGFHMILT 124
Qy 406 EAGC-----RPCSDPSSGSDIECNVETGRCVCKDNVEGFNCERCKPGFFNLESSNPR 457
Db 125 DAGCTQDQRLDLSKCDPAGIAGPC--DAGRCVCKPAVTGERCDRCRSYYNLDDGGNPE 182
Qy 458 GCTPCFCFGHSSVCTNAVGYSVYSISSTFQIDEDGWRAEORDGSEASLEWSSERQDIJAVI 517
Db 183 GCTQCFCYGHSSASCRSAEYSVHKITSTFHQDVGWKAQVNGSPAKLQWSQRHQDVFS 242
Qy 518 SDSYFPRYFIAPAKFLGKQVLSYQNLFSFSFRVDRDRDTRLSAEDLVLEGAGLRVSVPLIA 577
Db 243 AQRLDPVYFVAPAKFLGNQVSYGQSLSFYRVDGRGRHPSAHDVILEGAGLRITAPLMP 302
Qy 578 QGNSYPSETTVKYVFRLEATDYPRPALTPPFQKLLNLTISKIRGTYSERSAGYLLDD 637
Db 303 LGKTLPCGLTKTYTFRLNEHPSNNWSPQLSYFEYRRLRLNLTAIRIRATYGEYSTGYIDN 362
Qy 638 VTLASARPGVPATWVESCTCPVYGGQFCMCLSGYRRETPNLGPYSPCVLCACNGHS 697
Db 363 VTLISARPVSGAPAPWVEQCICPVYKGQFCQDCASGYKXDSARLPGFTGTCIPNCQG-G 421
Qy 698 ETCDPETGVNCRDNTAGPHCEKCSGDIYGDSTAGTSSDCQPCPCPGSSCAVVPKTKEV 757
Db 422 GACDPDTGDCYSGDENPDIEACDPIGFYNDPHDPRS--CKPCCHNGFSCSVMPETEEV 479
Qy 758 VCTNCPGTGTRKRCCLDDGYFGDPLGRNGPVRRLCRLCQSDNIDPNVAGNCNRLTGECL 817
Db 480 VCNNCPGVTGARCELCAADGYFGDPFGEHGPVRPCQPCQCNVNDVPSASGNCDRLLTGRCL 539
Qy 818 KCIYNTAGFYCDRCKDGGFFGNPLAPNPADKCKACNCNPYGTMTKQSSCNPVGTQCECLPH 877
Db 540 KCIHNTAGIYCDQCKAGYFGDPLAPNPADKCRACNCNPMGS----- 580
Qy 878 VTGQDCGACDPGFYNLQSGQGCERCDCHALGSTNGQCIRTGQCECQPGITGHCERCEV 937
Db 581 ----- 580
Qy 938 NHFGFEGCKPCDCHPEGSLSLQCKDDGRCECREGFGVGNRCDCQCEENYFYNRSWPGCQE 997
Db 581 -----EPVG-----CRSDGTCVCCKPGFGGPNCEH-----GAFS 608
Qy 998 CPACYRLVKDKVADHRVKLQELSLIANLGTGDEMVTDOAFEDRLKEAREVMDLLREAQ 1057
Db 609 CPACYNQVKIQMDQFMQQLQRMALISKAQGGDVVPDTELEGRMQQAQALQDLRDAQ 668
Qy 1058 DVKVDQNLMDRLQVRNNTLSSQISRLQNIIRNTIETGNLAQAARAHVENTERLIEIASR 1117
Db 669 ISEGASRSLGLQAKVRSQENSQSRLLDDLKMTVERVRALGSQYQNRVRDTHRLITQMQL 728
Qy 1118 ELEKAKVAAANVSVTQPESTGDPNNMTLLAEEARKLAERHKQAEADDIVRVAKTANDTSTE 1177
Db 729 SLAESEASLGNTNIPASDHYVVGNGFKSLAQEAATRLAESHVESASNMEQLTRETEDYSKQ 788
Qy 1178 AYNLLRLTL-----AGENQTAFAEIEELNRKYEQAQNTSQDLEKQAARVHEEAKRAGDK 1230
Db 789 ALSVRKALHEGVGSGSGSPDGAU-VQGLVEKLEKTKSLAQQLTREATQAEIEADRSYQH 847
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Db 789 ALSLVRKALHEGVGSGSGPDGAV-VQGLVEKLEKTKSLAQQLTREATQAEIEADRSYQH 847

QY 1231 AVEIYASVAGLSPLDSETLE-NEANNIKWEAENLEQLIDQKLKDYEDLREDMRGKELEVK 1289

Db 848 SLRLDLSVSRLLQGVSDQSFQVEEAKRIKQADSLSTLVTRHMEFKRTQKNLGNWKEEAQ 907

QY 1290 NLLEKGKTEQQTADQLLARADAAKALAEAAKGRDRTLQEANDILNNLKDFDRRVNDNKT 1349

Db 908 QLLQNGKSGREKSDQLLSRANLAKSRAQEALSMGNATFYEVESILKNLREFDLQVDNRKA 967

QY 1350 AAEEALRKIPAINQITITEANEKTRAQALGSAADATEAKNKAHEAERIAASAVQKNATS 1409

Db 968 EAEEAMKRLSVISQKVSDDSKTQQAERALGSAADAQRAKNGAGEALEISSEIEQEIGS 1027

QY 1410 TKAEAEERTFAEVTDLDNVNNMLKQLOEAEKELKRKQDDADQODMMAGMASQAAQEAEN 1469

Db 1028 LNLEANVTADGALAMEKGLASLKSEMREVEGELEKELEFDTNMDAVQMVITEAQKVDTR 1087

QY 1470 ARKAKNSVTSLSIINDLLEQLGQDQTLVDLNLKNEIEGTLNKADEMKSDDLDRKVSdle 1529

Db 1088 AKNAGVTIQDTLNTLDGLLHMDQPLSVDEEGLVLLLEQKLSRAKTQIN-SQLRPMMSLE 1146

QY 1530 NEAKKQEAAMDNRYNDIEEIMKDIRNLEDIRKTLPSGCFNTPSIEK 1575

Db 1147 ERARQQRGHLHLETSIDGILADVKNLENIRDNLPPGCYNTQALEQ 1192

Search completed: May 18, 2004, 15:42:59
Job time : 47.0948 secs

OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:58 ; Search time 14.504 Seconds
(without alignments)
10452.141 Million cell updates/sec

Title: US-10-037-182-16
Perfect score: 8544
Sequence: 1 QAAMDECTDEGRPQRCMPE.....EDIRKTLPSGCFNTPSIEKP 1576

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8540	100.0	1609	1 MMHUB2	laminin gamma-1 ch
2	8056	94.3	1607	1 MMMSB2	laminin gamma-1 ch
3	3433	40.2	1639	1 MMFFB2	laminin gamma-1 ch
4	3240	37.9	1557	2 T28811	hypothetical prote
5	2637	30.9	1193	2 A44018	laminin B2t chain
6	2454.5	28.7	1192	2 S69000	laminin gamma 2 ch
7	1782.5	20.9	3084	1 MMMSA	laminin alpha-1 ch
8	1774.5	20.8	3106	1 S53868	laminin alpha-2 ch
9	1726	20.2	3075	2 S14458	laminin alpha-1 ch
10	1673	19.6	1786	1 MMHUB1	laminin beta-1 cha
11	1669.5	19.5	1790	1 MMFFB1	laminin beta-1 cha
12	1643	19.2	1786	1 MMMSB1	laminin beta-1 cha
13	1626.5	19.0	2823	2 T23064	hypothetical prote
14	1626.5	19.0	2823	2 F87908	protein T22A3.8 [i
15	1626.5	19.0	3102	2 T43291	laminin alpha chai
16	1606.5	18.8	1808	2 T15099	hypothetical prote
17	1595.5	18.7	1801	1 MMRTS	laminin beta-2 cha
18	1578	18.5	1798	2 S53869	laminin beta-2 cha
19	1486.5	17.4	3712	2 S18253	laminin alpha-1 ch
20	1479.5	17.3	1797	2 A55677	laminin beta-2 cha
21	1394	16.3	3672	2 T23433	hypothetical prote
22	1394	16.3	3704	2 T37316	probable laminin a
23	1327.5	15.5	3635	2 T10053	laminin alpha 5 ch
24	1164.5	13.6	606	2 A54665	netrin-1 precursor
25	1061.5	12.4	581	2 B54665	netrin-2 precursor
26	986.5	11.5	612	2 JH0799	laminin-related pr
27	923	10.8	1170	2 A53612	laminin B1k chain
28	884.5	10.4	1168	2 I56985	kalinin B1 - mouse
29	880	10.3	4391	2 A38096	perlecan precursor

30	867.5	10.2	3707	2 S18252	heparan sulfate pr
31	630	7.4	1751	1 MMHUMH	laminin alpha-2 ch
32	609	7.1	1160	2 F88369	protein unc-52 [im
33	609	7.1	2295	2 C88369	protein unc-52 [im
34	609	7.1	3375	2 T19821	hypothetical prote
35	588	6.9	1620	2 T27283	hypothetical prote
36	574.5	6.7	1111	2 T26972	hypothetical prote
37	572.5	6.7	1816	1 S68960	laminin alpha-4 ch
38	549	6.4	1574	2 T13954	MEGF6 protein - ra
39	510	6.0	1713	2 A55347	adhesive ligand ep
40	485	5.7	303	2 B45067	laminin B1 Chain -
41	480.5	5.6	2524	2 A35844	Xotch protein - Af
42	479	5.6	400	2 T46388	hypothetical prote
43	452.5	5.3	2703	1 A24420	notch protein - fr
44	451	5.3	2437	2 S42612	transmembrane prot
45	450.5	5.3	2318	2 S45306	notch 3 protein -

ALIGNMENTS

RESULT 1

MMHUB2
laminin gamma-1 chain precursor - human
N;Alternate names: laminin chain B2
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text change 10-Dec-1999
C;Accession: S13548; A28158; S13549; B34961; S14664; S23567
R;Kallunki, T.; Ikonen, J.; Chow, L.T.; Kallunki, P.; Tryggvason, K.
J. Biol. Chem. 266, 221-228, 1991
A;Title: Structure of the human laminin B2 chain gene reveals extensive divergence from
A;Reference number: S13548; MUID:91093128; PMID:1985895
A;Accession: S13548
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1609 <KAL>
A;Cross-references: GB:M55217; NID:G186937
A;Note: the nucleotide sequence was submitted to GenBank, February 1991
R;Pikkarainen, T.; Kallunki, T.; Tryggvason, K.
J. Biol. Chem. 263, 6751-6758, 1988
A;Title: Human laminin B2 chain. Comparison of the complete amino acid sequence with the
A;Reference number: A28158; MUID:98198245; PMID:3360804
A;Accession: A28158
A;Molecule type: mRNA
A;Residues: 1-211, 'I', 213-1609 <PIK>
A;Cross-references: EMBL:J03202; NID:G186916; PIDN:AAA59488.1; PID:G307107
R;Eukushima, Y.; Pikkarainen, T.; Kallunki, T.; Eddy, R.L.; Byers, M.G.; Haley, L.L.; Hei
Cytogenet. Cell Genet. 48, 137-141, 1988
A;Title: Isolation of a human laminin B2 (LAMB2) cDNA clone and assignment of the gene to
A;Reference number: S13549; MUID:89169663; PMID:3234037
A;Accession: S13549
A;Molecule type: mRNA
A;Residues: 1393-1609 <FUK>
A;Cross-references: EMBL:M27654; NID:G186923; PIDN:AAA59489.1; PID:G186924
R;Olsen, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki, R.
Lab. Invest. 60, 772-782, 1989
A;Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 cha
A;Reference number: A34961; MUID:89280632; PMID:2733383
A;Accession: B34961
A;Molecule type: mRNA
A;Residues: 868-1551, 'N', 1553-1609 <OLS>
R;Santos, C.L.S.; Sabbaga, J.; Brentani, R.
DNA Seq. 1, 275-277, 1991
A;Title: Differences in human laminin B2 sequences.
A;Reference number: S14664; MUID:92216129; PMID:1806043
A;Accession: S14664
A;Molecule type: mRNA
A;Residues: 1282-1609 <SAN>
A;Cross-references: EMBL:X13939; NID:G34237; PIDN:CAA32122.1; PID:G34238
R;Vuolteenaho, R.; Kallunki, T.; Chow, L.; Ikonen, J.; Pikkarainen, T.; Tryggvason, K.
in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp. 175-193, Academic P
A;Title: Genes for the human laminin B1 and B2 chains.
A;Reference number: S23566

Qy 1561 KTLPSGCFNTPSIEKP 1576
|||||
Db 1594 KTLPSGCFNTPSIEKP 1609

RESULT 2

MMMSB2

laminin gamma-1 chain precursor - mouse

N;Alternate names: laminin chain B2

C;Species: Mus musculus (house mouse)

C;Date: 28-Feb-1986 #sequence revision 30-Jun-1991 #text change 10-Dec-1999

C;Accession: A28469; A27729; A28082; S02680; S05327; S02037; A02870; S13544; S14552

R;Sasaki, M.; Yamada, Y.

J. Biol. Chem. 262, 17111-17117, 1987

A;Title: The laminin B2 chain has a multidomain structure homologous to the B1 chain.

A;Reference number: A28469; MUID:88059118; PMID:3680290

A;Accession: A28469

A;Molecule type: mRNA

A;Residues: 1-1607 <SAS>

A;Cross-references: EMBL:J03484; NID:G198694; PIDN:AAA39405.1; PID:G2933688

R;Durkin, M.E.; Bartos, B.B.; Liu, S.H.; Phillips, S.L.; Chung, A.E.

Biochemistry 27, 5198-5204, 1988

A;Title: Primary structure of the mouse laminin B2 chain and comparison with laminin B1.

A;Reference number: A27729; MUID:89000737; PMID:3167041

A;Accession: A27729

A;Molecule type: mRNA

A;Residues: 1-263, 'D', 265-336, 'C', 338-446, 'PS', 449-661, 'S', 663-885, 887-1155, 1157-1433, 'A'

A;Cross-references: EMBL:J02930; NID:G198702; PIDN:AAA39408.1; PID:G2933691

A;Note: the authors translated the codon TAT for residue 544 as Asp and GCG for residue

R;Ogawa, K.; Burbelo, P.D.; Sasaki, M.; Yamada, Y.

J. Biol. Chem. 263, 8384-8389, 1988

A;Title: The laminin B2 chain promoter contains unique repeat sequences and is active in

A;Reference number: A28082; MUID:88228071; PMID:2836421

A;Accession: A28082

A;Molecule type: DNA

A;Residues: 1-215, 'A', 217-239 <OGA>

A;Cross-references: EMBL:J03749; NID:G198704; PIDN:AAA39409.1; PID:G554184

R;Fujiwara, S.; Shinkai, H.; Deutzmann, R.; Paulsson, M.; Timpl, R.

Biochem. J. 252, 453-461, 1988

A;Title: Structure and distribution of N-linked oligosaccharide chains on various domain

A;Reference number: S02678; MUID:88326259; PMID:2458101

A;Accession: S02680

A;Molecule type: protein

A;Residues: 227-238 <FUJ>

R;Hartl, L.; Oberbaeumer, I.; Deutzmann, R.

Eur. J. Biochem. 173, 629-635, 1988

A;Title: The N terminus of laminin A chain is homologous to the B chains.

A;Reference number: S00624; MUID:88225080; PMID:3267223

A;Accession: S05327

A;Molecule type: protein

A;Residues: 227-238, 387-393, 'F', 395-405, 881-912; 1022-1034 <HAR>

R;Deutzmann, R.; Huber, J.; Schmetz, K.A.; Oberbaeumer, I.; Hartl, L.

Eur. J. Biochem. 177, 35-45, 1988

A;Title: Structural study of long arm fragments of laminin. Evidence for repetitive C-te

A;Reference number: S01790; MUID:89030693; PMID:3181157

A;Accession: S02037

A;Molecule type: protein

A;Residues: 1362-1377, 'X', 1379-1392, 'X', 1394-1406 <DEU>

R;Barlow, D.P.; Green, N.M.; Kurkinen, M.; Hogan, B.L.M.

EMBO J. 3, 2355-2362, 1984

A;Title: Sequencing of laminin B chain cDNAs reveals C-terminal regions of coiled-coil a

A;Reference number: A02870; MUID:85051302; PMID:6209134

A;Accession: A02870

A;Molecule type: mRNA

A;Residues: 1391-1474, 'K', 1476-1575, 'N', 1577-1607 <BAR>

A;Cross-references: EMBL:X05211; NID:G52862; PIDN:CAA28838.1; PID:G817975

R;Paulsson, M.; Deutzmann, R.; Timpl, R.; Dalzoppo, D.; Odermatt, E.; Engel, J.

EMBO J. 4, 309-316, 1985

A;Title: Evidence for coiled-coil alpha-helical regions in the long arm of laminin.

A;Reference number: S13543; MUID:85257455; PMID:3848400

A;Accession: S13544

A;Molecule type: protein

A;Residues: 1506-1523, 'X', 1525 <PAU>

R;Olsen, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki,

Lab. Invest. 60, 772-782, 1989

A;Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 cha

A;Reference number: A34961; MUID:89280632; PMID:2733383

A;Accession: S14552

A;Molecule type: protein

A;Residues: 881-912; 1022-1034; 1364-1377; 1379-1392; 1394-1409; 1506-1525; 1593-1606 <OLS>

C;Genetics:

A;Gene: Lamb-2

A;Map position: 1

A;Introns: 138/1; 239/3

C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin

C;Function:

A;Description: interact with cells and with other basement membrane proteins to promote

C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology

C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular

Db 392 ACSPCHCSPVSLSTQCDSDSYGRCSCKPFGVMGDKCDRCQPGFHSLSLTAECRPPCSCDLRGST 451

QY 421 DECNVETGRCVCKDNVEGFNCERCCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGYSVY 480

Db 452 DECNVETGRCVCKDNVEGFNCERCCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGYSVY 511

QY 481 SISSTFQIDEDGWRABQRDQDGEASLEWSSERQDIAVISDSYFFPRYFIAPAKFLGKQVLSY 540

Db 512 DISSTFQIDEDGWRVQRDQDGEASLEWSSDRQDIAVISDSYFFPRYFIAPVKFLGNQVLSY 571

QY 541 GQNLSPSFRVDRRDTLSAEDLVLEGAGLRVSVPLIAQNSYPSETTVKYVFRLHEATDY 600

Db 572 GQNLSPSFRVDRRDTLSAEDLVLEGAGLRVSVPLIAQNSYPSETTVKYIIFRLHEATDY 631

QY 601 PWRPALTPFEFQKLLNLTLSIKIRGTYSERSAGYLDVDTLASARPGPGVPATWVESCTCP 660

Db 632 PWRPALSPFEFQKLLNLTLSIKIRGTYSERTAGYLDVDTLQ SARPGPGVPATWVESCTCP 691

QY 661 VYGGQFCFCEMCLSGYRRETPNLGPYSPCVLCACNHSETCDPETGVCNCRDNTAGPHCEK 720

Db 692 VYGGQFCETCLPGYRRETPSLGPYSPCVLCTCNHSETCDPETGVCNCRDNTAGPHCEK 751

QY 721 CSDGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKBWWCTNCPTGTTGKRCCELCDDGYFG 780

Db 752 CSDGYGDSSTLGTSSDCQPCPCPGSSCAIVPKTKBWWCTHCPTGTAGKRCCELCDDGYFG 811

QY 781 DPLGRNGPVRLCRLCQCSDNIDPNAVGNCRNLGTGCLKCIYNTAGFYCDRCKDGFNGNPL 840

Db 812 DPLGNGPVRLCRLCQCSDNIDPNAVGNCRNLGTGCLKCIYNTAGFYCDRCKEGFFGNPL 871

QY 841 APNPADKCKACACNPYGTGMQOSSCNPNVTGQCECLPHVVTGQDCGACDPGFNLSQSGQCE 900

Db 872 APNPADKCKACACNPYGTGVQOSSCNPNVTGQCQCLPHVSGRDCGTCDPGYNLSQSGQCE 931

QY 901 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCHERCCEVNHFGFGPEGCKPCDCHPEGSLSL 960

Db 932 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCHERCCEVNHFGFGPEGCKPCDCHHEGSLSL 991

QY 961 QCKDGRCECREGFGVGNRCQDCEENYFYNRSWPGCQBCPACRYRLVKDKVADHRVKLQELE 1020

Db 992 QCKDGRCECREGFGVGNRCQDCEENYFYNRSWPGCQBCPACRYRLVKDKAAHRVKLQELE 1051

QY 1021 SLIANLGTGDEMVTDOAFEDRLKEAREVMDLLREAQDVKDQVNDQNLMDRLQVNNLTSSQ 1080

Db 1052 SLIANLGTGDDMVTDOAFEDRLKEAREVTDLLREAGEVKDQVNDQNLMDRLQVNSSLSHQ 1111

QY 1081 ISRLQIRNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSUTQPESTGDP 1140

Db 1112 ISRLQIRNTIETGILAEARASRVSESTEOLIEIASRELEKAKMAAANVSITQPESTGEP 1171

QY 1141 NNMTLLAEARKLAERHKQEAADDIVRVAKTANDTSTEAYNLLRLTLAGENQTAFEIEELN 1200

Db 1172 NNMTLLAEARRLAERHKQEAADDIVRVAKTANETSABAYNLLRLTLAGENQTALEIEELN 1231

QY 1201 RKYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPLDSETLENEANNIKMEA 1260

Db 1232 RKYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEA 1291

QY 1261 ENLEQLIDQKLXDYEDLREDMRGKEVKNLLEKKGTEQQTADQLLARADAAKALAEAA 1320

Db 1292 ADLDRLLIDQKLXDYEDLREDMRGKEHEVKNLLEKKGAEQQTADQLLARADAAKALAEAA 1351

QY 1321 KKGRDTLQEBANDILNNLKDFRRVNDNKTAEEALRKJPAINQTTITEANEKTRAQQAALG 1380

Db 1352 KKGRSTLQEBANDILNNLKDFRRVNDNKTAEEALRRIPAINRTIAEANEKTREAQLALG 1411

QY 1381 SAAADATEAKNKAHEAERIAASAVQKATSTKAAERTFAEVTDLCDNEVNNMLKQLQEAEBK 1440

Db 1412 NAAADATEAKNKAHEAERIAASAVQKATSTTKADAERTFGEVTDLDNEVNGMLRQLEEAEN 1471

QY 1441 ELKRKQDDADQDMMWAGMASQAQAEALNARKAKNSVTSLSLSIINDLLEQLGQLDFTVDLN 1500

Db 1472 ELKRKQDDADQDMMWAGMASQAQAEALNARKAKNSVSSLLSQNLNLLDQLGQLDFTVDLN 1531

RESULT 3

MMFFB2
laminin gamma-1 chain precursor - fruit fly (Drosophila melanogaster)
N;Alternate names: laminin chain B2
C;Species: Drosophila melanogaster
C;Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text_change 16-Jun-2000
C;Accession: A31483; A33737; S01733; A40502
R;Chi, H.C.; Hui, C.F.
J. Biol. Chem. 264, 1543-1550, 1989
A;Title: Primary structure of the Drosophila laminin B2 chain and comparison with human,
A;Reference number: A31483; MUID:89109164; PMID:2912972
A;Accession: A31483
A;Molecule type: mRNA
A;Residues: 1-1639 <CH1>
A;Cross-references: EMBL:M25063; NID:g157803; PIDN:AAA28664.1; PID:g157804
R;Montell, D.J.; Goodman, C.S.
J. Cell Biol. 109, 2441-2453, 1989
A;Title: Drosophila laminin: sequence of B2 subunit and expression of all three subunits
A;Reference number: A33737; MUID:90037237; PMID:2808533
A;Accession: A33737
A;Molecule type: mRNA
A;Residues: 1-39, 'T', 41-891, 'L', 893-1106, 'T', 1108-1459, 'HV', 1462-1581, 'G', 1583-1639 <MON
A;Note: 831-Tyr was also found
R;Chi, H.C.; Hui, C.F.
Nucleic Acids Res. 16, 7205-7206, 1988
A;Title: cDNA and amino acid sequences of Drosophila laminin B2 chain.
A;Reference number: S01733; MUID:88303364; PMID:3405777
A;Accession: S01733
A;Molecule type: mRNA
A;Residues: 344-1639 <CH2>
A;Cross-references: EMBL:X07806; NID:g8179; PIDN:CAA30665.1; PID:g1335618
A;Note: the authors translated the codon GGC for residue 409 as Phe
R;Chi, H.C.; Juminaga, D.; Wang, S.Y.; Hui, C.F.
DNA Cell Biol. 10, 451-466, 1991
A;Title: Structure of the Drosophila gene for the laminin B2 chain.
A;Reference number: A40502; MUID:91299161; PMID:1840513
A;Accession: A40502
A;Molecule type: DNA
A;Residues: 1-891, 'L', 893-1639 <CH3>
A;Cross-references: GB:M58417; NID:g157805; PIDN:AAA28665.1; PID:g157806
C;Genetics:
A;Gene: lamB2
A;Cross-references: FlyBase:FBgn0002528
A;Map position: 3L 67C
A;Introns: 65/3; 110/2; 153/1; 358/1; 495/2; 1357/2; 1469/3; 1570/1
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C;Function:
A;Description: interact with cells and with other basement membrane proteins to promote
C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular
F;1-33/Domain: signal sequence #status predicted <SIG>
F;34-1639/Product: laminin gamma-1 chain #status predicted <MAT>
F;34-297/Domain: VI <DOM6>
F;298-528/Domain: V <DOM5>
F;299-356/Domain: laminin-type EGF-like homology <LE01>
F;359-411/Domain: laminin-type EGF-like homology <LE02>
F;414-458/Domain: laminin-type EGF-like homology <LE03>
F;461-511/Domain: laminin-type EGF-like homology <LE04>
F;514-523/Domain: laminin-type EGF-like homology #status atypical <LE05>
F;529-705/Domain: IV <DOM4>
F;706-1057/Domain: III <DOM3>
F;710-741/Domain: laminin-type EGF-like homology #status atypical <LE06>
F;744-790/Domain: laminin-type EGF-like homology <LE07>

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:26:08 ; Search time 8.96059 Seconds
(without alignments)
9158.169 Million cell updates/sec

Title: US-10-037-182-16
Perfect score: 8544
Sequence: 1 QAAMDECTDEGGRPQRCMPE.....EDIRKTLPSGCFNTPSIEKP 1576

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8540	100.0	1609	1 LMG1_HUMAN	P11047 homo sapien
2	8056	94.3	1607	1 LMG1_MOUSE	P02468 mus musculu
3	3600	42.1	1587	1 LMG3_HUMAN	Q9y6n6 homo sapien
4	3482.5	40.8	1581	1 LMG3_MOUSE	Q9r0b6 mus musculu
5	3440	40.3	1639	1 LMG1_DROME	P15215 drosophila
6	3222	37.7	1535	1 LML1_CAEEL	Q18823 caenorhabdi
7	2637	30.9	1193	1 LMG2_HUMAN	Q13753 homo sapien
8	2529	29.6	1191	1 LMG2_MOUSE	Q61092 mus musculu
9	1782.5	20.9	3084	1 LMA1_MOUSE	P19137 mus musculu
10	1776	20.8	3110	1 LMA2_HUMAN	P24043 homo sapien
11	1774.5	20.8	3106	1 LMA2_MOUSE	Q60675 mus musculu
12	1726	20.2	3075	1 LMA1_MOUSE	P25391 homo sapien
13	1673	19.6	1786	1 LMB1_HUMAN	P07942 homo sapien
14	1669.5	19.5	1790	1 LMB1_DROME	P11046 drosophila
15	1643	19.2	1786	1 LMB1_MOUSE	P02469 mus musculu
16	1595.5	18.7	1801	1 LMB2_RAT	P15800 rattus norv
17	1572	18.4	1798	1 LMB2_HUMAN	P55268 homo sapien
18	1554	18.2	1799	1 LMB2_MOUSE	Q61292 mus musculu
19	1486.5	17.4	3712	1 LMA_DROME	Q00174 drosophila
20	1394	16.3	3672	1 LML2_CAEEL	Q21313 caenorhabdi
21	1359	15.9	3718	1 LMA5_MOUSE	Q61001 mus musculu
22	1296.5	15.2	3695	1 LMA5_HUMAN	O15230 homo sapien
23	1164.5	13.6	606	1 NET1_MOUSE	Q09118 mus musculu
24	1157	13.5	604	1 NET1_HUMAN	O95631 homo sapien
25	1156	13.5	604	1 NET1_MOUSE	Q61789 mus musculu
26	1141.5	13.4	3333	1 LMA3_MOUSE	Q90922 gallus gall
27	1061.5	12.4	581	1 NET2_CHICK	Q90923 gallus gall
28	986.5	11.5	612	1 UNC6_CAEEL	P34710 caenorhabdi
29	930	10.9	1172	1 LMB3_HUMAN	Q13751 homo sapien
30	887	10.4	727	1 NETA_DROME	Q24567 drosophila
31	883.5	10.3	1168	1 LMB3_MOUSE	Q61087 mus musculu
32	880	10.3	4391	1 PGEM_HUMAN	P98160 homo sapien
33	867.5	10.2	3707	1 PGEM_MOUSE	Q05793 mus musculu

Q24568 drosophila
Q8r4g0 mus musculu
Q06561 caenorhabdi
Q96cw9 homo sapien
Q16363 homo sapien
P97927 mus musculu
Q8r4f1 mus musculu
Q16787 homo sapien
Q01635 gallus gall
P21783 xenopus lae
P07207 drosophila
P46530 brachydanio

34 849 9.9 793 1 NETB_DROME
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36 609 7.1 3375 1 UN52_CAEEL
37 580.5 6.8 530 1 NTC2_HUMAN
38 571.5 6.7 1816 1 LMA4_HUMAN
39 554.5 6.5 1816 1 LMA4_MOUSE
40 545 6.4 589 1 NTC2_MOUSE
41 510 6.0 1713 1 LMA3_HUMAN
42 485 5.7 303 1 LMB1_CHICK
43 472 5.5 2524 1 NOTC_XENLA
44 453.5 5.3 2703 1 NOTC_DROME
45 451 5.3 2437 1 NTC1_BRARE

ALIGNMENTS

RESULT 1
LMG1_HUMAN
ID LMG1_HUMAN STANDARD; PRT; 1609 AA.
AC P11047;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Laminin gamma-1 chain precursor (Laminin B2 chain).
GN LAMC1 OR LAMB2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=91093128; PubMed=1985895;
RA Kallunki T., Ikonen J., Chow L.T., Kallunki P., Tryggvason K.;
RT "Structure of the human laminin B2 chain gene reveals extensive
RT divergence from the laminin B1 chain gene.";
RL J. Biol. Chem. 266:221-228(1991).
RN [2]
SEQUENCE FROM N.A.
RX MEDLINE=88198245; PubMed=3360804;
RA Pikkarainen T., Kallunki T., Tryggvason K.;
RT "Human laminin B2 chain. Comparison of the complete amino acid
RT sequence with the B1 chain reveals variability in sequence homology
RT between different structural domains.";
RL J. Biol. Chem. 263:6751-6758(1988).
RN [3]
SEQUENCE OF 1393-1609 FROM N.A.
RX MEDLINE=89169663; PubMed=3234037;
RA Fukushima Y., Pikkarainen T., Kallunki T., Eddy R.L., Byers M.G.,
RA Haley L.L., Henry W.M., Tryggvason K., Shows T.B.;
RT "Isolation of a human laminin B2 (LAMB2) cDNA clone and assignment of
RT the gene to chromosome region 1q25-->q31.";
RL Cytogenet. Cell Genet. 48:137-141(1988).
RN [4]
SEQUENCE OF 1282-1609 FROM N.A.
RC TISSUE=Endothelial cells;
RX MEDLINE=92216129; PubMed=1806043;
RA Santos C.L.S., Sabbaga J., Brentani R.;
RT "Differences in human laminin B2 sequences.";
RL DNA Seq. 1:275-277(1991).
RN [5]
CARBOHYDRATE-LINKAGE SITE ASN-650.
RX MEDLINE=22660472; PubMed=12754519;
RA Zhang H., Li X.-J., Martin D.B., Aebersold R.;
RT "Identification and quantification of N-linked glycoproteins using
RT hydrazide chemistry, stable isotope labeling and mass spectrometry.";
RL Nat. Biotechnol. 21:660-666(2003).
CC -I- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components.
CC -I- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC different polypeptide chains (alpha, beta, gamma), which are bound

to each other by disulfide bonds into a cross-shaped molecule comprising one long and three short arms with globules at each end. The gamma-1 chain is a subunit of laminin-1 (EHS laminin), laminin-2 (merosin), laminin-3 (S-laminin), laminin-4 (S-merosin), laminin-6 (K-laminin) and laminin-7 (KS-laminin).

CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Found in the basement membranes (major component).
CC -!- DOMAIN: The alpha-helical domains I and II are thought to interact with other laminin chains to form a coiled coil structure.
CC -!- DOMAIN: Domains VI and IV are globular.
CC -!- SIMILARITY: Contains 1 laminin N-terminal domain.
CC -!- SIMILARITY: Contains 11 laminin EGF-like domains.
CC -!- SIMILARITY: Contains 1 laminin IV domain.

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DR EMBL; M55210; AAA59492.1; -.
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DR Genew; HGNC:6492; LAMC1.
DR MIM; 150290; -.
DR GO; GO:0005604; C:basement membrane; TAS.
DR GO; GO:0007492; P:endoderm development; TAS.
DR GO; GO:0006461; P:protein complex assembly; TAS.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR008212; Lam_N2.
DR InterPro; IPR000034; Laminin_B.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR008211; LamNT.
DR Pfam; PF00052; laminin_B; 1.
DR Pfam; PF00053; laminin_EGF; 9.
DR Pfam; PF00055; laminin_Nterm; 1.
DR PRINTS; PR00011; EGFLAMININ.
DR PRODOM; PD002082; Lam_N2; 1.
DR SMART; SM00180; EGF_Lam; 8.
DR SMART; SM00281; LamB; 1.
DR SMART; SM00136; LamNT; 1.
DR PROSITE; PS00022; EGF_1; 8.

DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 11.
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal; Polymorphism.
FT SIGNAL 1 33
FT CHAIN 34 1609 LAMININ GAMMA-1 CHAIN.
FT DOMAIN 34 285 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 286 341 LAMININ EGF-LIKE 1.
FT DOMAIN 342 397 LAMININ EGF-LIKE 2.
FT DOMAIN 398 444 LAMININ EGF-LIKE 3.
FT DOMAIN 445 494 LAMININ EGF-LIKE 4.
FT DOMAIN 495 504 LAMININ EGF-LIKE 5 (N-TERMINAL).
FT DOMAIN 505 689 LAMININ DOMAIN IV.
FT DOMAIN 690 723 LAMININ EGF-LIKE 5 (C-TERMINAL).
FT DOMAIN 724 772 LAMININ EGF-LIKE 6.
FT DOMAIN 773 827 LAMININ EGF-LIKE 7.
FT DOMAIN 828 883 LAMININ EGF-LIKE 8.
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FT CARBOHYD 650 650 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 1107 1107 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1161 1161 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1175 1175 N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match				100.0%; Score 8540; DB 1; Length 1609;			
Best Local Similarity				99.9%; Pred. No. 2.9e-308;			
Matches 1575; Conservative				0; Mismatches 1; Indels 0; Gaps 0;			
QY	1	QAAMDECTDEGGRPQRCMPEFVNAAFNVTVATNTCGTPPEEYCVQGTGVTKSCHLCD	60				
Db	34	QAAMDECTDEGGRPQRCMPEFVNAAFNVTVATNTCGTPPEEYCVQGTGVTKSCHLCD	93				
QY	61	ACQPHLQHGAFLTDYNNQADTTWQSQTMLAGVQYPSSINLTLLHLGKAFDITYVRLKFH	120				
Db	94	ACQPHLQHGAFLTDYNNQADTTWQSQTMLAGVQYPSSINLTLLHLGKAFDITYVRLKFH	153				
QY	121	TSRPESFAIYKRTREDGPWIPYQYYSGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDIS	180				
Db	154	TSRPESFAIYKRTREDGPWIPYQYYSGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDFS	213				
QY	181	PLTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVNDPKVLYKSY	240				
Db	214	PLTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVNDPKVLYKSY	273				
QY	241	YYAISDFAVGGRCKCNHGASECMKNEFDKLVNCCKHNTYGVDCCKLPPFNDRPWRATA	300				
Db	274	YYAISDFAVGGRCKCNHGASECMKNEFDKLVNCCKHNTYGVDCCKLPPFNDRPWRATA	333				
QY	301	ESASECLPCDCNGRSQECVFPDPPELYRSTGHGGHCTNCQDNTDGAHCERCENFRLGNNE	360				
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QY	361	ACSSCHCSPVGSLSSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCPCSDPSGSI	420				
Db	394	ACSSCHCSPVGSLSSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCPCSDPSGSI	453				
QY	421	DECNVETGRCVCKDNVEGNCERCCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGYSVY	480				
Db	454	DECNVETGRCVCKDNVEGNCERCCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGYSVY	513				
QY	481	SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY	540				
Db	514	SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY	573				
QY	541	GQNLFSFRVDRRDTRLSABDLVLEGAGLRVSVPVLIAGQNSYPSSETTVKYVFRLLHEATDY	600				
Db	574	GQNLFSFRVDRRDTRLSABDLVLEGAGLRVSVPVLIAGQNSYPSSETTVKYVFRLLHEATDY	633				
QY	601	PWRPALTPFEFQKLLNLTISKIRGTYSERSAGYLDVTLASARPGPGVPATWVESCTCP	660				
Db	634	PWRPALTPFEFQKLLNLTISKIRGTYSERSAGYLDVTLASARPGPGVPATWVESCTCP	693				
QY	661	VGYGGQFCMCLSGYRRTPNLGPYSPCVLCACNGHSETCDPETGVNCNRDNTAGPHCEK	720				
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QY	721	CSDGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKWVCTNCPTGTTGKRCELCDGGYFG	780				
Db	754	CSDGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKWVCTNCPTGTTGKRCELCDGGYFG	813				
QY	781	DPLGRNGPVLRLCQCSNDIDPNAVGNCRNLGTGECLKCIYNTAGFYCDRCCKDGGFGNPL	840				
Db	814	DPLGRNGPVLRLCQCSNDIDPNAVGNCRNLGTGECLKCIYNTAGFYCDRCCKDGGFGNPL	873				
QY	841	APNPADKCKACNCNPYGTMKQSSCNPNVTGQCECLPHVVTGQDCGACDPGFYNLQSGQGE	900				
Db	874	APNPADKCKACNCNPYGTMKQSSCNPNVTGQCECLPHVVTGQDCGACDPGFYNLQSGQGE	933				
QY	901	RCDCHALGSTNGQCDIRTGQCECQPGITGQHCHERCEVNHFGFPEGCKPCDCHPEGSLSL	960				
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QY	961	QCKDDGRCECREGFGVGNRCQDQCEENYFYNRSWPCQCECPACYRLVKDKVADHRVKLQELE	1020				
Db	994	QCKDDGRCECREGFGVGNRCQDQCEENYFYNRSWPCQCECPACYRLVKDKVADHRVKLQELE	1053				

QY	1021	SLIANLGTGDEMVTDAQAFEDRLKEAEREVMDLLREACQVKDQVQDQNLMDRLQRVNNTLSSQ	1080
Db	1054	SLIANLGTGDEMVTDAQAFEDRLKEAEREVMDLLREACQVKDQVQDQNLMDRLQRVNNTLSSQ	1113
QY	1081	ISRLQIRNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP	1140
Db	1114	ISRLQIRNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP	1173
QY	1141	NNMTLLAEEARKLAERHKQEADDIVRVAKTANDTSTEAYNLLRLTLAGENQTAFAIEELN	1200
Db	1174	NNMTLLAEEARKLAERHKQEADDIVRVAKTANDTSTEAYNLLRLTLAGENQTAFAIEELN	1233
QY	1201	RKYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIIVASVAQLSPDSETLENEANNIKMEA	1260
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QY	1261	ENLEQLIDQKLKDYEDLREDMRGKELEVKNLLEKKGTEQQTADQLLARADAAKALAEAA	1320
Db	1294	ENLEQLIDQKLKDYEDLREDMRGKELEVKNLLEKKGTEQQTADQLLARADAAKALAEAA	1353
QY	1321	KKGRDTLQEANDILNLLKDFRRVNDNKTAAEEALRKIPAINQTITEANEKTRBAQQALG	1380
Db	1354	KKGRDTLQEANDILNLLKDFRRVNDNKTAAEEALRKIPAINQTITEANEKTRBAQQALG	1413
QY	1381	SAAADATEAKNKAHEAERIAASAVQKNATSTKAEABRTFAEVTDLDNVNNMLKQLEAEK	1440
Db	1414	SAAADATEAKNKAHEAERIAASAVQKNATSTKAEABRTFAEVTDLDNVNNMLKQLEAEK	1473
QY	1441	ELKRQDDADQDMMAGMASQAQAEAEINARKAKNSVTSLLSIINDLLEQLGQDQDVTDLN	1500
Db	1474	ELKRQDDADQDMMAGMASQAQAEAEINARKAKNSVTSLLSIINDLLEQLGQDQDVTDLN	1533
QY	1501	KLNEIEGTNLKAKDEMKVSDLDKRVSDLENEAKKQEAAMDYNRDIEEIMKDINLEDIR	1560
Db	1534	KLNEIEGTNLKAKDEMKVSDLDKRVSDLENEAKKQEAAMDYNRDIEEIMKDINLEDIR	1593
QY	1561	KTLPSCGCFNTPSIEKP	1576
Db	1594	KTLPSCGCFNTPSIEKP	1609

RESULT 2

LMG1_MOUSE			
ID	LMG1_MOUSE	STANDARD;	PRT; 1607 AA.
AC	P02468;		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	01-JUL-1989 (Rel. 11, Last sequence update)		
DT	15-MAR-2004 (Rel. 43, Last annotation update)		
DE	Laminin gamma-1 chain precursor (Laminin B2 chain).		
GN	LAMC1 OR LAMC-1 OR LAMB-2.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=88059118; PubMed=3680290;		
RA	Sasaki M., Yamada Y.;		
RT	"The laminin B2 chain has a multidomain structure homologous to the		
RT	B1 chain."		
RL	J. Biol. Chem. 262:17111-17117(1987).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=89000737; PubMed=3167041;		
RA	Durkin M.E., Bartos B.B., Liu S.-H., Phillips S.L., Chung A.E.;		
RT	"Primary structure of the mouse laminin B2 chain and comparison with		
RT	laminin B1."		
RL	Biochemistry 27:5198-5204(1988).		
RN	[3]		
RP	SEQUENCE OF 1-239 FROM N.A.		
RX	MEDLINE=88228071; PubMed=2836421;		
RA	Ogawa K., Burbelo P.D., Sasaki M., Yamada Y.;		
RT	"The laminin B2 chain promoter contains unique repeat sequences and		

RT is active in transient transfection.";
RL J. Biol. Chem. 263:8384-8389(1988).
RN [4]
RP SEQUENCE OF 1391-1607 FROM N.A.
RX MEDLINE=85051302; PubMed=6209134;
RA Barlow D.P., Green N.M., Kurkinen M., Hogan B.L.M.;
RT "Sequencing of laminin B chain cDNAs reveals C-terminal regions of
RT coiled-coil alpha-helix.";
RL EMBO J. 3:2355-2362(1984).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 771-932.
RX MEDLINE=96196434; PubMed=8648630;
RA Stetefeld J., Mayer U., Timpl R., Huber R.;
RT "Crystal structure of three consecutive laminin-type epidermal growth
RT factor-like (LE) modules of laminin gamma1 chain harboring the
RT nidogen binding site.";
RL J. Mol. Biol. 257:644-657(1996).
RN [6]
RP STRUCTURE BY NMR OF 824-881.
RX MEDLINE=96196435; PubMed=8648631;
RA Baumgartner R., Czisch M., Mayer U., Poeschl E., Huber R.,
RA Timpl R., Holak T.A.;
RT "Structure of the nidogen binding LE module of the laminin gamma1
RT chain in solution.";
RL J. Mol. Biol. 257:658-668(1996).
RN [7]
CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components.
CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC different polypeptide chains (alpha, beta, gamma), which are bound
CC to each other by disulfide bonds into a cross-shaped molecule
CC comprising one long and three short arms with globules at each
CC end. The gamma-1 chain is a subunit of laminin-1 (EHS laminin),
CC laminin-2 (merosin), laminin-3 (S-laminin), laminin-4 (S-merosin),
CC laminin-6 (K-laminin) and laminin-7 (KS-laminin).
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Found in the basement membranes (major
CC component).
CC -!- DOMAIN: The alpha-helical domains I and II are thought to interact
CC with other laminin chains to form a coiled coil structure.
CC -!- DOMAIN: Domains VI and IV are globular.
CC -!- SIMILARITY: Contains 1 laminin N-terminal domain.
CC -!- SIMILARITY: Contains 11 laminin EGF-like domains.
CC -!- SIMILARITY: Contains 1 laminin IV domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X05211; CAA28838.1; -
DR EMBL; J03484; AAA39405.1; -
DR EMBL; J02930; AAA39408.1; -
DR EMBL; J03749; AAA39409.1; -
DR PIR; A28469; MMSB2.
DR PDB; 1KLO; 20-AUG-97.
DR PDB; 1TLE; 12-FEB-97.
DR MGD; MGI:99914; Lamc1.
DR GO; GO:0005604; C:basement membrane; IDA.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR008212; Lam_N2.
DR InterPro; IPR000034; Laminin_B.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR008211; LamNT.
DR Pfam; PF00052; laminin_B; 1.
DR Pfam; PF00053; laminin_EGF; 9.
DR Pfam; PF00055; laminin_Nterm; 1.
DR PRINTS; PR00011; EGFLAMININ.
DR ProDom; PD002082; Lam_N2; 1.

DR SMART; SM00180; EGF_Lam; 8.
DR SMART; SM00281; LamB; 1.
DR SMART; SM00136; LamNT; 1.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 10.
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal; 3D-structure.
FT SIGNAL 1 33
FT CHAIN 34 1607 LAMININ GAMMA-1 CHAIN.
FT DOMAIN 34 283 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 284 339 LAMININ EGF-LIKE 1.
FT DOMAIN 340 395 LAMININ EGF-LIKE 2.
FT DOMAIN 396 442 LAMININ EGF-LIKE 3.
FT DOMAIN 443 492 LAMININ EGF-LIKE 4.
FT DOMAIN 493 502 LAMININ EGF-LIKE 5 (N-TERMINAL).
FT DOMAIN 503 587 LAMININ DOMAIN IV.
FT DOMAIN 588 721 LAMININ EGF-LIKE 5 (C-TERMINAL).
FT DOMAIN 722 770 LAMININ EGF-LIKE 6.
FT DOMAIN 771 825 LAMININ EGF-LIKE 7.
FT DOMAIN 826 881 LAMININ EGF-LIKE 8 (NIDOGEN-BINDING).
FT DOMAIN 882 932 LAMININ EGF-LIKE 9.
FT DOMAIN 933 980 LAMININ EGF-LIKE 10.
FT DOMAIN 981 1028 LAMININ EGF-LIKE 11.
FT DOMAIN 1029 1607 DOMAIN II AND I.
FT DOMAIN 1034 1594 COILED COIL (POTENTIAL).
FT DISULFID 340 349 BY SIMILARITY.
FT DISULFID 342 365 BY SIMILARITY.
FT DISULFID 368 377 BY SIMILARITY.
FT DISULFID 380 393 BY SIMILARITY.
FT DISULFID 396 408 BY SIMILARITY.
FT DISULFID 398 414 BY SIMILARITY.
FT DISULFID 416 425 BY SIMILARITY.
FT DISULFID 428 440 BY SIMILARITY.
FT DISULFID 443 454 BY SIMILARITY.
FT DISULFID 445 461 BY SIMILARITY.
FT DISULFID 463 472 BY SIMILARITY.
FT DISULFID 475 490 BY SIMILARITY.
FT DISULFID 722 731 BY SIMILARITY.
FT DISULFID 724 738 BY SIMILARITY.
FT DISULFID 740 749 BY SIMILARITY.
FT DISULFID 752 768 BY SIMILARITY.
FT DISULFID 771 779 BY SIMILARITY.
FT DISULFID 773 790 BY SIMILARITY.
FT DISULFID 793 802 BY SIMILARITY.
FT DISULFID 805 823 BY SIMILARITY.
FT DISULFID 826 840 BY SIMILARITY.
FT DISULFID 828 847 BY SIMILARITY.
FT DISULFID 850 859 BY SIMILARITY.
FT DISULFID 862 879 BY SIMILARITY.
FT DISULFID 882 896 BY SIMILARITY.
FT DISULFID 884 903 BY SIMILARITY.
FT DISULFID 905 914 BY SIMILARITY.
FT DISULFID 917 930 BY SIMILARITY.
FT DISULFID 933 945 BY SIMILARITY.
FT DISULFID 935 952 BY SIMILARITY.
FT DISULFID 954 963 BY SIMILARITY.
FT DISULFID 966 978 BY SIMILARITY.
FT DISULFID 981 993 BY SIMILARITY.
FT DISULFID 983 999 BY SIMILARITY.
FT DISULFID 1001 1010 BY SIMILARITY.
FT DISULFID 1013 1026 BY SIMILARITY.
FT DISULFID 1029 1029 INTERCHAIN (PROBABLE).
FT DISULFID 1032 1032 INTERCHAIN (WITH BETA-1 CHAIN).
FT DISULFID 1598 1598 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 58 58 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 574 574 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 648 648 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1020 1020 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1105 1105 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1159 1159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1173 1173 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT	CARBOHYD	1203	1203	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1221	1221	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1239	1239	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1378	1378	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1393	1393	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1437	1437	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CONFLICT	216	216	G -> A (IN REF. 3).	
FT	CONFLICT	260	260	E -> D (IN REF. 2).	
FT	CONFLICT	337	337	S -> C (IN REF. 2).	
FT	CONFLICT	447	448	LR -> PS (IN REF. 2).	
FT	CONFLICT	544	544	D -> Y (IN REF. 2).	
FT	CONFLICT	662	662	T -> S (IN REF. 2).	
FT	CONFLICT	886	886	MISSING (IN REF. 2).	
FT	CONFLICT	1158	1158	MISSING (IN REF. 2).	
FT	CONFLICT	1434	1434	V -> A (IN REF. 2).	
FT	CONFLICT	1475	1475	R -> K (IN REF. 4).	
FT	CONFLICT	1576	1576	D -> N (IN REF. 4).	
FT	TURN	775	776		
FT	STRAND	779	781		
FT	STRAND	788	790		
FT	TURN	795	796		
FT	STRAND	797	798		
FT	TURN	800	801		
FT	STRAND	804	805		
Query Match					
Best Local Similarity 94.3%; Score 8056; DB 1; Length 1607;					
Matches 1469; Conservative 59; Mismatches 48; Indels 0; Gaps 0;					
Qy	1	QAAMDECTDEGRRPQRCMP	FEVNAAFNVTVATNTCGTPPEEYCVQ	TGVTGVTKSKHLCD	60
Db	32	RAAMDECADEGRRPQRCMP	FEVNAAFNVTVATNTCGTPPEEYCVQ	TGVTGVTKSKHLCD	91
Qy	61	AGQHLQHGAAFLTDYNNQAD	ITWQSQTMLAGVQYPPSSINLTLHLGKAFD	ITVRLKFH	120
Db	92	AGQHLQHGAAFLTDYNNQAD	ITWQSQTMLAGVQYPPNSINLTLHLGKAFD	ITVRLKFH	151
Qy	121	TSRPESFAIKRTREDGPWIP	QYYSGSCENTYSKANRGFIR	TGGDEQQAALCTDEFSDIS	180
Db	152	TSRPESFAIKRTREDGPWIP	QYYSGSCENTYSKANRGFIR	TGGDEQQAALCTDEFSDIS	211
Qy	181	PLTGGNVAFSTLEGRPSAY	NFDNSPVLOEWVTATDIRVILNRLNT	FGDEVENDPKVLKSY	240
Db	212	PLTGGNVAFSTLEGRPSAY	NFDNSPVLOEWVTATDIRVILNRLNT	FGDEVENEKVLKSY	271
Qy	241	YYAISDFAVGGRCKCNH	GHASECMKNEFDKLVNCNKENTYGV	DCEKCLPFFNDRPWRATA	300
Db	272	YYAISDFAVGGRCKCNH	GHASECVKNEFDKLMCNCKENTYGV	DCEKCLPFFNDRPWRATA	331
Qy	301	ESASECLPCDCNRSQECY	FDPELYRSTGHGHCTNCQDNTDGAH	CERCRCRENFRLGNNE	360
Db	332	ESASECLPCDCNRSQECY	FDPELYRSTGHGHCTNCNCRDNTDGA	KCERCRCRENFRLGNTE	391
Qy	361	ACSSCHCSPVGSLS	TQCDSYGRCSCKPGVMGDKCDRCQ	PGFHSLTEAGCRPCSDPSGSI	420
Db	392	ACSPCHCSPVGSLS	TQCDSYGRCSCKPGVMGDKCDRCQ	PGFHSLTEAGCRPCSDLRGST	451
Qy	421	DECNVETGRCVCKDN	VEGFNCERCKPGFFNLESSNPRGCT	PCFCFGHSSVCTNAVGYSVY	480
Db	452	DECNVETGRCVCKDN	VEGFNCERCKPGFFNLESSNPKGCT	PCFCFGHSSVCTNAVGYSVY	511
Qy	481	SISSTFOIDEDGWRAE	QORDGSEASLEWSSERQDIAVISDSY	PPRYFIAPAKFLGQVLSY	540
Db	512	DISSTFOIDEDGWRVE	QORDGSEASLEWSSDRQDIAVISDSY	PPRYFIAPVKFLGQVLSY	571
Qy	541	GQNLSPSFRVDRRL	TRLSAEDLVLEGAGLRVSVPLIAQ	NSYPSSETTVKYVFRLHEATDY	600
Db	572	GQNLSPSFRVDRRL	TRLSAEDLVLEGAGLRVSVPLIAQ	NSYPSSETTVKYIFRLHEATDY	631
Qy	601	PWRPALTPPEFQKLL	NNLTSIKIRGTYSERSAGYLD	DDVTLASARPGVPATWYESCTCP	660
Db	632	PWRPALTPPEFQKLL	NNLTSIKIRGTYSERTAGYLD	DDVTLQSRPGVPATWYESCTCP	691

Qy	661	VYGGQFC	EMCLSGYRR	ETNLGPSPCVL	CACNGHSETCD	PETGVCNCRDNTAGPHCEK	720									
Db	692	VYGGQFC	ETCLPGYRR	ETPSLGPSPCVL	CTCNGHSETCD	PETGVCDCHDNTAGPHCEK	751									
Qy	721	CSDGYG	SDSTAGTSSD	QPCPCPGSSCAV	VPKTKVVCTNCPT	GTGTTGKCELCDDGYFG	780									
Db	752	CSDGYG	SDSTLGTSSD	QPCPCPGSSCAI	VPKTKVVCTHCPT	GTGTTAGKCELCDDGYFG	811									
Qy	781	DPLGRNG	PVRLCRLCQCS	DNIDPNAVGN	CNRLTGECLKCI	YNTAGFYCDRCKDGFENPL	840									
Db	812	DPLGSNG	PVRLCRPCQC	NDNIDPNAVGN	CNRLTGECLKCI	YNTAGFYCDRCKEGFFENPL	871									
Qy	841	APNPAD	CKKACNCPYGT	MTKQSSCN	PVTGQCECLPH	VTGQDCGACDPGFYNLQSGQCE	900									
Db	872	APNPAD	CKKACACNFYGT	VQVQSSCN	PVTGQCCLPH	VSGRDCGTCDPGYYNLQSGQCE	931									
Qy	901	RCDCHAL	GSTNGQCDIR	TGQCECQPGIT	GQHCHCER	CEVNHFGFEGCKPCDCHPEGSLSL	960									
Db	932	RCDCHAL	GSTNGQCDIR	TGQCECQPGIT	GQHCHCER	CETNHFFGFEGCKPCDCHHEGSLSL	991									
Qy	961	QCKDDG	CECREG	FVGNRC	QCCEENFYNR	SWPGCQEC	PACRYLVKDKVADHRVKLQBLE	1020								
Db	992	QCKDDG	CECREG	FVGNRC	QCCEENFYNR	SWPGCQEC	PACRYLVKDKAAEHRVKLQBLE	1051								
Qy	1021	SLIANL	GTGDEM	VTDOAFED	RLKEAREV	MDLLREAOQV	KDVQDNLM	DRLQRVNNTLSQ	1080							
Db	1052	SLIANL	GTGDDM	VTDOAFED	RLKEAREV	TDLLREAOQV	KDVQDNLM	DRLQRVNSSLHSQ	1111							
Qy	1081	ISRLQNI	RNTIET	GNLAEQAR	AHVENTER	LIEIASRELE	KAQVAAANVS	VTQPESTGDP	1140							
Db	1112	ISRLQNI	RNTIET	GNLAEAR	SRVSTEQL	IEIASRELE	KAQVAAANVS	ITQPESTGEP	1171							
Qy	1141	NNMTLL	AEEARKLA	ERHKQEA	DDIVRVAKT	ANDTSTEAYN	LLRLTLAGENQ	TAFIEELN	1200							
Db	1172	NNMTLL	AEEARRLA	ERHKQEA	DDIVRVAKT	ANETSAEAYN	LLRLTLAGENQ	TAFIEELN	1231							
Qy	1201	RKYEQA	KNISQDLE	KQAARVHEE	AKRAGDKAVEI	YASVAQLSP	LDSETLE	NEANNIKMEA	1260							
Db	1232	RKYEQA	KNISQDLE	KQAARVHEE	AKRAGDKAVEI	YASVAQLTP	VDSEALE	NEANKIKKEA	1291							
Qy	1261	ENLEQL	IDQKL	DYEDLRED	MRGKELEVN	LLKKGKTE	QOTADQLLARADA	AKALAEAA	1320							
Db	1292	ADLRLID	QKL	DYEDLRED	MRGKEHEVN	LLKKGKAE	QOTADQLLARADA	AKALAEAA	1351							
Qy	1321	KKGRDT	LQEANDI	LNNLKDF	RRRVNDN	KNTAAEEALRKI	PAINQTI	TEANEK	TREAOQALG	1380						
Db	1352	KKGRST	LQEANDI	LNNLKDF	RRRVNDN	KNTAAEEALRRI	PAINRTIA	EANEK	TREAOQALG	1411						
Qy	1381	SAAADATE	AKNKAHEA	ERIASAVQ	KNATSTKAAE	ERTFAE	VTDL	DNEVN	NMLKQLQEA	1440						
Db	1412	NAAADATE	AKNKAHEA	ERIASAVQ	KNATSTKADA	ERTFG	VTDL	DNEV	NGMLRQLEA	1471						
Qy	1441	ELKRQD	DADQDMM	MAGMASQA	QAEAEIN	ARKANS	VT	SILLSI	IINDL	LEQL	QGLD	TVDLN	1500			
Db	1472	ELKRQD	DADQDMM	MAGMASQA	QAEAEIN	ARKANS	VS	SILLSI	QLNN	LLDQ	LG	LD	TVDLN	1531		
Qy	1501	KLNEI	ECTLN	AKDEM	KVSD	LD	RKVS	D	LENEAK	QEA	AIMD	YN	RDIEE	IMKDIR	NLEDIR	1560
Db	1532	KLNEI	EGSLN	AKDEM	KASD	LD	RKVS	D	LESEARK	QEA	AIMD	YN	RDIAE	IKDIH	NLEDIK	1591
Qy	1561	KTLPS	GCG	ENTP	SI	EKP	1576									
Db	1592	KTLPT	GCG	ENTP	SI	EKP	1607									

RESULT 3
LMG3_HUMAN
ID LMG3 HUMAN STANDARD; PRT; 1587 AA.
AC Q9Y6N6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Laminin gamma-3 chain precursor (Laminin 12 gamma 3).

GN LAMC3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=99242614; PubMed=10225960;
RA Koch M., Olson P.F., Albus A., Jin W., Hunter D.D., Brunken W.J.,
RA Burgeson R.E., Champlaud M.F.;
RT "Characterization and expression of the laminin gamma3 chain: a novel,
RT non-basement membrane-associated, laminin chain.";
RL J. Cell Biol. 145:605-618(1999).
CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components.
CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC different polypeptide chains (alpha, beta, gamma), which are bound
CC to each other by disulfide bonds into a cross-shaped molecule
CC comprising one long and three short arms with globules at each
CC end. The gamma-3 chain is a subunit of laminin-12.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Broadly expressed in: skin, heart, lung, and
CC the reproductive tracts.
CC -!- DOMAIN: The alpha-helical domains I and II are thought to interact
CC with other laminin chains to form a coiled coil structure.
CC -!- DOMAIN: Domain IV is globular.
CC -!- SIMILARITY: Contains 1 laminin N-terminal domain.
CC -!- SIMILARITY: Contains 11 laminin EGF-like domains.
CC -!- SIMILARITY: Contains 1 laminin IV domain.
CC -----
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CC -----
CC EMBL; AF041835; AAD36991.1; --
CC HSSP; P02468; 1TLE.
CC Genew; HGNC:6494; LAMC3.
CC MIM; 604349; --
CC GO; GO:0005578; C:extracellular matrix; TAS.
CC GO; GO:0016020; C:membrane; TAS.
CC GO; GO:0005198; F:structural molecule activity; TAS.
CC InterPro; IPR006209; EGF-like.
CC InterPro; IPR008212; Lam_N2.
CC InterPro; IPR000034; Laminin_B.
CC InterPro; IPR002049; Laminin_EGF.
CC InterPro; IPR008211; LamNT.
CC Pfam; PF00052; laminin_B; 1.
CC Pfam; PF00053; laminin_EGF; 9.
CC Pfam; PF00055; laminin_Nterm; 1.
CC PRINTS; PR00011; EGFLAMININ.
CC ProDom; PD002082; Lam_N2; 1.
CC SMART; SM00180; EGF_Lam; 9.
CC SMART; SM00136; LamNT; 1.
CC PROSITE; PS00022; EGF_1; 7.
CC PROSITE; PS01186; EGF_2; 2.
CC PROSITE; PS01248; LAMININ_TYPE_EGF; 10.
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
FT SIGNAL 1
FT CHAIN 20 1587 LAMININ GAMMA-3 CHAIN.
FT DOMAIN 20 270 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 271 326 LAMININ EGF-LIKE 1.
FT DOMAIN 327 382 LAMININ EGF-LIKE 2.
FT DOMAIN 383 429 LAMININ EGF-LIKE 3.
FT DOMAIN 430 479 LAMININ EGF-LIKE 4.
FT DOMAIN 480 489 LAMININ EGF-LIKE 5 (N-TERMINAL).

FT	DOMAIN	490	672	LAMININ DOMAIN IV.
FT	DOMAIN	673	706	LAMININ EGF-LIKE 5 (C-TERMINAL).
FT	DOMAIN	707	754	LAMININ EGF-LIKE 6.
FT	DOMAIN	755	809	LAMININ EGF-LIKE 7.
FT	DOMAIN	810	865	LAMININ EGF-LIKE 8.
FT	DOMAIN	866	916	LAMININ EGF-LIKE 9.
FT	DOMAIN	917	964	LAMININ EGF-LIKE 10.
FT	DOMAIN	965	1013	LAMININ EGF-LIKE 11.
FT	DOMAIN	1014	1587	DOMAIN II AND I.
FT	DOMAIN	1071	1141	COILED COIL (POTENTIAL).
FT	DOMAIN	1200	1229	COILED COIL (POTENTIAL).
FT	DOMAIN	1424	1504	COILED COIL (POTENTIAL).
FT	DOMAIN	1535	1579	COILED COIL (POTENTIAL).
FT	SITE	1059	1061	CELL ATTACHMENT SITE (POTENTIAL).
FT	CARBOHYD	87	87	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	119	119	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	295	295	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	328	328	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	631	631	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	837	837	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	980	980	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1185	1185	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1518	1518	N-LINKED (GLCNAC. .) (POTENTIAL).
SQ	SEQUENCE	1587 AA;	172051 MW;	3CB6E09B5F203319 CRC64;

Query Match 42.1%; Score 3600; DB 1; Length 1587;
Best Local Similarity 43.5%; Pred. No. 5.4e-126;
Matches 695; Conservative 263; Mismatches 575; Indels 64; Gaps 20;

QY	2	AAMDECTDEGRPQRCMPEFVNAFNVTVVATNTCTGTPPEEYCVQGTGTGVTGKTSCHLCDA	61
DB	20	AGMGACYDAGRPQRCPLPFVFAAFGRLAQAASHTCGSPDFCFPHVGAAGAGAHQCRQDA	79
QY	62	GPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYPPSSINLTLLHKGAFDITYVRLKEHT	121
DB	80	ADPQRHNASYLTDFHSQDESTWQSPSMAFGVQYPTSVNITLRLKAYEITYVRLKEHT	139
QY	122	SRPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQALCTDFSDISP	181
DB	140	SRPESFAIYKRSRADGPWEYQYYSASQKTYGRPEGOYLPRGEDERVAFTSEFSDISP	199
QY	182	LTGGNVAFSTLEGRPSAYNFEDNSPVLQEWVTATDIRVTNRLNTFGDEVNDPKVLSYY	241
DB	200	LSGGNVAFSTLEGRPSAYNFEEPSGLQEWVTSTELLISLDRNLNTFGDDIFDKPKVLSYY	259
QY	242	YAISDFAVGGRCKNGHASECMKNEFFDKLVCKNKHNTYGVCEKCLPFENDRPWRATAE	301
DB	260	YAVSDFSVGGRCKNGHASECGPDVAGQLACRCQHNTTGTDCERCLPFFQDRPWARGTAE	319
QY	302	SASECLPCDNGRSQECYFDPYELRSTGHGHCTNCQDNTDGAHCERCENFFRLGNNEA	361
DB	320	AAHECLPCNCSGRSECTFDRELFRSTGHGGRCHCRDHTAGPHCERCQENFYHWDPRMP	379
QY	362	CSSCHCSPVGSLSLTCDSYGRCSCKPGVMGDKCDRCQPGFHSILTEAGCRPCSCDPSGSD	421
DB	380	CQPCDCQSAGSLHLQCDDTGTCAKPTVTGWKCDRLPGFHSLSGCGCRPCTCNPAGSLD	439
QY	422	ECNVETGRVCVKDNVEGFNCERCCKPFFNLESSNPRGCTPCFCFHSVSVCTNAVGSVYS	481
DB	440	TCDPRSGRCPCKENVEGNLDCRCRGTENLQPHNPAGCSSCFYGHSKVCASTAQFQVHH	499
QY	482	ISSTFQIDEDCWRAEQORDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSYG	541
DB	500	ILSDFHQAGAGWARSVGGSEHSPQWSPN----GVLLSPDEEELTAPGKFLGDQRFSG	555
QY	542	QNLSEFVRDTRRLSAEDLVLEGAGLRVSVPLIAQGNYSYSETTVKYVFLRH---EAT	598
DB	556	QPLILTFRVPFGDSPLPVQ--LRLEGTGLALS--LRHSSLSGPDARASQGGRAQVPLQET	612
QY	599	DYPWRPALTPPEFQKLLNLTSLIKRTGYSERSAG--YLDDEVILASARPPGVPATWVES	656
DB	613	SEDAVAPLPPPEHFQRLLANLTSLRLRVSPGSPAGPVFLTEVRLTSARPLSPASWVEI	672

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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:28 ; Search time 42.7526 Seconds
(without alignments)
11631.021 Million cell updates/sec

Title: US-10-037-182-16
Perfect score: 8544
Sequence: 1 QAAMDECTDEGRPQRCMP.....EDIRKTLPSGCFNTPSIEKP 1576

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL 25:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6203	72.6	1593	13 Q8JHV8	Q8jlv8 brachydanio
2	4789	56.1	1007	13 Q90ZN3	Q90zn3 gallus gall
3	3532.5	41.3	1623	5 Q9U3U7	Q9u3u7 anopheles g
4	2614.5	30.6	1190	6 Q8HZI9	Q8hzi9 equus cabal
5	2612.5	30.6	1196	6 Q867A2	Q867a2 canis famil
6	1712	20.0	1785	13 Q8JHV7	Q8jlv7 brachydanio
7	1705	20.0	529	4 Q8N2D6	Q8n2d6 homo sapien
8	1666	19.5	1792	13 Q57484	Q57484 gallus gall
9	1652	19.3	1761	4 Q86XN2	Q86xn2 homo sapien
10	1626.5	19.0	3102	5 Q45614	Q45614 caenorhabdi
11	1566	18.3	319	4 Q96BH6	Q96bh6 homo sapien
12	1562.5	18.3	1799	11 Q8R0Y0	Q8roY0 mus musculu
13	1517	17.8	351	11 P97552	P97552 rattus norv
14	1506.5	17.6	2731	5 Q9VJT5	Q9vjt5 drosophila
15	1506.5	17.6	3367	5 Q9XZC9	Q9xzc9 drosophila
16	1506.5	17.6	3375	5 Q8IP51	Q8ip51 drosophila

17	1485.5	17.4	1631	4 Q9Y6U6	Q9y6u6 homo sapien
18	1485.5	17.4	3712	5 Q9VRW0	Q9vrw0 drosophila
19	1476	17.3	1827	13 Q8JHV6	Q8jlv6 brachydanio
20	1394	16.3	3704	5 P91904	P91904 caenorhabdi
21	1295.5	15.2	3695	4 Q8TDF8	Q8tdf8 homo sapien
22	1197	14.0	1168	5 Q967S8	Q967s8 schistocerc
23	1155	13.5	604	11 Q924Z9	Q924z9 rattus norv
24	1151.5	13.5	603	13 Q42140	Q42140 brachydanio
25	1139.5	13.3	602	13 Q42203	Q42203 brachydanio
26	1137.5	13.3	569	13 Q57339	Q57339 xenopus lae
27	1136	13.3	1026	5 Q8SWY0	Q8swy0 drosophila
28	1131.5	13.2	464	11 Q61965	Q61965 mus musculu
29	1092	12.8	555	5 Q9NFW6	Q9nfw6 branchiosto
30	1086.5	12.7	1069	5 Q9BPS4	Q9bps2 bombyx mori
31	1071	12.5	1086	4 Q8TAS6	Q8tas6 homo sapien
32	1054.5	12.3	1067	5 Q44565	Q44565 caenorhabdi
33	1053.5	12.3	610	5 Q96659	Q96659 hirudo medi
34	1034	12.1	1546	4 Q9NS27	Q9ns27 homo sapien
35	1031	12.1	1461	11 Q9JLP3	Q9jlp3 mus musculu
36	1030	12.1	1546	4 Q75445	Q75445 homo sapien
37	979	11.5	1512	11 Q8K3K1	Q8k3k1 rattus norv
38	962.5	11.3	984	11 Q8K271	Q8k271 mus musculu
39	934.5	10.9	1486	4 Q14637	Q14637 homo sapien
40	918.5	10.8	695	11 Q8C9J2	Q8c9j2 mus musculu
41	902.5	10.6	1168	11 Q91V90	Q91v90 mus musculu
42	896	10.5	911	11 Q9CRX6	Q9crx6 mus musculu
43	879	10.3	667	5 Q9VY25	Q9vy25 drosophila
44	862	10.1	580	4 Q00634	Q00634 homo sapien
45	858	10.0	580	11 Q9RIA3	Q9ria3 mus musculu

ALIGNMENTS

RESULT 1
Q8JHV8
ID Q8JHV8 PRELIMINARY; PRT; 1593 AA.
AC Q8JHV8;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Laminin gamma 1.
GN LAMC1.
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22065263; PubMed=12070089;
RA Parsons M.J., Pollard S.M., Saude L., Feldman B., Coutinho P.,
Hirst E.M., Stemple D.L.;
RT "Zebrafish mutants identify an essential role for laminins in
notochord formation.";
RL Development 129:3137-3146(2002).
DR EMBL; AF468048; AAM61766.1; -;
DR GO; GO:0005198; F:extracellular matrix; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR000034; Laminin_B.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR008211; LamNT.
DR InterPro; IPR008212; Lam_N2.
DR Pfam; PF00052; laminin_B; 1.
DR Pfam; PF00053; laminin_EGF; 10.
DR Pfam; PF00055; laminin_Nterm; 1.
DR PRINTS; PR00011; EGFLAMININ.
DR PRODom; PD002082; Lam_N2; 1.
DR SMART; SM00180; EGF_Lam; 11.
DR SMART; SM00281; LamB; 1.
DR SMART; SM00136; LamNT; 1.
DR PROSITE; PS00022; EGF_1; 7.

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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:25:32 ; Search time 43.5393 Seconds
(without alignments)
10415.614 Million cell updates/sec

Title: US-10-037-182-18
Perfect score: 8694
Sequence: 1 MTGGGRAALALQPRGLWPL.....EDIKTLPTGCFNTPSIEKP 1605

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8694	100.0	1605	3 AAB19805	Aab19805 Mouse lam
2	8694	100.0	1605	3 AAB48454	Aab48454 Mouse lam
3	8694	100.0	1605	5 ABB81596	Abb81596 Mouse lam
4	8613	99.1	1607	2 AAW50897	Aaw50897 Mouse lam
5	8527	98.1	1572	3 AAB19806	Aab19806 Mouse lam
6	8527	98.1	1572	3 AAB48455	Aab48455 Mouse lam
7	8527	98.1	1572	5 ABB81597	Abb81597 Mouse lam
8	8148	93.7	1609	3 AAB19801	Aab19801 Human lam
9	8148	93.7	1609	3 AAB48452	Aab48452 Human lam
10	8148	93.7	1609	5 ABB81594	Abb81594 Human lam
11	8148	93.7	1609	7 ADC01887	Adc01887 Human lam
12	8148	93.7	1617	3 AAB19803	Aab19803 Human lam
13	8144	93.7	1609	2 AAW50898	Aaw50898 Human lam
14	8043	92.5	1576	3 AAB19802	Aab19802 Human lam
15	8043	92.5	1576	3 AAB48453	Aab48453 Human lam
16	8043	92.5	1576	5 ABB81595	Abb81595 Human lam
17	8043	92.5	1584	3 AAB19804	Aab19804 Human lam
18	3598.5	41.4	1587	3 AAB40917	Aab40917 Human ORF
19	3596.5	41.4	1587	5 AAM50361	Aam50361 Mouse lam
20	3596.5	41.4	1587	6 ABR58467	Abr58467 Human NOV
21	3593.5	41.3	1575	6 ABR58468	Abr58468 Human NOV
22	3476	40.0	1639	4 ABB59807	Abb59807 Drosophil
23	3445.5	39.6	1524	2 AAY15458	Aay15458 Human lam
24	2592	29.8	1193	5 AAE14712	Aae14712 Human lam
25	2592	29.8	1193	6 ABR48214	Abr48214 Human bla

26	2592	29.8	1193	6 ABU56513	Abu56513 Lung canc
27	2592	29.8	1193	6 ABU56696	Abu56696 Lung canc
28	2592	29.8	1193	6 ABR92103	Abr92103 Human cer
29	2592	29.8	1193	6 ADA74120	Ada74120 Human lam
30	2591	29.8	1193	2 AAR91427	Aar91427 Kalinin/1
31	2591	29.8	1193	3 AAB48468	Aab48468 Human lam
32	2591	29.8	1193	5 AAO14992	Aao14992 Laminin g
33	2584	29.7	1172	3 AAB48469	Aab48469 Human lam
34	2583	29.7	1193	3 AAB48470	Aab48470 Human lam
35	2577.5	29.6	1190	6 ADA74091	Ada74091 Equine la
36	2576	29.6	1172	3 AAB48471	Aab48471 Human lam
37	2477.5	28.5	1111	5 AAE14713	Aae14713 Human lam
38	2476.5	28.5	1111	2 AAR91428	Aar91428 Kalinin/1
39	2476.5	28.5	1111	5 AAO14993	Aao14993 Laminin g
40	2400.5	27.6	1171	3 AAB48473	Aab48473 Mouse lam
41	2400.5	27.6	1192	3 AAB48472	Aab48472 Mouse lam
42	2400.5	27.6	1192	5 AAE14711	Aae14711 Mouse lam
43	2400.5	27.6	1192	6 ADA74121	Ada74121 Murine la
44	2306.5	26.5	1171	2 AAW26583	Aaw26583 Rat hemid
45	1812.5	20.8	3106	3 AAB19795	Aab19795 Mouse lam

ALIGNMENTS

RESULT 1
AAB19805
ID AAB19805 standard; protein; 1605 AA.
XX

AC AAB19805;

XX 05-MAR-2001 (first entry)

XX Mouse laminin 2 gamma-1 chain.

DE

XX Laminin 2; mouse; nerve regeneration; angiogenic; cell adhesion;

KW degenerative muscle disorder; muscular dystrophy; cell therapy.

XX Mus musculus.

XX Key Location/Qualifiers

FT Peptide 1..33

FT Protein /label= Signal_peptide

FT 34..1605

FT /label= Mature_protein

XX WO200066730-A2.

XX 09-NOV-2000.

XX 28-APR-2000; 2000WO-US011378.

XX 30-APR-1999; 99US-0131720P.

XX 15-JUN-1999; 99US-0139198P.

XX 12-JUL-1999; 99US-0143289P.

XX 24-SEP-1999; 99US-0155945P.

XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.

XX Yurchenco P;

XX WPI; 2000-687537/67.

XX N-PSDB; AAA88905.

XX Purified laminin 2 protein, useful for research and therapeutic purposes

XX including peripheral nerve regeneration, treatment of degenerative muscle

XX disorders, angiogenesis regulation, and ex vivo cell therapy.

XX Claim 5; Page 288-294; 305pp; English.

XX The present sequence is that of the gamma-1 chain of mouse laminin 2.

XX Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1

XX (100 kDa) chains. It is thought to be specifically required for

CC stabilizing myotubes during skeletal muscle development, and for
CC preventing apoptosis. Genetic defects in human laminin 2 structure or
CC expression are associated with a major type of congenital muscular
CC dystrophy. Laminin 2 is also thought to be important in Schwann
CC cell/basal lamina interactions. The invention provides laminin 2 alpha-2,
CC beta-1 and gamma-1 chain polypeptides (see AAB19791-806) and the
CC polynucleotides encoding them (see AAA8891-906), methods for making
CC recombinant laminin 2, cells that express recombinant laminin 2, and
CC methods for using purified laminin 2 for research and therapeutic
CC purposes including peripheral nerve regeneration, treatment of
CC degenerative muscle disorders, angiogenesis regulation, promoting cell
CC attachment and migration, ex vivo cell therapy, improving the take of
CC grafts, improving the biocompatibility of medical devices and preparing
CC improved culture devices and media
XX

SQ Sequence 1605 AA;

Query Match 100.0%; Score 8694; DB 3; Length 1605;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1605; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTGGRAALALQPRGRLWPLLAVLAAGCVRAAMDECADEGRPQRCMPEFVNAFNV 60
DB 1 MTGGRAALALQPRGRLWPLLAVLAAGCVRAAMDECADEGRPQRCMPEFVNAFNV 60
QY 61 VVATNTCGTPPEEYCVQTVGTGVTKSKCHLSDAGQQLHQAFLTDYNNQADTTWQSQ 120
DB 61 VVATNTCGTPPEEYCVQTVGTGVTKSKCHLSDAGQQLHQAFLTDYNNQADTTWQSQ 120
QY 121 MLAGVQYPNSINLTHLGKAFDITYVRLKFHTSRPESFAIYKRTREDGWPWIPYQYISG 180
DB 121 MLAGVQYPNSINLTHLGKAFDITYVRLKFHTSRPESFAIYKRTREDGWPWIPYQYISG 180
QY 181 ENTYSKANRGFTRTGGDEQQAALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFDNSPVLQ 240
DB 181 ENTYSKANRGFTRTGGDEQQAALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFDNSPVLQ 240
QY 241 VWTATDIRVTNLNLTFTGDEVNDPKVLKSYYYAISDFAVGRCCKNGHASECVKNEFDK 300
DB 241 VWTATDIRVTNLNLTFTGDEVNDPKVLKSYYYAISDFAVGRCCKNGHASECVKNEFDK 300
QY 301 LMCNCKHNTYGVDCCKLPFFNDRPWRATASASECLPCDCNRSQECYFDPPELYRSTG 360
DB 301 LMCNCKHNTYGVDCCKLPFFNDRPWRATASASECLPCDCNRSQECYFDPPELYRSTG 360
QY 361 HGGHCTNCRDNTDGAKCERCENFFRLGNTEACSPCHCSPVGLSTQCDSYGRCSCKPGV 420
DB 361 HGGHCTNCRDNTDGAKCERCENFFRLGNTEACSPCHCSPVGLSTQCDSYGRCSCKPGV 420
QY 421 MGDKCDRCQPGHSLTEAGCRPCSCDFSGSTDECNVETGRCVCXNDVGEFNCERCKPGFF 480
DB 421 MGDKCDRCQPGHSLTEAGCRPCSCDFSGSTDECNVETGRCVCXNDVGEFNCERCKPGFF 480
QY 481 NLESSNPKGCTPCFCFHHSSVCTNAVGSYVDISSTFQIDEDGWRVEQORDGSEASLEWSS 540
DB 481 NLESSNPKGCTPCFCFHHSSVCTNAVGSYVDISSTFQIDEDGWRVEQORDGSEASLEWSS 540
QY 541 DRQYIAVISDSYFPRYFIAPVKFLGNQVLSYGQNLSPFSFRVDRDRLSAEDLVLEGAGL 600
DB 541 DRQYIAVISDSYFPRYFIAPVKFLGNQVLSYGQNLSPFSFRVDRDRLSAEDLVLEGAGL 600
QY 601 RVSVPPLIAQGNISYSETTVKYIFRLHEATDYPWRPALSPFFQKLLNLTSTIKIRGTSE 660
DB 601 RVSVPPLIAQGNISYSETTVKYIFRLHEATDYPWRPALSPFFQKLLNLTSTIKIRGTSE 660
QY 661 RSAGYLDVTLQSRAPGPGVPATWVESCTCPVGGQFCETCLPGYRRETSLGYPSPCV 720
DB 661 RSAGYLDVTLQSRAPGPGVPATWVESCTCPVGGQFCETCLPGYRRETSLGYPSPCV 720
QY 721 LCTCNGHSETCDPETGVCDNRDNTAGPHCKSCSDGYGDSLTGSSDCQPCPGGSSCA 780
DB 721 LCTCNGHSETCDPETGVCDNRDNTAGPHCKSCSDGYGDSLTGSSDCQPCPGGSSCA 780

QY 781 IVPKTKEVVCTHCPTGTAGKRCCLCDDGYFGDPLGSGNPVRLCRPCQCNNDIDPNAVNC 840
DB 781 IVPKTKEVVCTHCPTGTAGKRCCLCDDGYFGDPLGSGNPVRLCRPCQCNNDIDPNAVNC 840
QY 841 NRLTGECLKCIYNTAGFYCDRCCKEGFFGNPLAPNPADKCKACACNYGTVQQSSCNFVTG 900
DB 841 NRLTGECLKCIYNTAGFYCDRCCKEGFFGNPLAPNPADKCKACACNYGTVQQSSCNFVTG 900
QY 901 QCQCLPHVSGRDCGTCDPGYYNLQSGQGCERCDCCHALGSTNGQDRTGQCECQPGITGQ 960
DB 901 QCQCLPHVSGRDCGTCDPGYYNLQSGQGCERCDCCHALGSTNGQDRTGQCECQPGITGQ 960
QY 961 HCERCETNHFPGFEGCKPCDCCHHSGSLQCKDDGRCECEGFVGNRCDCQCEENYFYNR 1020
DB 961 HCERCETNHFPGFEGCKPCDCCHHSGSLQCKDDGRCECEGFVGNRCDCQCEENYFYNR 1020
QY 1021 SWPGCQCEPCACYRLVKDKAAEHRVKLQJLESILIANLGTGDDMVTDQAFEDRLKEAREVT 1080
DB 1021 SWPGCQCEPCACYRLVKDKAAEHRVKLQJLESILIANLGTGDDMVTDQAFEDRLKEAREVT 1080
QY 1081 DLLREAQEVKDVQNLMDRLQRVNSSLHLSQISRLQINRNTIETGILAEARARSVESTEQ 1140
DB 1081 DLLREAQEVKDVQNLMDRLQRVNSSLHLSQISRLQINRNTIETGILAEARARSVESTEQ 1140
QY 1141 LIEIASRELEKAKMAANVSITQPESTGEPNNMTLLAEARRILAEERHKEADDDIVRVAKTA 1200
DB 1141 LIEIASRELEKAKMAANVSITQPESTGEPNNMTLLAEARRILAEERHKEADDDIVRVAKTA 1200
QY 1201 NETSABEAYNLLRTLAGEQTALIEELNRKYEQAQKNISQDLEKQAAHVHEEAKRAGDKA 1260
DB 1201 NETSABEAYNLLRTLAGEQTALIEELNRKYEQAQKNISQDLEKQAAHVHEEAKRAGDKA 1260
QY 1261 VEIYASVAQLTPVDSEALENEANKIKKEAADLRLIDQKLKDYEDLREDMRGKEHEVKNL 1320
DB 1261 VEIYASVAQLTPVDSEALENEANKIKKEAADLRLIDQKLKDYEDLREDMRGKEHEVKNL 1320
QY 1321 LEKGKAEQQTADQLLARADAALAEAEAAKKGRSTLQEAANDILNNLKDFRRVNDNKATA 1380
DB 1321 LEKGKAEQQTADQLLARADAALAEAEAAKKGRSTLQEAANDILNNLKDFRRVNDNKATA 1380
QY 1381 EEALRRIPAINRTIAEANEKTRTREAQLALGNAADATEAKNKAHEAERIAAAQKNATSTK 1440
DB 1381 EEALRRIPAINRTIAEANEKTRTREAQLALGNAADATEAKNKAHEAERIAAAQKNATSTK 1440
QY 1441 ADAERTFGEVTDLDNEVNGMLRQLEAEANELKRKQDDADQDMMAGMASQAAQAEELNAR 1500
DB 1441 ADAERTFGEVTDLDNEVNGMLRQLEAEANELKRKQDDADQDMMAGMASQAAQAEELNAR 1500
QY 1501 KAKNSVSSLLSQLNNLLDQLGQDVTVDLKNLNEIEGSLNKADEMKAASDLDRKVSLESE 1560
DB 1501 KAKNSVSSLLSQLNNLLDQLGQDVTVDLKNLNEIEGSLNKADEMKAASDLDRKVSLESE 1560
QY 1561 ARKQEAAMIDYNRDIAEIIKDIHNLEDIKKTLPTGCFNTPSIEKP 1605
DB 1561 ARKQEAAMIDYNRDIAEIIKDIHNLEDIKKTLPTGCFNTPSIEKP 1605

RESULT 2

AAB48454

ID AAB48454 standard; protein; 1605 AA.

XX

AC AAB48454;

XX

DT 02-MAR-2001 (first entry)

XX

DE Mouse laminin 8 polypeptide, SEQ ID NO: 26.

XX

KW Mouse; laminin 8; neuroprotective; angiogenic; osteopathic;
KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;
KW vascular tissue injury; neural injury; angiogenesis regulation.

XX

OS Mus musculus.

XX

PN WO200066732-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US011543.
XX
PR 30-APR-1999; 99US-0131720P.
PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.
PR 11-FEB-2000; 2000US-0182012P.
XX
PA (BIOS-) BIOSTRATUM INC.
XX
PI Kortessmaa J, Tryggvason K;
XX
DR WPI; 2000-687539/67.
DR N-PSDB; AAC83715.
XX
XX
PT Purified laminin 8 protein, useful for research and therapeutic purposes
PT including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.
XX
PS Claim 5; Page 227-232; 245pp; English.
XX
CC The present sequence is a laminin 8 polypeptide chain. Laminins are a
CC family of heterotrimeric glycoproteins that function via binding
CC interactions with neighbouring cell receptors and by forming laminin
CC networks. They are signalling molecules which influence cellular
CC function. Laminin 8 is useful for treating injuries to tissue of
CC mesenchymal origin, such as bone, cartilage, tendon, and ligament,
CC treating injuries to vascular tissue, promoting cell attachment and
CC migration, ex vivo cell therapy, improving the biocompatibility of
CC medical devices, and preparing improved cell culture devices and media.
CC Laminin 8 is also useful for promoting re-endothelialisation at the site
CC of vascular injuries, improving the take of grafts, improving the
CC biocompatibility of medical devices, treating neural injuries (neural
CC regeneration), regulating angiogenesis, and promoting cell attachment and
CC migration
XX
SQ Sequence 1605 AA;
Query Match 100.0%; Score 8694; DB 3; Length 1605;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1605; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTGGGRAALALQPRGLWPLAVLAAGCVRAAMDECADEGGRPQRCMPFVNAAFNV 60
Db 1 MTGGGRAALALQPRGLWPLAVLAAGCVRAAMDECADEGGRPQRCMPFVNAAFNV 60
QY 61 VVATNTCGTPPEEYCVQGTGVTGKSCHLCDAGQHLQHGAFLTDYNNQADTTWQSQT 120
Db 61 VVATNTCGTPPEEYCVQGTGVTGKSCHLCDAGQHLQHGAFLTDYNNQADTTWQSQT 120
QY 121 MLAGVQYPNSINLTLLHKGAFDITYVRLKFHTSRPESFAIYKRTREDGWPWYQYSGSC 180
Db 121 MLAGVQYPNSINLTLLHKGAFDITYVRLKFHTSRPESFAIYKRTREDGWPWYQYSGSC 180
QY 181 ENTYSKANRGFIRTGDEQALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFDNSPVLQE 240
Db 181 ENTYSKANRGFIRTGDEQALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFDNSPVLQE 240
QY 241 WYTATDIRVTNLRLNTFGDEVFNDPKVLKSYYYAISDFAVGGRCKNGHASECVKNEFDK 300
Db 241 WYTATDIRVTNLRLNTFGDEVFNDPKVLKSYYYAISDFAVGGRCKNGHASECVKNEFDK 300
QY 301 LMCNCKHNTYGVDCCKLPFFNDRPWRRTAESAECPLPCDCNGRSQECYFDPPELYRSTG 360
Db 301 LMCNCKHNTYGVDCCKLPFFNDRPWRRTAESAECPLPCDCNGRSQECYFDPPELYRSTG 360
QY 361 HGGHCTNCRDNTDGAKCERCRENFFRLGNTEACSPCHCSPVGSLSLTCDSYGRCSCKPGV 420
Db 361 HGGHCTNCRDNTDGAKCERCRENFFRLGNTEACSPCHCSPVGSLSLTCDSYGRCSCKPGV 420

QY 421 MGDKCDRCQPGFHSLEAGCRPCSCDPSGSTDENVTGRCVCKDNVEGFNCERCKPGFF 480
Db 421 MGDKCDRCQPGFHSLEAGCRPCSCDPSGSTDENVTGRCVCKDNVEGFNCERCKPGFF 480
QY 481 NLESSNPKGCTPCFCFGHSSVCTNAVGSYVDISSTFQIDEDGWRVEORDGSEASLEWSS 540
Db 481 NLESSNPKGCTPCFCFGHSSVCTNAVGSYVDISSTFQIDEDGWRVEORDGSEASLEWSS 540
QY 541 DRQYIAVISDSYFPRYFIAPVKFLGNQVLSYGNLSFSFRVDRDRRLSADLVLGAGL 600
Db 541 DRQYIAVISDSYFPRYFIAPVKFLGNQVLSYGNLSFSFRVDRDRRLSADLVLGAGL 600
QY 601 RVSVPILIAQNSYSPSETTKYIFRLHEATDYPWPALSPFEFQKLLNNLTSTKIRGTYS 660
Db 601 RVSVPILIAQNSYSPSETTKYIFRLHEATDYPWPALSPFEFQKLLNNLTSTKIRGTYS 660
QY 661 RSAGYLDVTLQSAARPGVPATWVESCTCPVGYGQFCETCLPGYRRETSLGYPSPCV 720
Db 661 RSAGYLDVTLQSAARPGVPATWVESCTCPVGYGQFCETCLPGYRRETSLGYPSPCV 720
QY 721 LCTCNHGHSETCDPETGVCDCRDNTAGPHCEKSCDGYGDSLTLGTSSDCQPCPCGGSSCA 780
Db 721 LCTCNHGHSETCDPETGVCDCRDNTAGPHCEKSCDGYGDSLTLGTSSDCQPCPCGGSSCA 780
QY 781 IVPKTKEVVCTHCPTGTAGKRCCELDDGYFGDPLGNSGVPVRLCRPCCQNDNIDPNAVNC 840
Db 781 IVPKTKEVVCTHCPTGTAGKRCCELDDGYFGDPLGNSGVPVRLCRPCCQNDNIDPNAVNC 840
QY 841 NRLTGECLKCIYNTAGFYCDRCKEGFFGNPLAPNADKCKACACNYGTVQQSSCNPVTG 900
Db 841 NRLTGECLKCIYNTAGFYCDRCKEGFFGNPLAPNADKCKACACNYGTVQQSSCNPVTG 900
QY 901 QCQCLPHVSGRDCGTCDPGYNYLQSGQGCRCCHALGSTNGQCDIRTGCECQPGITGQ 960
Db 901 QCQCLPHVSGRDCGTCDPGYNYLQSGQGCRCCHALGSTNGQCDIRTGCECQPGITGQ 960
QY 961 HCERCETNHFGFPEGCKPCDCHHEGSLSQCKDDGRCECREGVGNRCDOCEENYFYNR 1020
Db 961 HCERCETNHFGFPEGCKPCDCHHEGSLSQCKDDGRCECREGVGNRCDOCEENYFYNR 1020
QY 1021 SWPGCECPACRYLVKDKAAEHRVKLQELSLIANLGTGDDMTDQAFEDRLKEAEREVT 1080
Db 1021 SWPGCECPACRYLVKDKAAEHRVKLQELSLIANLGTGDDMTDQAFEDRLKEAEREVT 1080
QY 1081 DLLREAQEVKDVQNLMDRLQVNSSLHSQISRLQINRTIETGILAEARARSVESTEQ 1140
Db 1081 DLLREAQEVKDVQNLMDRLQVNSSLHSQISRLQINRTIETGILAEARARSVESTEQ 1140
QY 1141 LJEIASRELEKAKMAANVSITQPESTGEPNMTLLAEARLAEERHKEQADDIVRVAKTA 1200
Db 1141 LJEIASRELEKAKMAANVSITQPESTGEPNMTLLAEARLAEERHKEQADDIVRVAKTA 1200
QY 1201 NETSABAYNLLRLTAGENQTALEIEELNRKYEQAKNISQDLEKQAAARVHEEAKRAGDKA 1260
Db 1201 NETSABAYNLLRLTAGENQTALEIEELNRKYEQAKNISQDLEKQAAARVHEEAKRAGDKA 1260
QY 1261 VEIYASVAQLTPVDSEALENEANKIKKEAADLRLIDQKLKDYEDLREDMRGKEHEVKNL 1320
Db 1261 VEIYASVAQLTPVDSEALENEANKIKKEAADLRLIDQKLKDYEDLREDMRGKEHEVKNL 1320
QY 1321 LEKGKAEQQTADQLLARADAAKALAEAAKKGRSTLQEAANDILNNLKDFDRVNDNKTA 1380
Db 1321 LEKGKAEQQTADQLLARADAAKALAEAAKKGRSTLQEAANDILNNLKDFDRVNDNKTA 1380
QY 1381 EEALRRIPAINRTIAEANEKTRQAQLALGNAADATEAKNKAHEAERIAAQAQKATSTK 1440
Db 1381 EEALRRIPAINRTIAEANEKTRQAQLALGNAADATEAKNKAHEAERIAAQAQKATSTK 1440
QY 1441 ADAERTFGEVTDLDNEVNGMLRQLEEAENELKRXQDDADQDMMAGMASQAQAEALNAR 1500
Db 1441 ADAERTFGEVTDLDNEVNGMLRQLEEAENELKRXQDDADQDMMAGMASQAQAEALNAR 1500
QY 1501 KAKNSVSVLLSQLNNLLDQLGQLDVTDLNKLNEIEGSLNKADEMKASDLDRKVSDDLESE 1560

Db 1501 KAKNSVSSLLSQLNLLDQLGQDVTVDLNLKNEIEGSLNKADEMKA SLDLRKVS DLESE 1560

QY 1561 ARKQEAAIMDYNRDIAEIIKDHNLEDIKKTLPTGCFNTPSIEKP 1605

Db 1561 ARKQEAAIMDYNRDIAEIIKDHNLEDIKKTLPTGCFNTPSIEKP 1605

RESULT 3

ABB81596

ID ABB81596 standard; protein; 1605 AA.

XX

AC ABB81596;

DT 19-SEP-2002 (first entry)

XX

DE Mouse laminin 10 third chain protein sequence SEQ ID NO:18.

XX

KW Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;

KW tissue repair development; laminin; healing; vascular tissue;

KW re-endothelialisation; vascular injury; cell attachment; cell stasis;

KW proliferation; migration.

XX

OS Mus musculus.

XX

FT Key Location/Qualifiers

FT Peptide 1. .33

FT Protein /label= signal

FT 34. .1605

FT /label= laminin_10_third_chain

XX

WO200250111-A2.

PN

XX

PD 27-JUN-2002.

XX

PF 21-DEC-2001; 2001WO-US051035.

XX

PR 21-DEC-2000; 2000US-0257449P.

PR 28-MAR-2001; 2001US-0279282P.

PR 13-NOV-2001; 2001US-00279282.

XX

PA (BIOS-) BIOSTRATUM INC.

XX

PI Tryggvason K, Doi M, Thyboll J;

XX

DR WPI; 2002-557650/59.

DR N-PSDB; ABQ72914.

XX

PT New human laminin-10 proteins, useful for accelerating the healing of

PT vascular tissue, improving the biocompatibility of grafts, or for

PT promoting re-endothelialization at the site of vascular injuries.

XX

PS Claim 9; Page 191-195; 231pp; English.

XX

CC The present invention describes human laminin alpha 5. Also described is

CC an isolated laminin 10. Laminin 10 has vulnery activity. Laminins are

CC useful in maintaining cell/tissue phenotype as well as promoting cell

CC growth and differentiation in tissue repair development. Specifically,

CC laminin 10 can be used for accelerating the healing injuries of vascular

CC tissue, improving the biocompatibility of grafts useful for treating such

CC injuries, for promoting re-endothelialisation at the site of vascular

CC injuries, and promote cell attachment and subsequent cell stasis,

CC proliferation, differentiation, and/or migration. The present sequence

CC represents a third chain protein of laminin 10, from the present

CC invention

XX

SQ Sequence 1605 AA;

Query Match 100.0%; Score 8694; DB 5; Length 1605;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1605; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTGGGRAALALQPRGLWPLLAVALAAGCVRAAMDECADEGGRPQRCMPEFVNAAFNVT 60

Db 1 MTGGGRAALALQPRGLWPLLAVALAAGCVRAAMDECADEGGRPQRCMPEFVNAAFNVT 60

QY 61 VVATNTCGTPPEEYCVQGTGVTGKSKCHLCDAGQQHLQHGAFLTDYNNQADTTWQSQT 120

Db 61 VVATNTCGTPPEEYCVQGTGVTGKSKCHLCDAGQQHLQHGAFLTDYNNQADTTWQSQT 120

QY 121 MLAGVQYVNSINLTLLHLGKAFDIYVRLKFHTSRPESFAIYKRTREDGPWIPYQYSSGC 180

Db 121 MLAGVQYVNSINLTLLHLGKAFDIYVRLKFHTSRPESFAIYKRTREDGPWIPYQYSSGC 180

QY 181 ENTYSKANRGFIRTTGGDEQQALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFDNSPVLQE 240

Db 181 ENTYSKANRGFIRTTGGDEQQALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFDNSPVLQE 240

QY 241 WVTATDIRVTNLRLNTFGDEVFNDPKVLKSYYYAISDFAVGRCCKNGHASECVKNEFDK 300

Db 241 WVTATDIRVTNLRLNTFGDEVFNDPKVLKSYYYAISDFAVGRCCKNGHASECVKNEFDK 300

QY 301 LMCNCKHNTYGVDCCKLPFFNDRPWRRAATAESASECLPCDCNGRSQECYFDPPELYRSTG 360

Db 301 LMCNCKHNTYGVDCCKLPFFNDRPWRRAATAESASECLPCDCNGRSQECYFDPPELYRSTG 360

QY 361 HGGHCTNCRDNTDGAKCERCENFFRLGNTEACSPCHCSPVGSLSLTCDSYGRCSCKPGV 420

Db 361 HGGHCTNCRDNTDGAKCERCENFFRLGNTEACSPCHCSPVGSLSLTCDSYGRCSCKPGV 420

QY 421 MGDKCDRCQPGFHSLTEAGCRPCSDPSSGSTDECNVETGRVCCKDNVEGENCERCKPGFF 480

Db 421 MGDKCDRCQPGFHSLTEAGCRPCSDPSSGSTDECNVETGRVCCKDNVEGENCERCKPGFF 480

QY 481 NLESSNPKGCTPCFCFGHSSVCTNAVGYSVYDISSTFQIDEDGWRVEQRDSEASLEWSS 540

Db 481 NLESSNPKGCTPCFCFGHSSVCTNAVGYSVYDISSTFQIDEDGWRVEQRDSEASLEWSS 540

QY 541 DRQYIAVISDSYFPRIYFIAPVKFLGNQVLSYGONLSFSFRVDRDRTRLAEDLVLEGAGL 600

Db 541 DRQYIAVISDSYFPRIYFIAPVKFLGNQVLSYGONLSFSFRVDRDRTRLAEDLVLEGAGL 600

QY 601 RVSVPPLIAQGNISYSPSETTVKIYIFRLHEATDYPWRPALSPPEFQKLLNNLTSIKIRGTYS 660

Db 601 RVSVPPLIAQGNISYSPSETTVKIYIFRLHEATDYPWRPALSPPEFQKLLNNLTSIKIRGTYS 660

QY 661 RSAGYLDVTLQSAARPGVPATWVESCTCPVGYGGQFCETCLPGYRRETPSLGPYSPCV 720

Db 661 RSAGYLDVTLQSAARPGVPATWVESCTCPVGYGGQFCETCLPGYRRETPSLGPYSPCV 720

QY 721 LCTCNHGHSETCDPETGVCDRCNDTAGPHCEKCSGDIYGYDSTLGTSSDCQPCPGSSCA 780

Db 721 LCTCNHGHSETCDPETGVCDRCNDTAGPHCEKCSGDIYGYDSTLGTSSDCQPCPGSSCA 780

QY 781 IVPKTKEVVCTHCPTGTAGKRCCLCDDGYFGDPLGSGNPGVRLCRPCQCNNDIDPNAVNGC 840

Db 781 IVPKTKEVVCTHCPTGTAGKRCCLCDDGYFGDPLGSGNPGVRLCRPCQCNNDIDPNAVNGC 840

QY 841 NRLTGECLKCIYNTAGFYCDRCKEGFFGNPLAPNPADKCKACACNYGTVQQSSCNPVTV 900

Db 841 NRLTGECLKCIYNTAGFYCDRCKEGFFGNPLAPNPADKCKACACNYGTVQQSSCNPVTV 900

QY 901 QCQCLPHVSGRDCGTCDPGYINLQSGQGCRCDCCHALGSTNGQCDIRTGCECQPGITGQ 960

Db 901 QCQCLPHVSGRDCGTCDPGYINLQSGQGCRCDCCHALGSTNGQCDIRTGCECQPGITGQ 960

QY 961 HCERCETNHFHFGFEGCKPCDCCHHEGSLQCKDDGRCECREGFGVGNRCDQCEENFYNR 1020

Db 961 HCERCETNHFHFGFEGCKPCDCCHHEGSLQCKDDGRCECREGFGVGNRCDQCEENFYNR 1020

QY 1021 SWPGCQCECPACYRLVKDKAAEHRVKLQELLESILIANLGTGDDMVTDOAFEDRLKEAEREVT 1080

Db 1021 SWPGCQCECPACYRLVKDKAAEHRVKLQELLESILIANLGTGDDMVTDOAFEDRLKEAEREVT 1080

QY 1081 DLUREAQEVKDVQNLMDRLQVRNSSLSHSQISRLQNRNTIETGILAEARARSRVESTEQ 1140

Db 1081 DLLREAQEVKVDQNLMDRLQRVNSSLSHSQISRLQIRNTIETGILAEARRSRVSTEQ 1140
QY 1141 LIEIASRELEKAKMAANVSITQPESTGEPNNMTLLAEAEARRLAERHKQEADDIVRVAKTA 1200
Db 1141 LIEIASRELEKAKMAANVSITQPESTGEPNNMTLLAEAEARRLAERHKQEADDIVRVAKTA 1200
QY 1201 NETSAEAYNLLRLTLAGENQTALEIEELNRKYEQAKNISQDLEKQAAARVHEEAKRAGDKA 1260
Db 1201 NETSAEAYNLLRLTLAGENQTALEIEELNRKYEQAKNISQDLEKQAAARVHEEAKRAGDKA 1260
QY 1261 VEIYASVAQLTPVDSEALENEANKIKKEAADLRLIDQKLKDYEDLREDNRGKEHEVKNL 1320
Db 1261 VEIYASVAQLTPVDSEALENEANKIKKEAADLRLIDQKLKDYEDLREDNRGKEHEVKNL 1320
QY 1321 LEKGKAEQQTADQLLARADAAKALAEAAKKGSRSTLQEANDILNNLKDFDRRVNDNKATA 1380
Db 1321 LEKGKAEQQTADQLLARADAAKALAEAAKKGSRSTLQEANDILNNLKDFDRRVNDNKATA 1380
QY 1381 BEALRRIPAINRTIAEANEKTRAEQALGNAADAAATEAKNKAHEAERIAASAAQKNATSTK 1440
Db 1381 BEALRRIPAINRTIAEANEKTRAEQALGNAADAAATEAKNKAHEAERIAASAAQKNATSTK 1440
QY 1441 ADAERTFGEVTDLDNEVNGMLRQLEEAENELKRKODDADQDMMAGMASQAAQAEELNAR 1500
Db 1441 ADAERTFGEVTDLDNEVNGMLRQLEEAENELKRKODDADQDMMAGMASQAAQAEELNAR 1500
QY 1501 KAKNSVSSLLSOLNNLLDQIGQLDQTDVNLKLNKNEIEGSLNKADEMKASDLDRKVSLESE 1560
Db 1501 KAKNSVSSLLSOLNNLLDQIGQLDQTDVNLKLNKNEIEGSLNKADEMKASDLDRKVSLESE 1560
QY 1561 ARKQEAAIMDYNRDIAEIIKDIHNLEDIKKTLPFGCFNTPSIEKP 1605
Db 1561 ARKQEAAIMDYNRDIAEIIKDIHNLEDIKKTLPFGCFNTPSIEKP 1605

RESULT 4

AAW50897
ID AAW50897 standard; protein; 1607 AA.

XX AC AAW50897;

XX DT 07-DEC-1998 (first entry)

XX DE Mouse laminin G1 chain.

XX KW Laminin; mouse; beta-amyloid; amyloidosis; Alzheimer's disease;
KW Down's syndrome; hereditary cerebral haemorrhage; inflammation;
KW malignancy; Familial Mediterranean Fever; multiple myeloma;
KW type II diabetes; prion disease; Creutzfeldt-Jacob disease; CJD;
KW Gertstmann-Straussler syndrome; kuru; scrapie; haemodialysis;
KW carpal tunnel syndrome; senile cardiac amyloid polynuropathy;
KW Familial Amyloidotic Polynuropathy; thyroid carcinoma; diagnosis;
KW therapy.

XX OS Mus sp.

XX PN WO9815179-A1.

XX PD 16-APR-1998.

XX PF 08-OCT-1997; 97WO-US018145.

XX PR 08-OCT-1996; 96US-0027981P.

XX PA (UNIW) UNIV WASHINGTON.

XX PI Castillo G, Snow AD;

XX DR WPI; 1998-240534/21.

XX PT Use of laminin and fragments - for developing products for use in the
PT diagnosis and treatment of amyloid disease, e.g. Alzheimer's disease or
PT CJD.

XX PS Claim 15; Page 102-105; 132pp; English.

XX CC This is the amino acid sequence of the mouse laminin G1 chain. The
CC primary object of the invention is to use laminin, laminin-derived
CC protein fragments and/or laminin-derived polypeptides as potent
CC inhibitors of amyloid formation, deposition, accumulation and/or
CC persistence in Alzheimer's disease and other amyloidosis. The laminin
CC products (see AAW50888-98) may include mouse or human laminin A or A1
CC chain, laminin B1 or B2 chain, laminin A2 chain (merosin), laminin G1
CC chain, the globular repeats of the laminin A1 chain and the beta-amyloid
CC binding domain of the laminin A chain. A claimed method for treating an
CC amyloid disease comprises administering a polypeptide having a
CC conformational similarity to a fragment of a laminin protein. A method
CC for diagnosing an amyloid disease involves determining levels of laminin
CC in a sample. Production of laminin or its fourth globular repeat in vivo
CC provides a method for in vivo inhibition of beta-amyloid amyloidosis. The
CC products and methods can be used for the diagnosis, prognosis, monitoring
CC and treatment of amyloidosis such as Alzheimer's disease, Down's syndrome
CC and hereditary cerebral haemorrhage with amyloidosis of the Dutch type
CC (where the specific amyloid is the beta-amyloid protein), the amyloidosis
CC associated with chronic inflammation, various forms of malignancy and
CC Familial Mediterranean Fever (AA amyloid or inflammation-association
CC amyloidosis), the amyloidosis associated with multiple myeloma and other
CC B-cell abnormalities (AL amyloid), the amyloidosis associated with type
CC II diabetes (amylin or islet amyloid), the amyloidosis associated with
CC prion diseases including Creutzfeldt-Jacob disease, Gertstmann-Straussler
CC syndrome, kuru and animal scrapie (PrP amyloid), the amyloidosis
CC associated with long-term haemodialysis and carpal tunnel syndrome (beta
CC 2-microglobulin amyloid), the amyloidosis associated with senile cardiac
CC amyloid and Familial Amyloidotic Polynuropathy (prealbumin or
CC transthyretin amyloid), and the amyloidosis associated with endocrine
CC tumours such as medullary carcinoma of the thyroid (variant of
CC procalcitonin)

XX SQ Sequence 1607 AA;

Query Match 99.1%; Score 8613; DB 2; Length 1607;

Best Local Similarity 99.3%; Pred. No. 0;

Matches 1596; Conservative 2; Mismatches 7; Indels 2; Gaps 2;

QY 1 MTGGGRAALALQPRGLWPELLAAVAGCVRAAMDECADEGGRPQRCMPEFVNAAFNVT 60
Db 1 MTGGGRAALALQPRGLWPELLAAVAGCVRAAMDECADEGGRPQRCMPEFVNAAFNVT 60
QY 61 VVAINTCGTPPEEYCVQGTGVTKSCHLCDAGQOHLQHGAFLTDYNNQADTTWWQSQT 120
Db 61 VVAINTCGTPPEEYCVQGTGVTKSCHLCDAGQOHLQHGAFLTDYNNQADTTWWQSQT 120
QY 121 MLAGVQYPNSINLTHLGKAFDITYVRLKFHTSRPESFAIYKRTREDGPMIPYQYSGSC 180
Db 121 MLAGVQYPNSINLTHLGKAFDITYVRLKFHTSRPESFAIYKRTREDGPMIPYQYSGSC 180
QY 181 ENTYSKANRGFIRTTGGDEQALCTDEFSDISPLTGNVAFSTLEGRPSAYNFDNSPVLQE 240
Db 181 ENTYSKANRGFIRTTGGDEQALCTDEFSDISPLTGNVAFSTLEGRPSAYNFDNSPVLQE 240
QY 241 WVTATDIRVTNLRLNTFGDEVNDPKVLKSYYYAISDFAVGGRCCKNGHASECVKNEFDK 300
Db 241 WVTATDIRVTNLRLNTFGDEVNDPKVLKSYYYAISDFAVGGRCCKNGHASECVKNEFDK 300
QY 301 LMCNCKHNTYGVDCCKCLPFENDRPWRRATAESASECLPCDCNGRSQECYFDPFLYRSTG 360
Db 301 LMCNCKHNTYGVDCCKCLPFENDRPWRRATAESASECLPCDCNGRSQECYFDPFLYRSTG 360
QY 361 HGGHCTNCRDNTDGAKCERCERENFFRLGNTEACSPCHCSPVGLSTQCDSYGRCSCKPGV 420
Db 361 HGGHCTNCRDNTDGAKCERCERENFFRLGNTEACSPCHCSPVGLSTQCDSYGRCSCKPGV 420
QY 421 MGDKCDRCQPGFHSLSLTAACRCPSCDPSGSTDECNVETGRCVCKDNVEGENCERCKPGFF 480
Db 421 MGDKCDRCQPGFHSLSLTAACRCPSCDPSGSTDECNVETGRCVCKDNVEGENCERCKPGFF 480

QY 481 NLESSNPKGCTPCFCFGHSSVCTNAVGYSVYDISSTFOIDEDGWRVEQRDGSEASLEWSS 540
Db 481 NLESSNPKGCTPCFCFGHSSVCTNAVGYSVYDISSTFOIDEDGWRVEQRDGSEASLEWSS 540
QY 541 DRQYIAVTSYFPRYFIAPVKFLGNQVLSYGONLSFSFRVDRDRDRLSAEDLVLEGAGL 600
Db 541 DRQDIAVTSYFPRYFIAPVKFLGNQVLSYGONLSFSFRVDRDRDRLSAEDLVLEGAGL 600
QY 601 RVSVPPLIAOGNSYPSETTVKYIFRLHEATDYPWRPALSPPEFQKLLNNLTSIKIRGTYS 660
Db 601 RVSVPPLIAOGNSYPSETTVKYIFRLHEATDYPWRPALSPPEFQKLLNNLTSIKIRGTYS 660
QY 661 RSAGYLDVTLQSAARPGVPATWVESCTCPVGYGGQFCETCLPGYRRETSPSLGPYSPCV 720
Db 661 RTAGYLDVTLQSAARPGVPATWVESCTCPVGYGGQFCETCLPGYRRETSPSLGPYSPCV 720
QY 721 LCTCNHGHSETCDPETGVCDNRDNTAGPHCEKCSGYYGDSLTGTSDDCQPCPCPGSSCA 780
Db 721 LCTCNHGHSETCDPETGVCDNRDNTAGPHCEKCSGYYGDSLTGTSDDCQPCPCPGSSCA 780
QY 781 IVPKTKEVVCTHCTPTGTAGKRCCLDDGDFGDPGLSGNPGVRLCRPCQCNNDIDPNAVNC 840
Db 781 IVPKTKEVVCTHCTPTGTAGKRCCLDDGDFGDPGLSGNPGVRLCRPCQCNNDIDPNAVNC 840
QY 841 NRLTGECLKIYNTAGFYCDRCCKEGFFGNPLAPNPADKCKACACN-YGTVQQSSCNPEVT 899
Db 841 NRLTGECLKIYNTAGFYCDRCCKEGFFGNPLAPNPADKCKACACNPGYGTVQQSSCNPEVT 900
QY 900 GQCQCLPHVSGRDCGTCDPGYYNLOSQGGCERCDCHALGSTNGQCDIRTGQCECQPGITG 959
Db 901 GQCQCLPHVSGRDCGTCDPGYYNLOSQGGCERCDCHALGSTNGQCDIRTGQCECQPGITG 960
QY 960 QHCERCETNHFPGFEGCKPCDCHHEGSLSLQCKDDGRCEGREGFVGNRCDCQCEENYFYN 1019
Db 961 QHCERCETNHFPGFEGCKPCDCHHEGSLSLQCKDDGRCEGREGFVGNRCDCQCEENYFYN 1020
QY 1020 RSWPGCQEQPACRYLVKDAAEHRVKLQELSLIANLGTGDDMTDQAFEDRLKBAEREV 1079
Db 1021 RSWPGCQEQPACRYLVKDAAEHRVKLQELSLIANLGTGDDMTDQAFEDRLKBAEREV 1080
QY 1080 TDLLREAEVQKVDQNLMDRLQRVNSSLHSQISRLQNRINRTIETGILAEARARSVESTE 1139
Db 1081 TDLLREAEVQKVDQNLMDRLQRVNSSLHSQISRLQNRINRTIETGILAEARARSVESTE 1140
QY 1140 QLIEIASRELEKAKM-AANVSITQPESTGEPNNMTLLAEAEARLAERHKEADDIRVAK 1198
Db 1141 QLIEIASRELEKAKMAAANVSITQPESTGEPNNMTLLAEAEARLAERHKEADDIRVAK 1200
QY 1199 TANETSAEAYNLLRLTLAGENQTALEIEELNRKYEQAQKNSQDLEKQAARVHEEAKRAGD 1258
Db 1201 TANETSAEAYNLLRLTLAGENQTALEIEELNRKYEQAQKNSQDLEKQAARVHEEAKRAGD 1260
QY 1259 KAVEIYASVAQLTPVDSEALENEANKIKKEAADLRLIDQKLKDYEDLREDMRGKEHEVK 1318
Db 1261 KAVEIYASVAQLTPVDSEALENEANKIKKEAADLRLIDQKLKDYEDLREDMRGKEHEVK 1320
QY 1319 NLLEKGKAEQQTADQLLARADAALAEAEAAKKGRSTLQEAANDILNNLKDFDRRVNDNKT 1378
Db 1321 NLLEKEKAEQQTADQLLARADAALAEAEAAKKGRSTLQEAANDILNNLKDFDRRVNDNKT 1380
QY 1379 AAEEALRRIPAINRTIAEANETREAOALGNAAADATEAKNKAHEAEERIASAAQKNATS 1438
Db 1381 AAEEALRRIPAINRTIAEANETREAOALGNAAADATEAKNKAHEAEERIASAVQKNATS 1440
QY 1439 TKADAERTFGEVTDLDNEVNGMLRQLEAEAEANELKRQDDADQDMMAGMASQAAQAEALN 1498
Db 1441 TKADAERTFGEVTDLDNEVNGMLRQLEAEAEANELKRQDDADQDMMAGMASQAAQAEALN 1500
QY 1499 ARKAKNSVSSLISQLNNLLDQLGQDLDVNLKLEIEGSLNKADEMKAQDLDRKVSLE 1558
Db 1501 ARKAKNSVSSLISQLNNLLDQLGQDLDVNLKLEIEGSLNKADEMKAQDLDRKVSLE 1560
QY 1559 SEARKQEAAMNDYNDIAEIIKDIHNLEDIKKTLPCTGCFNTPSIEKP 1605

Db 1561 SEARKQEAAMNDYNDIAEIIKDIHNLEDIKKTLPCTGCFNTPSIEKP 1607
RESULT 5
AAB19806
ID AAB19806 standard; protein; 1572 AA.
XX
AC AAB19806;
DT 05-MAR-2001 (first entry)
XX
DE Mouse laminin 2 mature gamma-1 chain.
XX
KW Laminin 2; mouse; nerve regeneration; angiogenic; cell adhesion; degenerative muscle disorder; muscular dystrophy; cell therapy.
KW
XX Mus musculus.
OS
XX WO2000066730-A2.
PN
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US011378.
XX
PR 30-APR-1999; 99US-0131720P.
PR 15-JUN-1999; 99US-0139198P.
PR 12-JUL-1999; 99US-0143289P.
PR 24-SEP-1999; 99US-0155945P.
XX
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
PI Yurchenco P;
XX
DR WPI; 2000-687537/67.
DR N-PSDB; AAA88906.
XX
PT Purified laminin 2 protein, useful for research and therapeutic purposes including peripheral nerve regeneration, treatment of degenerative muscle disorders, angiogenesis regulation, and ex vivo cell therapy.
XX
PS Claim 5; Page 302-306; 305pp; English.
XX
CC The present sequence is that of mouse laminin 2 gamma-1 chain mature protein. Laminin-2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1 (100 kDa) chains. It is thought to be specifically required for stabilizing myotubes during skeletal muscle development, and for preventing apoptosis. Genetic defects in human laminin 2 structure or expression are associated with a major type of congenital muscular dystrophy. Laminin 2 is also thought to be important in Schwann cell/basal lamina interactions. The invention provides laminin 2 alpha-2, beta-1 and gamma-1 chain polypeptides (see AAB19791-806) and the polynucleotides encoding them (see AAA8891-906), methods for making recombinant laminin 2, cells that express recombinant laminin 2, and methods for using purified laminin 2 for research and therapeutic purposes including peripheral nerve regeneration, treatment of degenerative muscle disorders, angiogenesis regulation, promoting cell attachment and migration, ex vivo cell therapy, improving the take of grafts, improving the biocompatibility of medical devices and preparing improved culture devices and media
XX
SQ Sequence 1572 AA;
Query Match 98.1%; Score 8527; DB 3; Length 1572;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 34 AMDECADEGGRPQRCMPFVNAAFNVTVATNTCGTPPEYCVQGTGVTGKSchLCDAG 93
Db 1 AMDECADEGGRPQRCMPFVNAAFNVTVATNTCGTPPEYCVQGTGVTGKSchLCDAG 60
QY 94 QQHLQHGAAFLTDYNNQADTTWQSQMTLAGVQYPSNINLTLHLKAFDITYVRLKFTS 153

Dbb 61 QOHLQHGAFLTDYNNQADTTWQSQTMLAGVQVPNSINLTLLHLGKAFTDITYVRLKPHTS 120
QY 154 RPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQALCTDFSDISPL 213
Dbb 121 RPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQALCTDFSDISPL 180
QY 214 TGGNVAFSTLEGRPSAYNFDSNPSVLQEWVTATDIRVTILNRLNTFGDEVFNDPKVLKSYYY 273
Dbb 181 TGGNVAFSTLEGRPSAYNFDSNPSVLQEWVTATDIRVTILNRLNTFGDEVFNDPKVLKSYYY 240
QY 274 AISDFAVGGRCKCNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPCFFNDRPWRRTAES 333
Dbb 241 AISDFAVGGRCKCNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPCFFNDRPWRRTAES 300
QY 334 ASECLPCDCNCRSQECYFDPPELYRSTGHGCHCTNCRDNTDGA KCRCRENFRLGNTTEAC 393
Dbb 301 ASECLPCDCNCRSQECYFDPPELYRSTGHGCHCTNCRDNTDGA KCRCRENFRLGNTTEAC 360
QY 394 SPCHCSPVGSLSLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSTDE 453
Dbb 361 SPCHCSPVGSLSLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSTDE 420
QY 454 CNVETGRVCVKDNVEGFNCERCKPGFFNLESSNPXGCTPCFCFGHSSVCTNAVGSYVDI 513
Dbb 421 CNVETGRVCVKDNVEGFNCERCKPGFFNLESSNPXGCTPCFCFGHSSVCTNAVGSYVDI 480
QY 514 SSTFQIDEDGWRVEQORDGSEASLEWSSDRQYIAVTSDSYPPRYFIA PVKELGNQVLSYGQ 573
Dbb 481 SSTFQIDEDGWRVEQORDGSEASLEWSSDRQYIAVTSDSYPPRYFIA PVKELGNQVLSYGQ 540
QY 574 NLSFSFRVDRRDLRLSAEDLVLEGAGLRVSPLIAQNSYPSSETTVKYIFRLHEATDYPW 633
Dbb 541 NLSFSFRVDRRDLRLSAEDLVLEGAGLRVSPLIAQNSYPSSETTVKYIFRLHEATDYPW 600
QY 634 RPALSPPEFQKLLNLTISIKIRGTYSERSAGYLDVTLQ SARPGVPATWVESCTCPVG 693
Dbb 601 RPALSPPEFQKLLNLTISIKIRGTYSERSAGYLDVTLQ SARPGVPATWVESCTCPVG 660
QY 694 YGQFCETCLPGYRRETPLSGPYSPCVLCTCNHSHSETCDPETGVCD CRDNTAGPHCEKCS 753
Dbb 661 YGQFCETCLPGYRRETPLSGPYSPCVLCTCNHSHSETCDPETGVCD CRDNTAGPHCEKCS 720
QY 754 DGYGDSLTGTSSDCQPCPCPGSSCAIVPKTKEVVCTHPTGTAGKRCELCD DGYFGDP 813
Dbb 721 DGYGDSLTGTSSDCQPCPCPGSSCAIVPKTKEVVCTHPTGTAGKRCELCD DGYFGDP 780
QY 814 LGSNGPVRLCRPCQCNNDNIDPNAVGNCRNLTGECCLKIYNTAGFYCD RCKEGFFGNPLAP 873
Dbb 781 LGSNGPVRLCRPCQCNNDNIDPNAVGNCRNLTGECCLKIYNTAGFYCD RCKEGFFGNPLAP 840
QY 874 NPADKCKACACNYGTVQQSSCNPVGTQCQCLPHVSGRDCGTC DPGYYNLQSGQCERCDC 933
Dbb 841 NPADKCKACACNYGTVQQSSCNPVGTQCQCLPHVSGRDCGTC DPGYYNLQSGQCERCDC 900
QY 934 CHALGSTNGQCDIRTGQCECOPGITGQH CERCETNHFHFGPGEGCKPCDCHHESLSLQCK 993
Dbb 901 CHALGSTNGQCDIRTGQCECOPGITGQH CERCETNHFHFGPGEGCKPCDCHHESLSLQCK 960
QY 994 DDGRCCEGFGVGNRCDCQCEENYFYNRSWPGCQEC PACYRLVKDKAAEHRVKLQELES LI 1053
Dbb 961 DDGRCCEGFGVGNRCDCQCEENYFYNRSWPGCQEC PACYRLVKDKAAEHRVKLQELES LI 1020
QY 1054 ANLGTGDDMVTDOAFEDRLKEAREVTDLLREAOEVKDV DQNLMDRLQRVNSSLHQSISR 1113
Dbb 1021 ANLGTGDDMVTDOAFEDRLKEAREVTDLLREAOEVKDV DQNLMDRLQRVNSSLHQSISR 1080
QY 1114 LQNIPTIETGILAEARARSRVESTEQ LIEIASRELEKAKWAANVSITQPESTGEPNMNT 1173
Dbb 1081 LQNIPTIETGILAEARARSRVESTEQ LIEIASRELEKAKWAANVSITQPESTGEPNMNT 1140
QY 1174 LLAEBARRLAERHKQEADDIRVAKTANETS AEAYNLLRTLAGENQTALEIHEELNRKYE 1233
Dbb 1141 LLAEBARRLAERHKQEADDIRVAKTANETS AEAYNLLRTLAGENQTALEIHEELNRKYE 1200

QY 1234 QAKNISQDLEKQOARVHEEAKRAGDKAVEIYASVAQITPVDSEAL ENEANKIKKBAADLD 1293
Dbb 1201 QAKNISQDLEKQOARVHEEAKRAGDKAVEIYASVAQITPVDSEAL ENEANKIKKBAADLD 1260
QY 1294 RLIDQKLKDYEDLREDMRGKEHEVKNLLEKGAEQQTADQ LLARADAAKALAEAAKKGKGR 1353
Dbb 1261 RLIDQKLKDYEDLREDMRGKEHEVKNLLEKGAEQQTADQ LLARADAAKALAEAAKKGKGR 1320
QY 1354 STLQEANDILNLLKDFDRVNDNKTAAEEALRRIPAINRTIA EANEKTRERAOALGNAAA 1413
Dbb 1321 STLQEANDILNLLKDFDRVNDNKTAAEEALRRIPAINRTIA EANEKTRERAOALGNAAA 1380
QY 1414 DATEAKNKAHEAERIAASAAQKNATSTKADAERTFGEVTD LLDNEVNGMLRQLEEAENELKR 1473
Dbb 1381 DATEAKNKAHEAERIAASAAQKNATSTKADAERTFGEVTD LLDNEVNGMLRQLEEAENELKR 1440
QY 1474 KQDDADQDDMMAGMASQAAQAEALNARKAKNSVSSLLS QLNNLLDQLGQDITVDLNLKLINE 1533
Dbb 1441 KQDDADQDDMMAGMASQAAQAEALNARKAKNSVSSLLS QLNNLLDQLGQDITVDLNLKLINE 1500
QY 1534 IEGLNKADEMKAASDLDRKVS DLESEARKQEAALMDYNR DIAEIIKDIHNLEDIKKTL P 1593
Dbb 1501 IEGLNKADEMKAASDLDRKVS DLESEARKQEAALMDYNR DIAEIIKDIHNLEDIKKTL P 1560
QY 1594 TGCFTNTPSIEKP 1605
Dbb 1561 TGCFTNTPSIEKP 1572

RESULT 6

AAB48455
ID AAB48455 standard; protein; 1572 AA.

AC AAB48455;

DT 02-MAR-2001 (first entry)

XX Mouse laminin 8 polypeptide, SEQ ID NO: 28.

DE Mouse; laminin 8; neuroprotective; angiogenic; osteopathic;
KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;
KW vascular tissue injury; neural injury; angiogenesis regulation.

OS Mus musculus.

XX WO200066732-A2.

XX 09-NOV-2000.

XX 28-APR-2000; 2000WO-US011543.

XX 30-APR-1999; 99US-0131720P.

PR 21-AUG-1999; 99US-0149738P.

PR 24-SEP-1999; 99US-0155945P.

PR 11-FEB-2000; 2000US-0182012P.

XX (BIOS-) BIOSTRATUM INC.

XX Kortessmaa J, Tryggvason K;

XX WPI; 2000-687539/67.

DR N-PSDB; AAC83716.

PT Purified laminin 8 protein, useful for research and therapeutic purposes
PT including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.

XX Claim 5; Page 240-245; 245pp; English.

XX The present sequence is a laminin 8 polypeptide chain. Laminins are a
CC family of heterotrimeric glycoproteins that function via binding
CC interactions with neighbouring cell receptors and by forming laminin

QY 779 CAIVPKTKEVVCTHPTGTAGKRCCELCDGDFGDPVLRCLRPCCQNDNIDPNAVG 838
Db 781 CAVVPKTKVCTNPTGTGKRCCELCDGDFGDPVLRCLRCQSDNIDPNAVG 840
QY 839 NCNRLTGECLKCIYNTAGFYCDRCCKEGFFGNPLAPNADKCKACACN-YGTVQQSSCNP 897
Db 841 NCNRLTGECLKCIYNTAGFYCDRCCKEGFFGNPLAPNADKCKACACNPGYTMKQSSCNP 900
QY 898 VTGQCQCCLPHVSGRDCGTDPGYNLSQGGCERCDCCHALGSTNGQCDIRTGQCECQPGI 957
Db 901 VTGQCCECLPHVTGQDCGACDPGFYNLSQGGCERCDCCHALGSTNGQCDIRTGQCECQPGI 960
QY 958 TGQHCERCETNHFVGGPEGCKPCDCHHEGSLSLQCKDDGRCECREGVGNRCDCQCEENYF 1017
Db 961 TGQHCERCETNHFVGGPEGCKPCDCHHEGSLSLQCKDDGRCECREGVGNRCDCQCEENYF 1020
QY 1018 YNRSWPGCQCEPCACYRLVKDKAAEHRVKLQELSLIANLGTGDDMTDQAFEDRLKEAER 1077
Db 1021 YNRSWPGCQCEPCACYRLVKDKVADHRVKLQELSLIANLGTGDDMTDQAFEDRLKEAER 1080
QY 1078 EYTDLLREAQEVKQVQDQNLMDRLQRVNSSLHSLQISRLQIRNIRNTIETGILAEARARSVES 1137
Db 1081 EYMDLLREAQVQVQDQNLMDRLQRVNSSLHSLQISRLQIRNIRNTIETGILAEARAHVEN 1140
QY 1138 TEOLTEIASRELEKAKM-AANVSITQPESTGEPNNMTLLAEAEARRLAERHKEADDIRV 1196
Db 1141 TERLIEIASRELEKAKVAAANVSITQPESTGEPNNMTLLAEAEARRLAERHKEADDIRV 1200
QY 1197 AKTANETSAAEYNLLRLTLAGENQTALEIEELNRYEQAKNISQDLEKQAAHVHEEAKRA 1256
Db 1201 AKTANDTSTEAYNLLRLTLAGENQTALEIEELNRYEQAKNISQDLEKQAAHVHEEAKRA 1260
QY 1257 GDKAVEIYASVAQLTPVDSALENEANKIKKEAADLRLIDQKLKDYEDLREDMRGKEHE 1316
Db 1261 GDKAVEIYASVAQLSPDSELENEANNIKMEAEENLEQLIDQKLKDYEDLREDMRGKELE 1320
QY 1317 VKNLEKGAEOQTADQALLAPADAALAEAEAAKGRSTLQEAANDILNLLKDFDRRVNDN 1376
Db 1321 VKNLEKKGKTEQQTADQALLAPADAALAEAEAAKGRSTLQEAANDILNLLKDFDRRVNDN 1380
QY 1377 KTAABEALRRIPAINRTIAEANEKTRQAQLALGNAAADATEAKNKAHEAEERIASAAQKNA 1436
Db 1381 KTAABEALRRIPAINRTIAEANEKTRQAQLALGNAAADATEAKNKAHEAEERIASAVQKNA 1440
QY 1437 TSTKADAERTFGEVTDLDNEVNGMLRQLEAEENELKPKQDDADQDMMAGNASQAQAEAE 1496
Db 1441 TSTKADAERTFAEVTOLDNEVNNMLKQLEAEKEKELKPKQDDADQDMMAGNASQAQAEAE 1500
QY 1497 LNARKAKNSVSSLLSQNLNLLDQLGQDQTDVNLKLEIEGSLNKAKEDEKASDLDKRVSD 1556
Db 1501 INARKAKNSVSSLLSIINDLLEQLGQDQTDVNLKLEIEGTLNKAKEDEKASDLDKRVSD 1560
QY 1557 LESEARKQEAAMIDYNRDIAEIKDIHNLEDIKKTLPTGCFNTPSIEKP 1605
Db 1561 LENEARKQEAAMIDYNRDIEEIMKDIRNLEDIRKTLPSGCFNTPSIEKP 1609

RESULT 10
ABB81594
ID ABB81594 standard; protein; 1609 AA.
XX
AC ABB81594;
XX
DT 19-SEP-2002 (first entry)
XX
DE Human laminin 10 third chain protein sequence SEQ ID NO:14.
XX
KW Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;
KW tissue repair development; laminin; healing; vascular tissue;
KW re-endothelialisation; vascular injury; cell attachment; cell stasis;
KW proliferation; migration.
XX

OS Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 1..33
FT /label= signal
FT Protein 34..1609
FT /label= laminin_10_third_chain
PN WO200250111-A2.
XX
XX 27-JUN-2002.
XX
XX 21-DEC-2001; 2001WO-US051035.
XX
XX 21-DEC-2000; 2000US-0257449P.
PR 28-MAR-2001; 2001US-0279282P.
PR 13-NOV-2001; 2001US-00279282.
XX
XX (BIOS-) BIOSTRATUM INC.
XX
XX Tryggvason K, Doi M, Thyboll J;
XX
XX WPI; 2002-557650/59.
DR N-PSDB; ABQ72912.
XX
PT New human laminin-10 proteins, useful for accelerating the healing of
PT vascular tissue, improving the biocompatibility of grafts, or for
PT promoting re-endothelialization at the site of vascular injuries.
XX
PS Claim 9; Page 165-170; 231pp; English.
XX
XX The present invention describes human laminin alpha 5. Also described is
CC an isolated laminin 10. Laminin 10 has vulnery activity. Laminins are
CC useful in maintaining cell/tissue phenotype as well as promoting cell
CC growth and differentiation in tissue repair development. Specifically,
CC laminin 10 can be used for accelerating the healing injuries of vascular
CC tissue, improving the biocompatibility of grafts useful for treating such
CC injuries, for promoting re-endothelialisation at the site of vascular
CC injuries, and promote cell attachment and subsequent cell stasis,
CC proliferation, differentiation, and/or migration. The present sequence
CC represents a third chain protein of laminin 10, from the present
XX invention
SQ Sequence 1609 AA;

Query Match 93.7%; Score 8148; DB 5; Length 1609;
Best Local Similarity 92.8%; Pred. No. 0;
Matches 1493; Conservative 59; Mismatches 53; Indels 4; Gaps 3;
QY 1 MTGGRAALALQPRGLWPELLAVL--AAVAGCVRAAMDECADEGGRPQRCMPEFVNAAFN 58
Db 1 MRGSHRAAPALRPRGLWPELLAVLAAAAAGCAQAMDECTDEGGRPQRCMPEFVNAAFN 60
QY 59 VTVVATNTCGTPPEEYCVQTVGTGVTKSCHLCDAGQOHLQHGAAFLTDYNNQADTTWQS 118
Db 61 VTVVATNTCGTPPEEYCVQTVGTGVTKSCHLCDAGQOHLQHGAAFLTDYNNQADTTWQS 120
QY 119 QTMLAGVQYVPSINLTLHLGKAFDITYVRLKFTSRPESPAIYKRTREDGPMWIPYQYVSG 178
Db 121 QTMLAGVQYVPSINLTLHLGKAFDITYVRLKFTSRPESPAIYKRTREDGPMWIPYQYVSG 180
QY 179 SCENTYSKANRGFIRTTGGDEQALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFDNSPVL 238
Db 181 SCENTYSKANRGFIRTTGGDEQALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFDNSPVL 240
QY 239 QEWVTATDIRVTNRLNTFGDEVFNDPKVLKSYIYAIISDFAVGGRCKCNHASECVKNEF 298
Db 241 QEWVTATDIRVTNRLNTFGDEVFNDPKVLKSYIYAIISDFAVGGRCKCNHASECVKNEF 300
QY 299 DKLMCNCKHNTYGVDCCKLPFFNDRPWRRTAESAECCLPCDCNCRSQECYFDPPELYRS 358
Db 301 DKLMCNCKHNTYGVDCCKLPFFNDRPWRRTAESAECCLPCDCNCRSQECYFDPPELYRS 360

QY 359 TGHGGHCTNCRDNTDGAKCERCRENFRILGNTEACSPCHSPVGSLSLTCQDSYGRCSCKP 418
Db 361 TGHGGHCTNCRDNTDGAKCERCRENFRILGNTEACSPCHSPVGSLSLTCQDSYGRCSCKP 420
QY 419 GVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSTDECNVEITGRVCCKDNVEGFNCERCKPG 478
Db 421 GVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSTDECNVEITGRVCCKDNVEGFNCERCKPG 480
QY 479 FFNLESSNPKGCTPCFCFGHSSVCTNAVGYSVYDIDISSTFQIDEDGWRVEQRDGSEASLEW 538
Db 481 FFNLESSNPGRGCTPCFCFGHSSVCTNAVGYSVYDIDISSTFQIDEDGWRVEQRDGSEASLEW 540
QY 539 SSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYGQNLFSFRVDRDRTRLSEAEDLVLEGA 598
Db 541 SSERQDIAVISDSYFPRYFIAPAKFLGKQVLSYGQNLFSFRVDRDRTRLSEAEDLVLEGA 600
QY 599 GLRVSVPLIAQGNPSYPSSETTVKYIFRLHEATDYPWRPALSPFEFOKLLNNLTSIKIRGTY 658
Db 601 GLRVSVPLIAQGNPSYPSSETTVKYVFRLEATDYPWRPALTPFEFOKLLNNLTSIKIRGTY 660
QY 659 SERSAGYLDVTLQOSARPGVPATWVESCTCPVGYGGQFCETCLPGYRRETSPSLGPYSP 718
Db 661 SERSAGYLDVTLASARPGVPATWVESCTCPVGYGGQFCETCLPGYRRETSPSLGPYSP 720
QY 719 CVLCTCNHGHSETCDPETGVCDNRDNTAGPHCKECSGSDGYGDSITLGTSSDCQPCPCPGSS 778
Db 721 CVLCAACNGHSETCDPETGVCDNRDNTAGPHCKECSGSDGYGDSITLGTSSDCQPCPCPGSS 780
QY 779 CAIVPKTKEVVCHCTPTGTAGKRCCELCDGDFGDPPLGNGPVRVLCPCQCNNDIDPNVAVG 838
Db 781 CAIVPKTKEVVCHCTPTGTGTGRCCELCDGDFGDPPLGNGPVRVLCPCQCNNDIDPNVAVG 840
QY 839 NCNRLTGECLKCIYNTAGFYCDRCCKEGFFGNPLAPNPADKCKACACN-YGTVQQOSSCNP 897
Db 841 NCNRLTGECLKCIYNTAGFYCDRCCKEGFFGNPLAPNPADKCKACACNPGYTMKQOSSCNP 900
QY 898 VTGQCQCLPHVSGRDCGTCDPGYNNLQSGGQRCDCCHALGSTNGQCDIRTGQCECQPGI 957
Db 901 VTGQCECLPHVSGRDCGTCDPGYNNLQSGGQRCDCCHALGSTNGQCDIRTGQCECQPGI 960
QY 958 TGQHCERCETNHFGEPEGCKPCDCHHGSLSLQCKDDGRCEGFGVGNRCQCEENYF 1017
Db 961 TGQHCERCETNHFGEPEGCKPCDCHHGSLSLQCKDDGRCEGFGVGNRCQCEENYF 1020
QY 1018 YNRSWPGQCECPACVRLVKDKAAEHRVKLESLIANLGTGDDMTDQAFEDRLKEAER 1077
Db 1021 YNRSWPGQCECPACVRLVKDKVADHRVKLESLIANLGTGDDMTDQAFEDRLKEAER 1080
QY 1078 EVDLLREAQEVKVDQNLMDRLQRVNSLSHLSQISRLQNRNIRNTIETGILAEARSRVES 1137
Db 1081 EVDLLREAQEVKVDQNLMDRLQRVNSLSHLSQISRLQNRNIRNTIETGILAEARSRVES 1140
QY 1138 TEQLIEIASRELEKAKM-AANVSITQPESTGPNNTLLAEARLAEHRKHQAEADDIVRV 1196
Db 1141 TERLIEIASRELEKAKM-AANVSITQPESTGPNNTLLAEARLAEHRKHQAEADDIVRV 1200
QY 1197 AKTANETSAAEYNLLRLTLAGEQTALIEEELNRKVEQAKNISQDLEKQAAARVHEEAKRA 1256
Db 1201 AKTANDTSTEAYNLLRLTLAGEQTALIEEELNRKVEQAKNISQDLEKQAAARVHEEAKRA 1260
QY 1257 GDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLRLIDQKLKDYEDLREDMRGKEHE 1316
Db 1261 GDKAVEIYASVAQLSPDSELTENEANNIKMEAEENLEQIDQKLKDYEDLREDMRGKEHE 1320
QY 1317 VKNLLEKGAEQQTADOLLARADAALAEAAKKGSRSTLQEAANDILNNLKDFFDRRVNDN 1376
Db 1321 VKNLLEKGTQEQQTADOLLARADAALAEAAKKGSRSTLQEAANDILNNLKDFFDRRVNDN 1380
QY 1377 KTAABEALRRIPAINRTIAEANEKTRAEQAALGNAADAATEAKNKAHEAERIASAAQKNA 1436
Db 1381 KTAABEALRKIPAINQTITEANEKTRAEQAALGNAADAATEAKNKAHEAERIASAVQKNA 1440
QY 1437 TSTKADAERTFGEVTDLDNEVNGMLRQLEEAENELKCRKQDDADQDMMAGMASQAQAEAE 1496

Db 1441 TSTKAEARTFAEVTDLNEVNNMLKQLQEAELKELKQKQDDADQDMMAGMASQAQAEAE 1500
QY 1497 LNARKAKNSVSSLLSQLNNLLDQLGQDQDVTDLNKLNEIEGSLNKADEMKAASDLDRKQVSD 1556
Db 1501 INARKAKNSVTSLSIINDLLEQLGQDQDVTDLNKLNEIEGTLNKADEMKAASDLDRKQVSD 1560
QY 1557 LESEARKQEAAIMDYNRDIAEIIKDIHNLEDIKKTLPCTGCFNTPSIEKP 1605
Db 1561 LENEAKQEAAIMDYNRDIEEIMKDIRNLEDIRKTLPSGCFNTPSIEKP 1609
RESULT 11
ADC01887
ID ADC01887 standard; protein; 1609 AA.
XX
AC ADC01887;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human laminin gamma 1 subunit.
XX
KW Cytostatic; human; ds; gene; laminin; tumour; laminin-x; beta3 subunit;
KW gammal subunit; alpha4 subunit; angiogenesis.
XX
OS Homo sapiens.
XX
PN US2003103975-A1.
XX
PD 05-JUN-2003.
XX
PF 18-NOV-2002; 2002US-00299058.
XX
PR 03-NOV-1999; 99US-0163199P.
PR 03-NOV-2000; 2000US-00706235.
XX
(JONE/) JONES J C R.
(GONZ/) GONZALES M.
PI Jones JCR, Gonzales M;
XX
XX WPI; 2003-755217/71.
DR N-PSDB; ADC01886.
XX
PT Antigenic fragment of alpha4 laminin, useful for preparing a composition for treating tumor.
XX
PS Disclosure; Page 42-46; 52pp; English.
XX
CC The invention relates to an antigenic fragment of the human alpha4 laminin subunit appearing as ADC01881. Also included are a chimaeric and/or fusion protein comprising the antigenic fragment, an antibody to the antigenic fragment, a cell line that produces the antibody, an isolated laminin complex (laminin-x, comprising an alpha4 subunit, a beta3 subunit or gammal subunit), modulating angiogenesis and a method of inducing tumours. The antigenic fragment of alpha4 laminin subunit is useful for preparing a composition (e.g. the antibody 2A3) for treating a tumour. The present sequence represents the human gamma 1 laminin subunit.
XX
SQ Sequence 1609 AA;
Query Match 93.7%; Score 8148; DB 7; Length 1609;
Best Local Similarity 92.8%; Pred. No. 0;
Matches 1493; Conservative 59; Mismatches 53; Indels 4; Gaps 3;
QY 1 MTGGGRAALALQPRGRWLPLLAFL--AAVAGCVRAAMDECADEGGRPQRCMPEFVNAAFN 58
Db 1 MRGSHRAAPALRPRGRWLPLLAFLAALAAAGCAQAAMDECTDEGGRPQRCMPEFVNAAFN 60
QY 59 VTVVATNTCGTPPEEYCVQTGVTGVTGKTSCHLCDAGSOOHLQHGAFLTDYNNQADTTWQOS 118
Db 61 VTVVATNTCGTPPEEYCVQTGVTGVTGKTSCHLCDAGPHLQHGAFLTDYNNQADTTWQOS 120

QY 119 QTMLAGVQYPNSINLTLLHLGKAFDITYVRLKFHTSRPESFAIYKRTREDGPMIPYQYSG 178
Db 121 QTMLAGVQYPSSINLTLLHLGKAFDITYVRLKFHTSRPESFAIYKRTREDGPMIPYQYSG 180
QY 179 SCENTYSKANRGFIRTTGGDEQQALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFDNSPVL 238
Db 181 SCENTYSKANRGFIRTTGGDEQQALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFDNSPVL 240
QY 239 QEWVTATDIRVTNLRLNTFGDEVNDPKVLKSYYYAISDFAVGGRCKCNGHASECVKNEF 298
Db 241 QEWVTATDIRVTNLRLNTFGDEVNDPKVLKSYYYAISDFAVGGRCKCNGHASECVKNEF 300
QY 299 DKLMCNCKHNTYGVDCCKLPPFNDRPWRRATAESASECLPCDCNGRSQECYFDPBLYRS 358
Db 301 DKLVNCKHNTYGVDCCKLPPFNDRPWRRATAESASECLPCDCNGRSQECYFDPBLYRS 360
QY 359 TGHGGHTCNCRDNTDGAKCERCENFRRLGNTAECSPCHCSPVGSLSSTQCDSYGRCSCKP 418
Db 361 TGHGGHTCNCRDNTDGAKCERCENFRRLGNTAECSPCHCSPVGSLSSTQCDSYGRCSCKP 420
QY 419 GVMGDKCDRCOPGFHSLTEAGCRPCSDPSSGSTDENVEGRVCCKDNVEGFNCERCKPG 478
Db 421 GVMGDKCDRCOPGFHSLTEAGCRPCSDPSSGSTDENVEGRVCCKDNVEGFNCERCKPG 480
QY 479 FFNLESSNPKGTCPCFCFGHSSVCTNAVGSYVDISSTFOIDEDGWRVEQRDGSEASLEW 538
Db 481 FFNLESSNPRGCTPCFCFGHSSVCTNAVGSYVSISSSTFOIDEDGWRVEQRDGSEASLEW 540
QY 539 SSDROYIAVISDSYFPYFIAPVKFLGNQVLSYQNLFSFRVDRDRTRLASAEDLVLEGA 598
Db 541 SSERQDIAVISDSYFPYFIAPAKFLGKQVLSYQNLFSFRVDRDRTRLASAEDLVLEGA 600
QY 599 GLRVSVPLIAQNSYSPSETTVKYIFRLHEATDYPWRPALSPPEFQKLLNLTISIIRGTY 658
Db 601 GLRVSVPLIAQNSYSPSETTVKYIFRLHEATDYPWRPALTPPEFQKLLNLTISIIRGTY 660
QY 659 SERSAGYLDVTLOSARPGVGPATWVESCPCPVYGGQFCETCLPGYRRETPLSGPYSP 718
Db 661 SERSAGYLDVTLASARPGVGPATWVESCPCPVYGGQFCETCLPGYRRETPLSGPYSP 720
QY 719 CVLCTONGHSEICDPETGVCDCRDNTAGHCEKCSGDIYGGDSTLGTSSDCQPCPCPGSS 778
Db 721 CVLCAONGHSEICDPETGVCDCRDNTAGHCEKCSGDIYGGDSTLGTSSDCQPCPCPGSS 780
QY 779 CAIVPKTKEVVCVTHCPTGTAGKRCCLDDGYFGDPLGNSGVPVRLCRPCQCNNDIDPNAV 838
Db 781 CAIVPKTKEVVCVTHCPTGTAGKRCCLDDGYFGDPLGNSGVPVRLCRPCQCNNDIDPNAV 840
QY 839 NCNRLTGECLKCIYNTAGFYCDRCCKEGFNGNPLAPNADKCKACACN-YGTVOQQSSCNP 897
Db 841 NCNRLTGECLKCIYNTAGFYCDRCCKEGFNGNPLAPNADKCKACACNPGYTMKQSSCNP 900
QY 898 VTGQCQCLPHVSGRDCGTCDFGYNLSQGGCERCDCHALGSTNGQCDIRTGQCECQPGI 957
Db 901 VTGQCQCLPHVSGRDCGTCDFGYNLSQGGCERCDCHALGSTNGQCDIRTGQCECQPGI 960
QY 958 TGQHCERCETNHFGEPEGCKPCDCHHEGSLSQCKDDGRCECREGVGNRCDCQCEENYF 1017
Db 961 TGQHCERCETNHFGEPEGCKPCDCHHEGSLSQCKDDGRCECREGVGNRCDCQCEENYF 1020
QY 1018 YNRSWPGCQECPCYRLVKDKAAEHRVKLQELSLIANLGTGDDMVTDOAFEDRLKEAER 1077
Db 1021 YNRSWPGCQECPCYRLVKDKAAEHRVKLQELSLIANLGTGDDMVTDOAFEDRLKEAER 1080
QY 1078 EVTDLLREAQEVKDVNDLMDRLQVRNSSLHSQISRLQNRNTIETGILAEARSRVES 1137
Db 1081 EVMDDLREAQVQDVNDLMDRLQVRNSSLHSQISRLQNRNTIETGILAEARSRVES 1140
QY 1138 TEOLIEIASRELEKAKM-AANVSITQPESTGEPPNMTLLAEARLAEHRKQEAADDIVRV 1196
Db 1141 TERLIEIASRELEKAKVAAANVSITQPESTGEPPNMTLLAEARLAEHRKQEAADDIVRV 1200

QY 1197 AKTANETSABAYNLLRLTLAGENQTALEIEELNRKYEAKNISQDLEKQAAARVHEEAKRA 1256
Db 1201 AKTANDTSTAYNLLRLTLAGENQTALEIEELNRKYEAKNISQDLEKQAAARVHEEAKRA 1260
QY 1257 GDKAVEIYASVAQLTPVDSEALENEANKIKKEAADRLIDQKLKDYEDLREDMRGKEHE 1316
Db 1261 GDKAVEIYASVAQLSPDSELTENEANNIKMEABENLEQLIDQKLKDYEDLREDMRGKEHE 1320
QY 1317 VKNLLEKGAEQQTADQLLARADAALAEBAKKGKGRSTLOEANDILNNLKDFFDRRVNDN 1376
Db 1321 VKNLLEKGAEQQTADQLLARADAALAEBAKKGKGRSTLOEANDILNNLKDFFDRRVNDN 1380
QY 1377 KTAEEALRRIPAINRTIAEANEKTRQAQALGNAADATEAKNKAHEAERIAASAAQKNA 1436
Db 1381 KTAEEALRRIPAINRTIAEANEKTRQAQALGNAADATEAKNKAHEAERIAASAAQKNA 1440
QY 1437 TSTKADAERTFGEVTDLDNEVNGMLRQLEBAENELKRRKQDDADQDMMAGMASQAAQEA 1496
Db 1441 TSTKADAERTFGEVTDLDNEVNGMLRQLEBAENELKRRKQDDADQDMMAGMASQAAQEA 1500
QY 1497 LNARKAKNSVSSLLSQNLNLLDQLGQDVTVDLNLKLEIEGSLNKADEMKAASDLDRKVSD 1556
Db 1501 INARKAKNSVSSLLSQNLNLLDQLGQDVTVDLNLKLEIEGSLNKADEMKAASDLDRKVSD 1560
QY 1557 LESEARKQEAAMIDYNRDIAEIIKDHNLEDIKTLPTGCFNTPSIEKP 1605
Db 1561 LENEAKKQEAAMIDYNRDIEEIMKDIRNLEDIRKTLPSGCFNTPSIEKP 1609
RESULT 12
AAB19803
ID AAB19803 standard; protein; 1617 AA.
XX
AC AAB19803;
XX
DT 05-MAR-2001 (first entry)
XX Human laminin 2 gamma-1 chain with C-terminal FLAG epitope.
DE Laminin 2; human; nerve regeneration; angiogenic; cell adhesion;
KW degenerative muscle disorder; muscular dystrophy; cell therapy.
XX Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..33
FT /label= Signal_peptide
FT Protein 34..1609
FT /label= Mature_protein
FT Peptide 1610..1617
FT /label= FLAG
XX WO200066730-A2.
XX
XX 09-NOV-2000.
XX 28-APR-2000; 2000WO-US011378.
XX
XX 30-APR-1999; 99US-0131720P.
PR 15-JUN-1999; 99US-0139198P.
PR 12-JUL-1999; 99US-0143289P.
PR 24-SEP-1999; 99US-0155945P.
XX
XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX Yurchenco P;
XX
XX WPI; 2000-687537/67.
DR N-PSDB; AAA88903.
XX Purified laminin 2 protein, useful for research and therapeutic purposes
PT including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.

XX	PS	Claim 5; Page 263-268; 305pp; English.	Db	661	SERSAGYLDVTLASARPGVGPATWVESCTCPVGYGGQFCMCLSGYRRETPLNLPYSP	720
XX	CC	The present sequence is that of the gamma-1 chain of human laminin 2, with an additional C-terminal FLAG epitope, resulting from expression in transfected cells from mammalian expression vectors. Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1 (100 kDa) chains. It is thought to be specifically required for stabilizing myotubes during skeletal muscle development, and for preventing apoptosis. Genetic defects in its structure or expression are associated with a major type of congenital muscular dystrophy. Laminin 2 is also thought to be important in Schwann cell/basal lamina interactions. The invention provides laminin 2 alpha-2, beta-1 and gamma-1 chain polypeptides (see AAB19791-806) and the polynucleotides encoding them (see AAA8891-906), methods for making recombinant laminin 2, cells that express recombinant laminin 2, and methods for using purified laminin 2 for research and therapeutic purposes including peripheral nerve regeneration, treatment of degenerative muscle disorders, angiogenesis regulation, promoting cell attachment and migration, ex vivo cell therapy, improving the take of grafts, improving the biocompatibility of medical devices and preparing improved culture devices and media	Qy	719	CVLCTCNHSETCDPETGVCDRCNDTAGPHCEKCSGYYGDSLTGTSSDCQPCPCPGSS	778
XX	CC		Db	721	CVLCACNHSSETCDPETGVCDRCNDTAGPHCEKCSGYYGDSLTGTSSDCQPCPCPGSS	780
XX	CC		Qy	779	CAIVPKTKEVVTCHCPTGTAGKRCCLCDDGYFGDPLGNSGPNVLCRPPCCQNDNIDPNAVG	838
XX	CC		Db	781	CAVVPKTKEVVTCTNCPTGTTGKRCCLCDDGYFGDPLGRNGPVRCLCCQCSNDIDPNAVG	840
XX	CC		Qy	839	NCNRLTGECLKIYNTAGFYCDRCKEGFFGNPLAPNPADKCKACACN-YGTVQQQSSCNP	897
XX	CC		Db	841	NCNRLTGECLKIYNTAGFYCDRCCKDGFNGPLAPNPADKCKACNCPYGTMTKQQSSCNP	900
XX	CC		Qy	898	VTGQCQCCLPHVSGRDCGTDPGYYNLQSGQGCERCDCCHALGSTNGQCDIRTGQCECQPGI	957
XX	CC		Db	901	VTGQCECLPHVTGQDCGACDPGFYNLQSGQGCERCDCCHALGSTNGQCDIRTGQCECQPGI	960
XX	CC		Qy	958	TGQHCERCETNHFPGPEGCKPCDCHHEGSLQCKDDGRCEBGFVGNRCDCQCEENYF	1017
XX	CC		Db	961	TGQHCERCEVNHFGPEGCKPCDCHHEGSLQCKDDGRCEBGFVGNRCDCQCEENYF	1020
XX	SQ	Sequence 1617 AA;	Qy	1018	YNRSWPGCQCEPCACYRLVKDKAAEHRVKLQLESILIANLGTGDDMTDQAFEDRLKEAER	1077
		Query Match 93.7%; Score 8148; DB 3; Length 1617;	Db	1021	YNRSWPGCQCEPCACYRLVKDKVADHRVKLQLESILIANLGTGDEMVTDQAFEDRLKEAER	1080
		Best Local Similarity 92.8%; Pred. No. 0;	Qy	1078	EVTDLLREAQEVKVDVQNLMDRLQVRNSSLHSQISRLQINRNTIETGILAEARSRVES	1137
		Matches 1493; Conservative 59; Mismatches 53; Indels 4; Gaps 3;	Db	1081	EVMDLLREAQVDKVDVQNLMDRLQVRNNTLSSQISRLQINRNTIETGNLAERAHVEN	1140
Qy	1	MTGGGRAALALQPRGLWPLLAVL--AAVAGCVRAAMDECADEGRRPQRCMPEFVNAAFN	Qy	1139	TEQLIEIASRELEKAKM-AANVSITQPESTGEPPNNMTLLAEERLAEERHKKQEAADDIVRV	1196
Db	1	MRGSHRAAPALPRGRLPVLAVALAAAGCAQAAMDECTDEGRRPQRCMPEFVNAAFN	Db	1141	TERLIEIASRELEKAKVAAANVSITQPESTGDPNNMTLLAEERLAEERHKKQEAADDIVRV	1200
Qy	59	VTVAATNCTGTPPEEYCVQGTGVTGKTSCHLCDAGQOHLQHGAAFLTDYNNQADTTWQOS	Qy	1197	AKTANETSAEAYNLLRLTAGENQTALEIEELNRKYEQAQKNIQDLEKQAARVHEEAKRA	1256
Db	61	VTVAATNCTGTPPEEYCVQGTGVTGKTSCHLCDAGQPHLQHGAAFLTDYNNQADTTWQOS	Db	1201	AKTANDTSTEAYNLLRLTAGENQTAFEIEELNRKYEQAQKNIQDLEKQAARVHEEAKRA	1260
Qy	119	QTMLAGVQYPNSINLTLLHLGKAFDITYVRLKFHTSRPESFAIYKRTREDGPWIPYQYISG	Qy	1257	GDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLRLIDQKLKDYEDLREDMRGKEHE	1316
Db	121	QTMLAGVQYPPSSINLTLLHLGKAFDITYVRLKFHTSRPESFAIYKRTREDGPWIPYQYISG	Db	1261	GDKAVEIYASVAQLSPLDSETLENEANNIKAEAELEQLIDQKLKDYEDLREDMRGKELE	1320
Qy	179	SCENTYSKANRGFIRTTGGDEQQAALCTDEFSDISPLTGGNVAFSTILEGRPSAYNFDNSPVL	Qy	1317	VKNLLEKGAEOQTADQLLARADAAKALAEAAKKGRSTLOEANDILNNLKDFDRRVNDN	1376
Db	181	SCENTYSKANRGFIRTTGGDEQQAALCTDEFSDISPLTGGNVAFSTILEGRPSAYNFDNSPVL	Db	1321	VKNLLEKGTQEQQTADQLLARADAAKALAEAAKKGRDRTLOEANDILNNLKDFDRRVNDN	1380
Qy	239	QEWVTATDIRVTNRLNTFGDEVNDPKVLSYYAISDEAVGGRCKNGHASECVKNEF	Qy	1377	KTAAEEALRRIPAINRTIAEANEKTRAEQAALGNAADAATEAKNKAHEAERIAASAAQKNA	1436
Db	241	QEWVTATDIRVTNRLNTFGDEVNDPKVLSYYAISDFAVGGRCKNGHASECMKNEF	Db	1381	KTAAEEALRKIPAINQITTEANEKTRAEQAALGSAADAATEAKNKAHEAERIAASAVQKNA	1440
Qy	299	DKLMCNCKHNTYGVDCCKLPLFFNDRPWRRTAESAECPLPCDNGRSQECYFDPPELYRS	Qy	1437	TSTKADAERTFGEVTDLDNEVNGMLRQLEAEAEELKRRKQDDADQDMMAGMASQAAQAEAE	1496
Db	301	DKLVCNCKHNTYGVDCCKLPLFFNDRPWRRTAESAECPLPCDNGRSQECYFDPPELYRS	Db	1441	TSTKAEARTFAEVTDLNEVNNMLKQLEAEAEELKRRKQDDADQDMMAGMASQAAQAEAE	1500
Qy	359	TGHGGHCTNCRDNTDGAKCRCRENFRLGNTEACSPCHCSPVGSLSSTQCDSYGRCSCKP	Qy	1497	LNARKAKNSVSSLSQLNNLLDQLGQLDVTDLNKLNEIEGSLNKADEMKAESDLDRKVSD	1556
Db	361	TGHGGHCTNCRDNTDGAHCRCRENFRLGNNEACSSCHCSPVGSLSSTQCDSYGRCSCKP	Db	1501	INARKAKNSVTSLSISINDLLEQLGQLDVTDLNKLNEIEGTLNKADEMKVSDLDRKVSD	1560
Qy	419	GVMGDKCDRCQPGFHSILTEAGCRPCSDPSGSTDECNVETGRCVCKDNVEGFNCERCKPG	Qy	1557	LESEARKQEAAIMDYNRDIAEIIKDIHNLEDIKKTLPTGCFNTPSIEKP	1605
Db	421	GVMGDKCDRCQPGFHSILTEAGCRPCSDPSGSIDECNVETGRCVCKDNVEGFNCERCKPG	Db	1561	LENEAKQEAAIMDYNRDIEEIMKDIRNLEDIRKTLPSGCFNTPSIEKP	1609
Qy	479	FENLESSNPKGCTPCFCFGHSSVCTNAVGYSYVDISSTFQIDEDGWRVEQRDGSSEASLEW				
Db	481	FENLESSNPGRGCTPCFCFGHSSVCTNAVGYSYVISSTFQIDEDGWRABQRDGSSEASLEW				
Qy	539	SSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYGQNLFSFRVDRDRTRLSAEDLVLEGA				
Db	541	SSERQDIAVISDSYFPRYFIAPAKFLGKQVLSYGQNLFSFRVDRDRTRLSAEDLVLEGA				
Qy	599	GLRVSVPPLIAQGNVSFSETTVKYIFRLHEATDYPWRPALSPFEFQKLNNLTISKIRGTY				
Db	601	GLRVSVPPLIAQGNVSFSETTVKYVFLRLHEATDYPWRPALTPFEFQKLNNLTISKIRGTY				
Qy	659	SERSAGYLDVTLQASARPGVGPATWVESCTCPVGYGGQFCETCLPGLYRRETPLSLGPYSP				

RESULT 13
AAW50898
ID AAW50898 standard; protein; 1609 AA.
XX
AC AAW50898;
XX
DT 07-DEC-1998 (first entry)
XX
DE Human laminin G1 chain.

Qy	1138	TEQLIETASRELEKAKM- AANVSITQPESTGEPNNMTLLAAEEARRLAEERHKQEADDIVRV	1196
Db	1141	TERLIEIASRELEKAKVAAANVSVTQPESTGDPNNMTLLAAEEARKLAEERHKQEADDIVRV	1200
Qy	1197	AKTANETSABAYNLLRLTLAGENQTALIEIHELNRKYEQAKNISQDLEKQAARVHEEAKRA	1256
Db	1201	AKTANDTSTEAYNLLRLTLAGENQTAFEIHELNRKYEQAKNISQDLEKQAARVHEEAKRA	1260
Qy	1257	GDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLRLIDQKLKYEDILREDMRGKEHE	1316
Db	1261	GDKAVEIYASVAQLSPDSETLENEANNIKWEAENLEQLIDQKLKYEDILREDMRGKELE	1320
Qy	1317	VKNLLEKGAEBEQOTADQLLARADAAKALAEBAAKKGRSTLQEAANDILNNLKDFDRRVNDN	1376
Db	1321	VKNLLEKXGTEQOTADQLLARADAAKALAEBAAKKGRDRTLQEAANDILNNLKDFDRRVNDN	1380
Qy	1377	KTAAEEALRRIPAINRTIAEANEKTREAOALGNAAADATEAKNKAHEAERIAASAAQKNA	1436
Db	1381	KTAAEEALRKIPAINQITI TEANEKTREAOQALGSAAADATEAKNKAHEAERIAASAVQKNA	1440
Qy	1437	TSTKADAERTFGEVTDLDNEVNGMLRQLEEAENELKRKQDDADQDMMAGMASQAQAEAE	1496
Db	1441	TSTKAAERTFAEVTDLDNEVNNMLKQLEAEKELKRKQDDADQDMMAGMASQAQAEAE	1500
Qy	1497	LNARKAKNSVSSLLSQLNNLLDQLGQDVTDLNKLNEIEGSLNKAKDEMKASDLDKRKUSD	1556
Db	1501	INARKAKNSVTSLLSIINDLLEQLGQDVTDLNKLNEIEGTLNKAKDEMKVSDLDKRKUSD	1560
Qy	1557	LESEARKQEAAIMDYNRDI AEIIKOIHNLEDIKKTLPTGCFNTPTPSIEKP	1605
Db	1561	LENEAKKQEAAIMDYNRDI EEEIMKDIRNLEDIRKTLPSGCFNTPTPSIEKP	1609

RESULT 14

AAB19802
 ID AAB19802 standard; protein; 1576 AA.
 XX
 AC AAB19802;
 XX
 DT 05-MAR-2001 (first entry)
 XX
 DE Human laminin 2 mature gamma-1 chain.
 XX
 KW Laminin 2; human; nerve regeneration; angiogenic; cell adhesion;
 KW degenerative muscle disorder; muscular dystrophy; cell therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200066730-A2.
 XX
 PD 09-NOV-2000.
 XX
 PF 28-APR-2000; 2000WO-US011378.
 XX
 PR 30-APR-1999; 99US-0131720P.
 PR 15-JUN-1999; 99US-0139198P.
 PR 12-JUL-1999; 99US-0143289P.
 PR 24-SEP-1999; 99US-0155945P.
 XX
 PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
 XX
 PI Yurchenco P;
 XX
 DR WPI; 2000-687537/67.
 DR N-PSDB; AAA88902.
 XX
 PT Purified laminin 2 protein, useful for research and therapeutic purposes
 PT including peripheral nerve regeneration, treatment of degenerative muscle
 PT disorders, angiogenesis regulation, and ex vivo cell therapy.
 XX
 PS Claim 5; Page 251-256; 305pp; English.
 XX
 CC The present sequence is that of human laminin 2 gamma-1 chain mature

protein. Laminin-2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1 (100 kDa) chains. It is thought to be specifically required for stabilizing myotubes during skeletal muscle development, and for preventing apoptosis. Genetic defects in its structure or expression are associated with a major type of congenital muscular dystrophy. Laminin 2 is also thought to be important in Schwann cell/basal lamina interactions. The invention provides laminin 2 alpha-2, beta-1 and gamma-1 chain polypeptides (see AAB19791-806) and the polynucleotides encoding them (see AAA8891-906), methods for making recombinant laminin 2, cells that express recombinant laminin 2, and methods for using purified laminin 2 for research and therapeutic purposes including peripheral nerve regeneration, treatment of degenerative muscle disorders, angiogenesis regulation, promoting cell attachment and migration, ex vivo cell therapy, improving the take of grafts, improving the biocompatibility of medical devices and preparing improved culture devices and media

Sequence 1576 AA;

Query Match 92.5%; Score 8043; DB 3; Length 1576;

Best Local Similarity 93.3%; Pred. No. 0;		Matches 1470; Conservative 57; Mismatches 47; Indels 2; Gaps 2;	
QY	32	RAAMDECADEGGRPQRCMPEFVNAAFNVTVATNTCGTPPEEYCVQGTGVTGKSCHLCD	91
Db	1	QAAMDECTDEGGRPQRCMPEFVNAAFNVTVATNTCGTPPEEYCVQGTGVTGKSCHLCD	60
QY	92	AGQQLHQHGA AFLTDYNNQADTTWQSQOTMLAGVQYPNSINLTILHLGKAFDITYVRLKFX	151
Db	61	AGQPHLQHGA AFLTDYNNQADTTWQSQOTMLAGVQYPSSINLTILHLGKAFDITYVRLKFX	120
QY	152	TSRPESFAIYKRTREDGPWIPYQYISGSCENTYSKANRGFIRTGDEQQAALCTDEFSDIS	211
Db	121	TSRPESFAIYKRTREDGPWIPYQYISGSCENTYSKANRGFIRTGDEQQAALCTDEFSDIS	180
QY	212	PLTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTILNRLNTFGDEVFNDPKVLKSY	271
Db	181	PLTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTILNRLNTFGDEVFNDPKVLKSY	240
QY	272	YYAISDFAVGGRCKCNHGHASECVKNEFDKLMCNCKHNTYGVDCBKCLPFENDRPWRATA	331
Db	241	YYAISDFAVGGRCKCNHGHASECMKNEFDKLVNCKHNTYGVDCBKCLPFENDRPWRATA	300
QY	332	ESASECULPCDCNCRSQECYFDPPELYRSTGHGGHCTNCRDNTDGAKCERCENFFRLGNTE	391
Db	301	ESASECULPCDCNCRSQECYFDPPELYRSTGHGGHCTNCRDNTDGAKCERCENFFRLGNTE	360
QY	392	ACSPCHCSPVGSLSLSTQCDSYGRCSCKPGVMGDKCDRCQCPGFHSLTEAGCRPCSCDPSGST	451
Db	361	ACSSCHCSPVGSLSLSTQCDSYGRCSCKPGVMGDKCDRCQCPGFHSLTEAGCRPCSCDPSGSI	420
QY	452	DECNVETGRCVCVKDNVEGFNCERCCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGYSVY	511
Db	421	DECNVETGRCVCVKDNVEGFNCERCCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGYSVY	480
QY	512	DISSTFQIDEDGWRVEQRDGSEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSY	571
Db	481	SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY	540
QY	572	GONLSFSPRVDRDTRLAEDLVLEGAGLRVSVPLIAQGNSSYPSETTVKYIFRLHEATDY	631
Db	541	GONLSFSPRVDRDTRLAEDLVLEGAGLRVSVPLIAQGNSSYPSETTVKYVFRLEHATDY	600
QY	632	PWRPALSPFEFQKLLNNLTISKIRGTYSERSAGYLDVTLQSA RGPVGPATWVESCTCP	691
Db	601	PWRPALTPFEFQKLLNNLTISKIRGTYSERSAGYLDVTLASARPGVGPATWVESCTCP	660
QY	692	VGYGQGFCTCLPGYRRETPSLGPYSPCVLCTCNHGHSETCDPETGVDCRDNNTAGPHCEK	751
Db	661	VGYGQGFCEMCLSGYRRETPNLGPYSPCVLCA CNHGHSETCDPETGVNCRDNNTAGPHCEK	720
QY	752	CSDGYYG DSTLGTSSDCQPCPCPGSSCAIVPKTKEVVCTHCPTGTAGKRCCLCDDGYFG	811

Claim 5: Page 251-256: 305pp: English:

The present sequence is that of human laminin 2 gamma-1 chain mature

Db 361 ACSSCHCSPVGSLSLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSI 420
QY 452 DECNVETGRVCVKDNVEGFNCERCCKPGFFNFLESSNPKGCTPCFCFGHSSVCTNAVGYSVY 511
Db 421 DECNVETGRVCVKDNVEGFNCERCCKPGFFNFLESSNPRGCTPCFCFGHSSVCTNAVGYSVY 480
QY 512 DISSTFQIDEDGWRVEQORDGSEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSY 571
Db 481 SISSTFQIDEDGWRAEQORDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY 540
QY 572 GQNLFSFRVDRDRTRLASAEDLVLEGAGLRVSVPLIAQGNYSYSETTVKYIFRLHEATDY 631
Db 541 GQNLFSFRVDRDRTRLASAEDLVLEGAGLRVSVPLIAQGNYSYSETTVKYIFRLHEATDY 600
QY 632 PWRPALSPFEFQKLLNNLTSIKIRGTYSERSAGYLDVTLQSA RPPGVPATWVESCTCP 691
Db 601 PWRPALTPFEFQKLLNNLTSIKIRGTYSERSAGYLDVTLASARPPGVPATWVESCTCP 660
QY 692 VGYGGQFCETCLPGYRRETSLGPYSPCVLCTCNGHSETCDPETGVCD CRDNTAGPHCEK 751
Db 661 VGYGGQFCEMCLSGYRRET PNLGPYSPCVLCACNGHSETCDPETGV C NCRDNTAGPHCEK 720
QY 752 CSDGYYGDSLTGLTSSDCQPCPCPGSSCAIVPKTKEVVC THCPTGTAGRCCEL CDDGYFG 811
Db 721 CSDGYYGDSLTAGTSSDCQPCPCPGSSCAIVPKTKEVVC TNCPTGTGRCCEL CDDGYFG 780
QY 812 DPLGNSGPVRLC RPOCNDNIDPNAVGN CNRLTGECLKCIYNTAGFYCDRCKEGFFGNPL 871
Db 781 DPLGRNGPVRLCRLCQCSDNIDPNAVGN CNRLTGECLKCIYNTAGFYCDRCXDGFFGNPL 840
QY 872 APNPADKCKACACN-YGTVOQOSSCNPV TGQCQCLPHVSGRDCGTDPGYYNLQSGQGCE 930
Db 841 APNPADKCKACNCNPYGTMKQOSSCNPV TGQCECLPHVTGQDCGACDPGFYNLQSGQGCE 900
QY 931 RCDCHALGSTNGQCDIR TGQCECQPGITGQHCE RCETNHF GFGPEGCKPCDCHHEGSLSL 990
Db 901 RCDCHALGSTNGQCDIR TGQCECQPGITGQHCE RCCEVNHFGF GPEGCKPCDCHPEGSLSL 960
QY 991 QCKDDGRCECREGFGVGNRCDCQCEENYFYNRSWPGCQCEPAC YRLVKDKAAEHRVKLQELE 1050
Db 961 QCKDDGRCECREGFGVGNRCDCQCEENYFYNRSWPGCQCEPAC YRLVKDKVADHRVKLQELE 1020
QY 1051 SLIANLGTGDDMVTDQAFEDRLKEAEREVTDLLREAEV KVDQNLMDRLQRVNSSLHSQ 1110
Db 1021 SLIANLGTGDEMVTDOAFEDRLKEAEREVMDLLREAEV KVDQNLMDRLQRVNNTLSSQ 1080
QY 1111 ISRLQNI RNTIETGILAEARSRVSTEQLEIETIASRELEKAKM-AANVSITQPESTGEP 1169
Db 1081 ISRLQNI RNTIETGNLAEQARAHVENTERLEIETIASRELEKAKVAAANVSVTQPESTGDP 1140
QY 1170 NNMTL LAEEARRLAE RHKQEAADDIVRVAKTANETS AEAYNLLRLTAGENQTALEIEELN 1229
Db 1141 NNMTL LAEEARKLAE RHKQEAADDIVRVAKTANDTSTEAYNLLRLTAGENQTA FEIEELN 1200
QY 1230 RKYEQAKNISQDLEKQAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEA 1289
Db 1201 RKYEQAKNISQDLEKQAARVHEEAKRAGDKAVEIYASVAQLSP L DSELENEANNIKMEA 1260
QY 1290 ADLDR LIDQKLKDYEDLREDMRGKEHEVKNLLEKGAEQQTADQLLARADA AKALAEAEA 1349
Db 1261 ENLEQLIDQKLKDYEDLREDMRGKEHEVKNLLEKKGTEQQTADQLLARADA AKALAEAEA 1320
QY 1350 KKG RSTLQEA NDILNNLKD FRRVNDNKTAAEEALRRIPAINRTIAEANEKTR EAQALG 1409
Db 1321 KKG RDTLQEA NDILNNLKD FRRVNDNKTAAEEALRKIPAINQTIT EANEKTR EAQALG 1380
QY 1410 NAAADATEAKNKAHEAEERIAAQAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAEN 1469
Db 1381 SAAADATEAKNKAHEAEERIAASAVQKNATSTKABAERTFAEVTDL DNEVNNMLKQLQEA EK 1440
QY 1470 ELK RKQDDADQDMMAGMASQAQAEALNARKAKNSVSSLLS QLNLLDQLGQLD TVDLN 1529
Db 1441 ELK RKQDDADQDMMAGMASQAQAEINARKAKNSVTSLLSIINDLLEQLGQLD TVDLN 1500

QY 1530 KLNEIEGSLNKA KDEM KASDLDRKVSDDLSEARKQEA A IMDYNRDIAEIIKDIHNLEDIK 1589
Db 1501 KLNEIEGTLNKA KDEM KVSDDLDRKVSDDLSENEAKQEA A IMDYNRDIEEIMKDIRNLEDIR 1560
QY 1590 KTLPTGCFNTPSIEKP 1605
Db 1561 KTLPSGCFNTPSIEKP 1576

Search completed: May 18, 2004, 14:42:31
Job time : 49.6393 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:58 ; Search time 15.8753 Seconds
(without alignments)
10452.141 Million cell updates/sec

Title: US-10-037-182-12
Perfect score: 9429
Sequence: 1 EPYCIVSHLQBDKKCFICDS.....EVRSLKDISEKVAVYSTCL 1725

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	9429	100.0	1786	1 MMMSB1	laminin beta-1 cha
2	8873	94.1	1786	1 MMHUB1	laminin beta-1 cha
3	4936	52.3	1801	1 MMRTS	laminin beta-2 cha
4	4892	51.9	1798	2 S53869	laminin beta-2 cha
5	4746.5	50.3	1797	2 A55677	laminin beta-2 cha
6	3733.5	39.6	1790	1 MMFFB1	laminin beta-1 cha
7	3646	38.7	1808	2 T15099	hypothetical prote
8	1730	18.3	3672	2 T23433	hypothetical prote
9	1730	18.3	3704	2 T37316	probable laminin a
10	1678.5	17.8	1639	1 MMFFB2	laminin gamma-1 ch
11	1649	17.5	3712	2 S18253	laminin alpha-1 ch
12	1618.5	17.2	1609	1 MMHUB2	laminin gamma-1 ch
13	1610.5	17.1	1607	1 MMMSB2	laminin gamma-1 ch
14	1608	17.1	1557	2 T28811	hypothetical prote
15	1584	16.8	3635	2 T10053	laminin alpha 5 ch
16	1575	16.7	303	2 B45067	laminin B1 chain -
17	1535	16.3	3075	2 S14458	laminin alpha-1 ch
18	1497.5	15.9	3106	1 S53868	laminin alpha-2 ch
19	1482	15.7	3084	1 MMMSA	laminin alpha-1 ch
20	1428.5	15.2	1170	2 A53612	laminin B1k chain
21	1395.5	14.8	1168	2 I56985	kalinin B1 - mouse
22	1276.5	13.5	2823	2 T23064	hypothetical prote
23	1276.5	13.5	2823	2 F87908	protein T22A3.8 [i
24	1276.5	13.5	3102	2 T43291	laminin alpha chai
25	978.5	10.4	616	2 I38231	S-laminin - human
26	858.5	9.1	1193	2 A44018	laminin B2t chain
27	850.5	9.0	1192	2 S69000	laminin gamma 2 ch
28	682.5	7.2	1620	2 T27283	hypothetical prote
29	680	7.2	1574	2 T13954	MEGF6 protein - ra

30	661.5	7.0	1111	2	T26972	hypothetical prote
31	659.5	7.0	606	2	A54665	netrin-1 precursor
32	656	7.0	3707	2	S18252	heparan sulfate pr
33	647.5	6.9	4391	2	A38096	perlecan precursor
34	593	6.3	581	2	B54665	netrin-2 precursor
35	583	6.2	612	2	JH0799	laminin-related pr
36	561	5.9	400	2	T46383	hypothetical prote
37	560.5	5.9	1816	1	S68960	laminin alpha-4 ch
38	555.5	5.9	1751	1	MMHUMH	laminin alpha-2 ch
39	531	5.6	2524	2	A35844	laminin alpha-2 Af
40	527	5.6	2321	2	S78549	notch3 protein - h
41	511.5	5.4	2703	1	A24420	notch protein - fr
42	510	5.4	2295	2	C88369	protein unc-52 [im
43	510	5.4	3375	2	T19821	hypothetical prote
44	507	5.4	1160	2	F88369	protein unc-52 [im
45	506	5.4	2318	2	S45306	notch 3 protein -

ALIGNMENTS

RESULT 1

MMMSB1
N;Laminin beta-1 chain precursor - mouse
N;Alternate names: laminin chain B1
C;Species: Mus musculus (house mouse)
C;Date: 28-Feb-1986 #sequence revision 30-Jun-1991 #text_change 10-Dec-1999
C;Accession: A26413; S02679; S05326; S14877; A02871; S02036; S13543
R;Sasaki, M.; Kato, S.; Kohno, K.; Martin, G.R.; Yamada, Y.
Proc. Natl. Acad. Sci. U.S.A. 84, 935-939, 1987
A;Title: Sequence of the cDNA encoding the laminin B1 chain reveals a multidomain protei
A;Reference number: A26413; MUID:87147212; PMID:3493487
A;Accession: A26413
A;Molecule type: mRNA
A;Residues: 1-1786 <SAS>
A;Cross-references: EMBL:M15525; NID:g198700
A;Note: translation in GenBank has additional 48 residues at the amino end
R;Fujiwara, S.; Shinkai, H.; Deutzmann, R.; Paulsson, M.; Timpl, R.
Biochem. J. 252; 453-461, 1988
A;Title: Structure and distribution of N-linked oligosaccharide chains on various domains
A;Reference number: S02678; MUID:88326259; PMID:2458101
A;Accession: S02679
A;Molecule type: protein
A;Residues: 28-42;932-946 <FUJ>
R;Hartl, L.; Oberbaeumer, I.; Deutzmann, R.
Eur. J. Biochem. 173, 629-635, 1988
A;Title: The N terminus of laminin A chain is homologous to the B chains.
A;Reference number: S00624; MUID:88225080; PMID:3267223
A;Accession: S05326
A;Molecule type: protein
A;Residues: 457-466;854-868;932-946 <HAR>
R;Mann, K.; Deutzmann, R.; Timpl, R.
Eur. J. Biochem. 178, 71-80, 1988
A;Title: Characterization of proteolytic fragments of the laminin-nidogen complex and the
A;Reference number: S08895; MUID:89078415; PMID:2462498
A;Accession: S14877
A;Molecule type: protein
A;Residues: 590-620 <MAN>
R;Barlow, D.P.; Green, N.M.; Kurkinen, M.; Hogan, B.L.M.
EMBO J. 3, 2355-2362, 1984
A;Title: Sequencing of laminin B chain cDNAs reveals C-terminal regions of coiled-coil a
A;Reference number: A02870; MUID:85051302; PMID:6209134
A;Accession: A02871
A;Molecule type: mRNA
A;Residues: 1292-1530, 'MEMP', 1535-1691, 'C', 1693-1748, 'N', 1750-1786 <BAR>
A;Cross-references: EMBL:X05212; NID:g52861; PIDN:CAA28839.1; PID:g809042
R;Deutzmann, R.; Huber, J.; Schmetz, K.A.; Oberbaeumer, I.; Hartl, L.
Eur. J. Biochem. 177, 35-45, 1988
A;Title: Structural study of long arm fragments of laminin. Evidence for repetitive C-ter
A;Reference number: S01790; MUID:89030693; PMID:3181157
A;Accession: S02036
A;Molecule type: protein
A;Residues: 1561-1587 <DEU>

R:Paulsson, M.; Deutzmann, R.; Timpl, R.; Dalzoppo, D.; Odermatt, E.; Engel, J.
EMBO J. 4, 309-316, 1985
A:Title: Evidence for coiled-coil alpha-helical regions in the long arm of laminin.
A:Reference number: S13543; MUID:85257455; PMID:3848400
A:Accession: S13543
A:Molecule type: protein
A:Residues: 1700-1748, N', 1750-1759 <PAU>
C:Genetics:
A:Gene: Lamb-1
A:Map position: 12
C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C:Function:
A:Description: interact with cells and with other basement membrane proteins to promote
C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-1786/Product: laminin beta-1 chain #status predicted <MAT>
F:22-270/Domain: VI <DOM6>
F:271-540/Domain: V <DOM5>
F:271-332/Domain: laminin-type EGF-like homology <LE01>
F:335-395/Domain: laminin-type EGF-like homology <LE02>
F:398-455/Domain: laminin-type EGF-like homology <LE03>
F:458-507/Domain: laminin-type EGF-like homology <LE04>
F:510-540/Domain: laminin-type EGF-like homology #status atypical <LE05>
F:541-772/Domain: IV <DOM4>
F:773-1182/Domain: III <DOM3>
F:773-818/Domain: laminin-type EGF-like homology <LE06>
F:821-864/Domain: laminin-type EGF-like homology <LE07>
F:867-914/Domain: laminin-type EGF-like homology <LE08>
F:917-973/Domain: laminin-type EGF-like homology <LE09>
F:976-1025/Domain: laminin-type EGF-like homology <LE10>
F:1028-1081/Domain: laminin-type EGF-like homology <LE11>
F:1084-1129/Domain: laminin-type EGF-like homology <LE12>
F:1132-1176/Domain: laminin-type EGF-like homology <LE13>
F:1183-1397/Domain: II <DOM2>
F:1183-1397/Region: heptad repeats
F:1398-1430/Domain: alpha <ALP>
F:1431-1786/Region: heptad repeats
F:1431-1786/Domain: I <DOM1>
F:22/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F:30-35/Disulfide bonds: #status predicted
F:120,356,519,677,1041,1195,1279,1336,1343,1487,1533,1542,1643/Binding site: carbohydra
F:1179,1182,1785/Disulfide bonds: interchain #status predicted

Query Match 100.0%; Score 9429; DB 1; Length 1786;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	EPYCIIVSHLQEDKKCFICDSRDPYHETLNDSHLIENVVTTTFAPNRLKIWQSENGVENV	60
Db	62	EPYCIIVSHLQEDKKCFICDSRDPYHETLNDSHLIENVVTTTFAPNRLKIWQSENGVENV	121
Qy	61	TIQLDLEAEFHFTHLIMTFKTRPAAMLIERSSDFGKTGWVYRYPAYDCESFPFGISTGP	120
Db	122	TIQLDLEAEFHFTHLIMTFKTRPAAMLIERSSDFGKTGWVYRYPAYDCESFPFGISTGP	181
Qy	121	MKKVDDIIICDSRYSIDIEPSTEGEVIFRALDPAPKIEDPYSPIQNLLKITNLRKFVKLH	180
Db	182	MKKVDDIIICDSRYSIDIEPSTEGEVIFRALDPAPKIEDPYSPIQNLLKITNLRKFVKLH	241
Qy	181	TLGDNLLDSRMEIREKYIYAYVDMVVRGNCFCYGHASECAPVDGVNVEEVEGMVHGHC	240
Db	242	TLGDNLLDSRMEIREKYIYAYVDMVVRGNCFCYGHASECAPVDGVNVEEVEGMVHGHC	301
Qy	241	HNTKGLNCELAMDYHDLPLWRPAEGRNSNACKKCNCSHCHFDMAVFLATGNVSGGV	300
Db	302	HNTKGLNCELAMDYHDLPLWRPAEGRNSNACKKCNCSHCHFDMAVFLATGNVSGGV	361
Qy	301	CDNCQHNTMGRNCEQCKPFYFQHPERDIRDNLCPECTCDPAGSENGICDGYTDFSVGL	360
Db	362	CDNCQHNTMGRNCEQCKPFYFQHPERDIRDNLCPECTCDPAGSENGICDGYTDFSVGL	421
Qy	361	IAGQCRCRKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGPNPCDSETGYCYC	420

Db	422	IAGQCRCRKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGPNPCDSETGYCYC	481
Qy	421	KRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCDLGGALNNSCEDSGQCSCLPHMIGRQCN	480
Db	482	KRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCDLGGALNNSCEDSGQCSCLPHMIGRQCN	541
Qy	481	EVESGYYFTTLDHYIYEAEEANLPGVVVERQYIQDRIPSWTGPVVRVPEGAYLEFFI	540
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Qy	541	DNIPYSMEYEILIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTVPDDDNQVVSLSPGS	600
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Qy	601	RYVVLPRPVCPEKGMNYYTVRLELPQYTAGSDVESPYTFIDSLVLMPYCKSLDIFTVGG	660
Db	662	RYVVLPRPVCPEKGMNYYTVRLELPQYTAGSDVESPYTFIDSLVLMPYCKSLDIFTVGG	721
Qy	661	GDGEVTNSAWETFORYRCLENSRSVVKTPMTDVCNIIIFSISALIHQTGLACECDPQGS	720
Db	722	GDGEVTNSAWETFORYRCLENSRSVVKTPMTDVCNIIIFSISALIHQTGLACECDPQGS	781
Qy	721	SSVCDPNGGQCCQCRPNVVGRTCNRCAPGTFFGPGNGCKPCDCHLQGSASAFCDAITGQ	780
Db	782	SSVCDPNGGQCCQCRPNVVGRTCNRCAPGTFFGPGNGCKPCDCHLQGSASAFCDAITGQ	841
Qy	781	CFQGIYARQCDCRCLPGYWGFPSCPCQCNHGDALDCTVTGECISCDYTTGHNCRCLAG	840
Db	842	CFQGIYARQCDCRCLPGYWGFPSCPCQCNHGDALDCTVTGECISCDYTTGHNCRCLAG	901
Qy	841	YVGDPPIIGSGDHCRPCPCPDGPDGSGRPFARSCYQDPVTLQLACVCDPQYIGSRCD	900
Db	902	YVGDPPIIGSGDHCRPCPCPDGPDGSGRPFARSCYQDPVTLQLACVCDPQYIGSRCD	961
Qy	901	FFGNPSDFGSGCQPCQCHNIDTTDPEACDKDTGRCLKCLYHTEGDHQCQLCQYGYGD	960
Db	962	FFGNPSDFGSGCQPCQCHNIDTTDPEACDKDTGRCLKCLYHTEGDHQCQLCQYGYGD	1021
Qy	961	RQDCRKVCNVLGTVKEHNGSDCHCDKATGQCSCLPNVIGQNCDCRCAPNTWQLASGTG	1020
Db	1022	RQDCRKVCNVLGTVKEHNGSDCHCDKATGQCSCLPNVIGQNCDCRCAPNTWQLASGTG	1081
Qy	1021	GPCNCNAHSGFPGSCNEFTGQCQCMPGFGGRTCECQELFWGDPDVECRACDCDPRG	1080
Db	1082	GPCNCNAHSGFPGSCNEFTGQCQCMPGFGGRTCECQELFWGDPDVECRACDCDPRG	1141
Qy	1081	PQCDQSTGQCVCVEGVEGPRCDKCTRGYSGVFPDCTPCHQCFCALWDALIGELTNR	1140
Db	1142	PQCDQSTGQCVCVEGVEGPRCDKCTRGYSGVFPDCTPCHQCFCALWDALIGELTNR	1201
Qy	1141	EKAKALKISGVIGPYRETVDVSEKKNVETKIDILAQSPAAEPLKNIGILFEEAEKLT	1200
Db	1202	EKAKALKISGVIGPYRETVDVSEKKNVETKIDILAQSPAAEPLKNIGILFEEAEKLT	1261
Qy	1201	EKAAQVEVKLTDTASQSNSTAGELGALQAEAESLDKTVKELAEQLEFIKNSDIQAL	1260
Db	1262	EKAAQVEVKLTDTASQSNSTAGELGALQAEAESLDKTVKELAEQLEFIKNSDIQAL	1321
Qy	1261	TKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRVEDLMLERESPFKEQEEQARLL	1320
Db	1322	TKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRVEDLMLERESPFKEQEEQARLL	1381
Qy	1321	AGKLSLDLSAAQMTCTGTPPGADCSSECGPNCRCTDEGEKKCGGPGCGGLVTVAH	1380
Db	1382	AGKLSLDLSAAQMTCTGTPPGADCSSECGPNCRCTDEGEKKCGGPGCGGLVTVAH	1441
Qy	1381	QKAMDFDRDVLALAEVEQLSKMVSEAKVRADEAKQNAQDVLLKTNATKEKVDKSN	1440
Db	1442	QKAMDFDRDVLALAEVEQLSKMVSEAKVRADEAKQNAQDVLLKTNATKEKVDKSN	1501
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Db 1502 NLIKQIRNFLTSDADLDSIEAVANEVLKSGNASTPQQLNLTEDIRERVETLSQVEVIL 1561

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RESULT 2

MMHUB1

laminin beta-1 chain precursor - human

N;Alternate names: laminin chain B1

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 19-Jan-2001

C;Accession: S13547; A28483; A26994; S23566

R;Vuolteenaho, R.; Chow, L.T.; Tryggvason, K.

J;Biol. Chem. 265, 15611-15616, 1990

A;Title: Structure of the human laminin B1 chain gene.

A;Reference number: S13547; MUID:90368768; PMID:1975589

A;Accession: S13547

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-1786 <VUO>

A;Cross-references: GB:M61951; GB:J02778; NID:g186911; PIDN:AAA59486.1; PID:g186913

A;Note: the nucleotide sequence was submitted to GenBank, February 1991

R;Pikkarainen, T.; Eddy, R.; Fukushima, Y.; Byers, M.; Shows, T.; Pihlajaniemi, T.; Sara J. Biol. Chem. 262, 10454-10462, 1987

A;Title: Human laminin B1 chain. A multidomain protein with gene (LAMB1) locus in the q2

A;Reference number: A28483; MUID:87280097; PMID:3611077

A;Accession: A28483

A;Molecule type: mRNA

A;Residues: 1-1786 <PIK>

A;Cross-references: GB:M61951; GB:J02778; NID:g186911; PIDN:AAA59486.1; PID:g186913

R;Jaye, M.; Modi, W.S.; Ricca, G.A.; Mudd, R.; Chiu, I.M.; O'Brien, S.J.; Drohan, W.N. Am. J. Hum. Genet. 41, 605-615, 1987

A;Title: Isolation of a cDNA clone for the human laminin-B1 chain and its gene localized

A;Reference number: A26994; MUID:88021029; PMID:3661559

A;Accession: A26994

A;Molecule type: mRNA

A;Residues: 1276-1469, 'V', 1471-1695, 'G', 1697-1709 <JAY>

A;Cross-references: EMBL:M20206; NID:g186914; PIDN:AAA59487.1; PID:g186915

R;Vuolteenaho, R.; Kallunki, T.; Chow, L.; Ikonen, J.; Pikkarainen, T.; Tryggvason, K. in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp. 175-193, Academic P

A;Title: Genes for the human laminin B1 and B2 chains.

A;Reference number: S23566

A;Accession: S23566

A;Molecule type: DNA

A;Residues: 762-1786 <VU2>

A;Note: mRNA was also sequenced

C;Genetics:

A;Gene: GDB:LAMB1

A;Cross-references: GDB:119357; OMIM:150240

A;Map position: 7q31.1-7q31.3

A;Introns: 13/1; 71/3; 117/1; 141/3; 204/3; 226/1; 293/3; 334/1; 397/1; 457/1; 494/3; 5264/3; 1513/1; 1582/2; 1629/3; 1688/3; 1742/1

C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin

C;Function:

A;Description: interact with cells and with other basement membrane proteins to promote

C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology

C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-1786/Product: laminin beta-1 chain #status predicted <MAT>

F;22-270/Domain: VI <DOM6>

F;271-548/Domain: V <DOM5>

F;271-332/Domain: laminin-type EGF-like homology <LE01>

F;335-395/Domain: laminin-type EGF-like homology <LE02>

F;398-455/Domain: laminin-type EGF-like homology <LE03>

F;458-507/Domain: laminin-type EGF-like homology <LE04>

F;463-468/Region: cell adhesion #status predicted

F;510-540/Domain: laminin-type EGF-like homology #status atypical <LE05>

F;549-774/Domain: IV <DOM4>

F;662-668/Region: cell adhesion #status predicted

F;773-818/Domain: laminin-type EGF-like homology <LE06>

F;775-1178/Domain: III <DOM3>

F;821-864/Domain: laminin-type EGF-like homology <LE07>

F;867-914/Domain: laminin-type EGF-like homology <LE08>

F;917-973/Domain: laminin-type EGF-like homology <LE09>

F;923-927/Region: cell adhesion #status predicted

F;950-954/Region: cell adhesion #status predicted

F;976-1025/Domain: laminin-type EGF-like homology <LE10>

F;1028-1081/Domain: laminin-type EGF-like homology <LE11>

F;1084-1129/Domain: laminin-type EGF-like homology <LE12>

F;1132-1176/Domain: laminin-type EGF-like homology <LE13>

F;1179-1397/Domain: II <DOM2>

F;1179-1397/Region: heptad repeats

F;1398-1430/Domain: alpha <ALP>

F;1431-1786/Domain: I <DOM1>

F;1431-1786/Region: heptad repeats

F;30-35/Disulfide bonds: #status predicted

F;120,356,519,677,965,1041,1195,1279,1336,1343,1487,1542,1643/Binding site: carbohydrate

F;1179,1182,1785/Disulfide bonds: interchain #status predicted

Query Match 94.1%; Score 8873; DB 1; Length 1786;

Best Local Similarity 92.9%; Pred. No. 0;

Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

QY 1 EPYCIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVVTTFAPNRLKIWKQSENGVENV 60

Db 62 EPYCIVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVVTTFAPNRLKIWKQSENGVENV 121

QY 61 TIQLDLEAEFHFTHLMTFKTRPAAMLIERSDFGKTGWVYRYFAYDCEASFFGISTGP 120

Db 122 TIQLDLEAEFHFTHLMTFKTRPAAMLIERSDFGKTGWVYRYFAYDCEASFFGISTGP 181

QY 121 MKKYDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPRIONLLKIITNLRIKFVKLH 180

Db 182 MKKYDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPRIONLLKIITNLRIKFVKLH 241

QY 181 TLGDNLLDSRMEIREKYIYAVYDMVRGNCFCYGHASECAPVDGVNNEEVEGMVGHCMCR 240

Db 242 TLGDNLLDSRMEIREKYIYAVYDMVRGNCFCYGHASECAPVDGVNNEEVEGMVGHCMCR 301

QY 241 HNTKGLNCELMDFYHDLPMWRPAEGRNSNACKKNCNEHSSSCHFDMAVFLATCNVSGGV 300

Db 302 HNTKGLNCELMDFYHDLPMWRPAEGRNSNACKKNCNEHSSSCHFDMAVFLATCNVSGGV 361

QY 301 CDNCQHTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 360

Db 362 CDNCQHTMGRNCEQCKPFYFQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFSTGL 421

QY 361 IAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGGNPCDSETGYCYC 420

Db 422 IAGQCRCKLNVEGEHCDVCKEGFYDLSSEDPFPGCKSCACNPLGTIPGGNPCDSETGHCYC 481

QY 421 KRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCDLGGALNNSCSEDSGQCSCLPHMIGRQCN 480

Db 482 KRLVTGQHCDQCLPEHWGLSNDLDGCRPCDCDLGGALNNSCFAESGQCSCLPHMIGRQCN 541

QY 481 EVESGYFTTLDHYIYEAEFANLPGVVVERQYIQDRIPSWTGPQFVRVPEGAYLEFFI 540

Db 542 EVEPGYVFATLDHYLYEAEFANLPGVSIIVERQYIQDRIPSWTGPQFVRVPEGAYLEFFI 601

QY 541 DNIPYSMEYEILIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTVPDDDNQVVSLSPGS 600

Db 602 DNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPSTSSRCGNTIPDDDNQVVSLSPGS 661

QY 601 RYVLP RPVPCEKGMN YTVRLPQYTASGSDVESPYTFIDSLVLM PYCKSLDIFTVGGS 660
DB 662 RYVLP RPVPCEKGMN YTVRLPQYTASGSDVESPYTFIDSLVLM PYCKSLDIFTVGGS 721
QY 661 GDGEV TNSAWETFOR YRCLENSRSVVKTPMTDVCNII FSI ALIHQTGLACECDPQGS L 720
DB 722 GDGV TNSAWETFOR YRCLENSRSVVKTPMTDVCNII FSI ALIHQTGLACECDPQGS L 781
QY 721 SSVCDP NGGOCQCRPNVVGRTCNRCAPGTFFGPGNGCKPCDCHLQGSASAFCAITGOCH 780
DB 782 SSVCDP NGGOCQCRPNVVGRTCNRCAPGTFFGPGNGCKPCDCHLQGSVNAFCNPVTGOCH 841
QY 781 CFQGIYARQC DRCLPGYWGFPSCQPCQNGHALDCDVTVTGEC LSCQDYTTGHN CERCLAG 840
DB 842 CFQGVYARQC DRCLPGHWGFPSCQPCQNGHADDCDPTVTGEC LNCQDYTMGHN CERCLAG 901
QY 841 YYGDP IIGSGDHCRPCPCPDGPDGSGRQFARSCYQDPVTIQLACVCDP GYIGSRCDDCAGS 900
DB 902 YYGDP IIGSGDHCRPCPCPDGPDGSGRQFARSCYQDPVTIQLACVCDP GYIGSRCDDCAGS 961
QY 901 FFGNPSDFGSGCQPCQCHNIDTTDPEACDKDTGRCLKCLYHTEGDHCQLCQYGYG DAL 960
DB 962 YFGNPSDFGSGCQPCQCHNIDTTDPEACDKDTGRCLKCLYHTEGDHCQLCQYGYG DAL 1021
QY 961 RQDCRKVCNVLGTVKEHCNGSDCHCDKATGCSCCLPNVIGQNCDCRCAPNTWQLASGTGC 1020
DB 1022 RQDCRKVCNVLGTVKEHCNGSDCHCDKATGCSCCLPNVIGQNCDCRCAPNTWQLASGTGC 1081
QY 1021 GPCNCNAAHSFGPSCNEFTGQCQCMPGFGGRTCSCEQLFWGDPDVECRACDCDPRGIET 1080
DB 1082 DPCNCNAAHSFGPSCNEFTGQCQCMPGFGGRTCSCEQLFWGDPDVECRACDCDPRGIET 1141
QY 1081 PQCDQSTGQCVCVEGVEGPRCDKCTRGYSGVFPDCTPCHQCQFALWDVIAELTNRTHKFL 1140
DB 1142 PQCDQSTGQCVCVEGVEGPRCDKCTRGYSGVFPDCTPCHQCQFALWDVIAELTNRTHKFL 1201
QY 1141 EKAKALKISGVIGPYRETVDVSEKKNVNEIKDILAQSPAABPLKNIGILFEEAEKLT KDVT 1200
DB 1202 EKAKALKISGVIGPYRETVDVSEKKNVNEIKDILAQSPAABPLKNIGILFEEAEKLT KDVT 1261
QY 1201 EKMAQVEVKLTDTASQSNSTAGELGALQABAEKSLDKTVKELAEQLEFIKNSDIQALDSI 1260
DB 1262 EMMAQVEVKLTDTASQSNSTAGELGALQABAEKSLDKTVKELAEQLEFIKNSDIQALDSI 1321
QY 1261 TKYFQMSLEAEKRVNASTDPNSTVEQSA LTRDRVEDLMLERESPFKEQEEQEARLDEL 1320
DB 1322 TKYFQMSLEAEKRVNASTDPNSTVEQSA LTRDRVEDLMLERESPFKEQEEQEARLDEL 1381
QY 1321 AGKLQSLDLSAAQMTCGTPPGADCSSECGGNCRCTDEGEKKCGGPGCGGLVTVAHSAW 1380
DB 1382 AGKLQSLDLSAAQMTCGTPPGADCSSECGGNCRCTDEGEKKCGGPGCGGLVTVAHSAW 1441
QY 1381 QKAMDFDRDVL SALAEVEQLSKMVSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDLR 1440
DB 1442 QKAMDLQDVL SALAEVEQLSKMVSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDLR 1501
QY 1441 NLIKQIRNFLTQDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVIL 1500
DB 1502 NLIKQIRNFLTQDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVIL 1561
QY 1501 QQSAADIARAE LLEAEKRAKSA TDVKVTADVMVKEALEEAEKAQVAAEKA I KQADEDIQ 1560
DB 1562 QHSAADIARAE LLEAEKRAKSA TDVKVTADVMVKEALEEAEKAQVAAEKA I KQADEDIQ 1621
QY 1561 GTQNLLTSI ESETAASEETLTNASQRI SKLERNVEELKRKAAQNSEAEYIEKVVYSVKQ 1620
DB 1622 GTQNLLTSI ESETAASEETLTNASQRI SKLERNVEELKRKAAQNSEAEYIEKVVYSVKQ 1681
QY 1621 NADDVKKTL DGE LDEKYKVESLIAQKTEESADARRKAE LLONEAKTL LAQANSKLQ LLE 1680
DB 1682 SAE DVKKTL DGE LDEKYKVESLIAQKTEESADARRKAE LLONEAKTL LAQANSKLQ LLE 1741

QY 1681 DLERKYEDNQYLEDKAQELVRLEGEVRSLLKDISEKVA VYSTCL 1725
DB 1742 DLERKYEDNQYLEDKAQELVRLEGEVRSLLKDISEKVA VYSTCL 1786
RESULT 3
MMRTS
laminin beta-2 chain precursor - rat
N;Alternate names: laminin chain B3; S-laminin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 10-Dec-1999
C;Accession: S03539
R;Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.
Nature 338, 229-234, 1989
A;Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the neuro
A;Reference number: S03539; MUID:89159410; PMID:2922051
A;Accession: S03539
A;Molecule type: mRNA
A;Residues: 1-1801 <HUN>
A;Cross-references: EMBL:X16563; NID:G57250; PIDN:CAA34561.1; PID:G57251
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C;Function:
A;Description: interact with cells and with other basement membrane proteins to promote
C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular
F;1-35/Domain: signal sequence #status predicted <SIG>
F;36-1801/Product: laminin beta-2 chain #status predicted <MAT>
F;36-285/Domain: VI <DOM6>
F;286-555/Domain: V <DOM5>
F;286-347/Domain: laminin-type EGF-like homology <LE01>
F;350-410/Domain: laminin-type EGF-like homology <LE02>
F;413-470/Domain: laminin-type EGF-like homology <LE03>
F;473-522/Domain: laminin-type EGF-like homology <LE04>
F;525-555/Domain: laminin-type EGF-like homology #status atypical <LE05>
F;556-784/Domain: IV <DOM4>
F;786-831/Domain: laminin-type EGF-like homology <LE06>
F;788-1196/Domain: III <DOM3>
F;834-877/Domain: laminin-type EGF-like homology <LE07>
F;880-927/Domain: laminin-type EGF-like homology <LE08>
F;930-986/Domain: laminin-type EGF-like homology <LE09>
F;989-1038/Domain: laminin-type EGF-like homology <LE10>
F;1041-1095/Domain: laminin-type EGF-like homology <LE11>
F;1098-1143/Domain: laminin-type EGF-like homology <LE12>
F;1146-1190/Domain: laminin-type EGF-like homology <LE13>
F;1197-1412/Domain: II <DOM2>
F;1197-1412/Region: heptad repeats
F;1413-1445/Domain: alpha <ALP>
F;1446-1801/Region: heptad repeats
F;1446-1801/Domain: I <DOM1>
F;45-50/Disulfide bonds: #status predicted
F;251,371,1088,1252,1311,1351,1502/Binding site: carbohydrate (Asn) (covalent) #status p
F;1193,1196,1800/Disulfide bonds: interchain #status predicted

Query Match 52.3%; Score 4936; DB 1; Length 1801;
Best Local Similarity 51.2%; Pred.No. 1.2e-181;
Matches 887; Conservative 297; Mismatches 530; Indels 20; Gaps 8;
QY 1 EPYCIVSHLQEDKKCFICDSRDPYHETLNPD SHLIENVTTFAPNRLKIWQSENGVENV 60
DB 77 QPYCIVSHLQDEKKCFICDSRRPFSARDNPNSHRIQNVVTSFAPQQRRTAWQSENGVPMV 136
QY 61 TIQLDLEAEFHFTHLIMTFKTRPAAMLIERSSDFGKTGWVYRYFAYDCESFPGISTGP 120
DB 137 TIQLDLEAEFHFTHLIMTFKTRPAAMLVERSADFGRTWRVYRYFSYDCGADFPGIPLAP 196
QY 121 MKKVDDIICDSRYSDIEPSTEGEVI FRALDPAFKIEDPYSPRIQNLKITNLRKFVKLH 180
DB 197 PRRWDDVVCESRYSEIEPSTEGEVIYRVLDPAIPIPDYSSRIQNLKITNLRVNLTRLH 256
QY 181 TLGDNLLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGVNVEEGVMVHGCMCR 240
DB 257 TLGDNLLDPRREIREKYYALYELVIRGNCFCYGHASQCAPAPGAPAHAEGMVHGACICK 316

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:26:08 ; Search time 9.80775 Seconds
(without alignments)
9158.169 Million cell updates/sec

Title: US-10-037-182-12
Perfect score: 9429
Sequence: 1 EPYCIVSHLQEDKKKFCIDS.....EVRSLKDISKAVAVSTCL 1725

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9429	100.0	1786	1 LMB1_MOUSE	P02469 mus musculus
2	8873	94.1	1786	1 LMB1_HUMAN	P07942 homo sapien
3	4936	52.3	1801	1 LMB2_RAT	P15800 rattus norv
4	4914	52.1	1799	1 LMB2_MOUSE	P61292 mus musculus
5	4890	51.9	1798	1 LMB2_HUMAN	P55268 homo sapien
6	3734.5	39.6	1790	1 LMB1_DROME	P11046 drosophila
7	1730	18.3	3672	1 LML2_CAEEL	Q21313 caenorhabdi
8	1682.5	17.8	1639	1 LMG1_DROME	P15215 drosophila
9	1649	17.5	3712	1 LMA_DROME	Q00174 drosophila
10	1618.5	17.2	1609	1 LMG1_HUMAN	P11047 homo sapien
11	1610.5	17.1	1607	1 LMG1_MOUSE	P02468 mus musculus
12	1608	17.1	1535	1 LML1_CAEEL	Q18823 caenorhabdi
13	1584	16.8	3718	1 LMA5_MOUSE	Q61001 mus musculus
14	1575	16.7	303	1 LMB1_CHICK	Q01635 gallus gall
15	1550	16.4	3695	1 LMA5_HUMAN	O15230 homo sapien
16	1535	16.3	3075	1 LMA1_HUMAN	P25391 homo sapien
17	1527.5	16.2	3110	1 LMA2_HUMAN	P24043 homo sapien
18	1497.5	15.9	3106	1 LMA2_MOUSE	Q60675 mus musculus
19	1484	15.7	1587	1 LMG3_HUMAN	Q9Y6N6 homo sapien
20	1482	15.7	3084	1 LMA1_MOUSE	P19137 mus musculus
21	1476.5	15.7	1581	1 LMG3_MOUSE	Q9R0B6 mus musculus
22	1438.5	15.3	1172	1 LMB3_HUMAN	Q13751 homo sapien
23	1394.5	14.8	1168	1 LMB3_MOUSE	Q61087 mus musculus
24	1330	14.1	3333	1 LMA3_MOUSE	Q61789 mus musculus
25	875	9.3	1191	1 LMG2_MOUSE	Q61092 mus musculus
26	862.5	9.1	1193	1 LMG2_HUMAN	Q13753 homo sapien
27	668.5	7.1	604	1 NET1_HUMAN	O95631 homo sapien
28	667	7.1	604	1 NET1_MOUSE	O09118 mus musculus
29	659.5	7.0	606	1 NET1_CHICK	Q90922 gallus gall
30	656	7.0	3707	1 PGBM_MOUSE	Q05793 mus musculus
31	647.5	6.9	4391	1 PGBM_HUMAN	P98160 homo sapien
32	593	6.3	581	1 NET2_CHICK	Q90923 gallus gall
33	583	6.2	612	1 UNC6_CAEEL	P34710 caenorhabdi

34	566.5	6.0	727	1 NETA_DROME	Q24567 drosophila
35	565.5	6.0	1816	1 LMA4_HUMAN	Q16363 homo sapien
36	559.5	5.9	1816	1 LMA4_MOUSE	P97927 mus musculus
37	537	5.7	2319	1 NTC3_RAT	Q9R172 rattus norv
38	532	5.6	400	1 LMB_HIRME	Q25092 hirudo medi
39	531	5.6	2524	1 NOTC_XENLA	P21783 xenopus lae
40	527	5.6	2321	1 NTC3_HUMAN	Q9UM47 homo sapien
41	511.5	5.4	2703	1 NOTC_DROME	P07207 drosophila
42	510	5.4	3375	1 UN52_CAEEL	Q06561 caenorhabdi
43	506	5.4	2318	1 NTC3_MOUSE	Q61982 mus musculus
44	497	5.3	2471	1 NTC2_RAT	Q9GW30 rattus norv
45	495.5	5.3	2556	1 NTC1_HUMAN	P46531 homo sapien

ALIGNMENTS

RESULT 1
LMB1_MOUSE
ID LMB1_MOUSE
AC P02469
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Laminin beta-1 chain precursor (Laminin B1 chain).
GN LAMB1-1 OR LAMB-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87147212; PubMed=3493487;
RA Sasaki M., Kato S., Kohno K., Martin G.R., Yamada Y.;
RT "Sequence of the cDNA encoding the laminin B1 chain reveals a
multidomain protein containing cysteine-rich repeats.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:935-939(1987).
RN [2]
RP SEQUENCE OF 1292-1786 FROM N.A.
RX MEDLINE=85051302; PubMed=6209134;
RA Barlow D.P., Green N.M., Kurkinen M., Hogan B.L.M.;
RT "Sequencing of laminin B chain cDNAs reveals C-terminal regions of
coiled-coil alpha-helix.";
RL EMBO J. 3:2355-2362(1984).
RN [3]
RP SEQUENCE OF 165-172; 539-547 AND 712-719.
RC STRAIN=BALB/c; TISSUE=Endothelial cells;
RX MEDLINE=97363207; PubMed=9219532;
RA Frieser M., Noeckel H., Pausch F., Roeder C., Hahn A., Deutzmann R.,
Sorokin L.M.;
RT "Cloning of the mouse laminin alpha 4 cDNA. Expression in a subset of
endothelium.";
RL Eur. J. Biochem. 246:727-735(1997).
CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
is thought to mediate the attachment, migration and organization
of cells into tissues during embryonic development by interacting
with other extracellular matrix components.
CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
different polypeptide chains (alpha, beta, gamma), which are bound
to each other by disulfide bonds into a cross-shaped molecule
comprising one long and three short arms with globules at each
end. The beta-1 chain is a subunit of laminin-1 (BHS laminin),
laminin-2 (merosin), and laminin-6 (K-laminin).
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Found in the basement membranes (major
component).
CC -!- SIMILARITY: Contains 1 laminin N-terminal domain.
CC -!- SIMILARITY: Contains 13 laminin EGF-like domains.
CC -!- SIMILARITY: Contains 1 laminin IV domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; M15525; AAA39407.1; ALT_INIT.
DR EMBL; X05212; CAA28839.1; --
DR PIR; A26413; MMSB1.
DR HSSP; P02468; 1KLO.
DR MGD; MGI:96743; Lamb1-1.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR008211; LamNT.
DR Pfam; PF00053; laminin_EGF; 13.
DR Pfam; PF00055; laminin_Nterm; 1.
DR PRINTS; PR00011; EGFLAMININ.
DR SMART; SM00180; EGF Lam; 11.
DR SMART; SM00136; LamNT; 1.
DR PROSITE; PS00022; EGF_1; 9.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 11.
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
FT SIGNAL 1 21
FT CHAIN 22 1786
FT DOMAIN 22 270 LAMININ BETA-1 CHAIN.
FT DOMAIN 271 334 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 335 397 LAMININ EGF-LIKE 1.
FT DOMAIN 398 457 LAMININ EGF-LIKE 2.
FT DOMAIN 458 509 LAMININ EGF-LIKE 3.
FT DOMAIN 510 540 LAMININ EGF-LIKE 4.
FT DOMAIN 541 772 LAMININ EGF-LIKE 5 (INCOMPLETE).
FT DOMAIN 773 820 LAMININ DOMAIN IV.
FT DOMAIN 821 866 LAMININ EGF-LIKE 6.
FT DOMAIN 867 916 LAMININ EGF-LIKE 7.
FT DOMAIN 917 975 LAMININ EGF-LIKE 8.
FT DOMAIN 976 1027 LAMININ EGF-LIKE 9.
FT DOMAIN 1028 1083 LAMININ EGF-LIKE 10.
FT DOMAIN 1084 1131 LAMININ EGF-LIKE 11.
FT DOMAIN 1132 1178 LAMININ EGF-LIKE 12.
FT DOMAIN 1179 1397 LAMININ EGF-LIKE 13.
FT DOMAIN 1398 1430 DOMAIN II.
FT DOMAIN 1431 1786 DOMAIN ALPHA.
FT DOMAIN 1787 1835 COILED COIL (POTENTIAL).
FT DOMAIN 1836 1888 COILED COIL (POTENTIAL).
FT DOMAIN 1889 1948 COILED COIL (POTENTIAL).
FT DISULFID 271 280 BY SIMILARITY.
FT DISULFID 273 298 BY SIMILARITY.
FT DISULFID 300 309 BY SIMILARITY.
FT DISULFID 312 332 BY SIMILARITY.
FT DISULFID 335 344 BY SIMILARITY.
FT DISULFID 337 362 BY SIMILARITY.
FT DISULFID 365 374 BY SIMILARITY.
FT DISULFID 377 395 BY SIMILARITY.
FT DISULFID 398 411 BY SIMILARITY.
FT DISULFID 400 426 BY SIMILARITY.
FT DISULFID 428 437 BY SIMILARITY.
FT DISULFID 440 455 BY SIMILARITY.
FT DISULFID 458 472 BY SIMILARITY.
FT DISULFID 460 479 BY SIMILARITY.
FT DISULFID 481 490 BY SIMILARITY.
FT DISULFID 493 507 BY SIMILARITY.
FT DISULFID 509 575 BY SIMILARITY.
FT DISULFID 577 792 BY SIMILARITY.
FT DISULFID 794 803 BY SIMILARITY.
FT DISULFID 806 818 BY SIMILARITY.
FT DISULFID 821 833 BY SIMILARITY.
FT DISULFID 833 840 BY SIMILARITY.
FT DISULFID 842 851 BY SIMILARITY.
FT DISULFID 854 864 BY SIMILARITY.
FT DISULFID 867 876 BY SIMILARITY.
FT DISULFID 869 883 BY SIMILARITY.
FT DISULFID 886 895 BY SIMILARITY.

FT DISULFID 898 914 BY SIMILARITY.
FT DISULFID 917 933 BY SIMILARITY.
FT DISULFID 919 944 BY SIMILARITY.
FT DISULFID 946 955 BY SIMILARITY.
FT DISULFID 958 973 BY SIMILARITY.
FT DISULFID 976 990 BY SIMILARITY.
FT DISULFID 1000 997 BY SIMILARITY.
FT DISULFID 1012 1009 BY SIMILARITY.
FT DISULFID 1084 1025 BY SIMILARITY.
FT DISULFID 1086 1096 BY SIMILARITY.
FT DISULFID 1105 1103 BY SIMILARITY.
FT DISULFID 1117 1114 BY SIMILARITY.
FT DISULFID 1132 1129 BY SIMILARITY.
FT DISULFID 1134 1144 BY SIMILARITY.
FT DISULFID 1153 1151 BY SIMILARITY.
FT DISULFID 1165 1162 BY SIMILARITY.
FT DISULFID 1179 1176 BY SIMILARITY.
FT DISULFID 1182 1179 INTERCHAIN (PROBABLE).
FT DISULFID 1185 1182 INTERCHAIN (PROBABLE).
FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 519 519 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 677 677 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1041 1041 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1195 1195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1279 1279 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1336 1336 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1343 1343 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1487 1487 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1533 1533 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1542 1542 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1643 1643 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 1531 1534 SGNA -> MEMP (IN REF. 2).
FT CONFLICT 1749 1749 D -> N (IN REF. 2).
SQ SEQUENCE 1786 AA; 196904 MW; 846671B7BF41A474 CRC64;

Query Match 100.0%; Score 9429; DB 1; Length 1786;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPYCIVSHLQEDKCFICDSRDPYHETLNPDSHLIENVVTTFAFNRLKIWWQSENGVENV 60
DB 62 EPYCIVSHLQEDKCFICDSRDPYHETLNPDSHLIENVVTTFAFNRLKIWWQSENGVENV 121
QY 61 TIQLDLEAEFFHFTLIMTKTFRPAAMLIERSSDFGKTGWVRYRYPAYDCESSFPGISTGP 120
DB 122 TIQLDLEAEFFHFTLIMTKTFRPAAMLIERSSDFGKTGWVRYRYPAYDCESSFPGISTGP 181
QY 121 MKKVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPRIQNLKITNLRIKFVKLH 180
DB 182 MKKVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPRIQNLKITNLRIKFVKLH 241
QY 181 TLGDNLLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGVNBEVEGMVHGHCMCR 240
DB 242 TLGDNLLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGVNBEVEGMVHGHCMCR 301
QY 241 HNTKGLNCELMDFYHDLPLWRPAEGRNSNACKKCNKNEHSSSCHFDMAVFLATGNVSGGV 300
DB 302 HNTKGLNCELMDFYHDLPLWRPAEGRNSNACKKCNKNEHSSSCHFDMAVFLATGNVSGGV 361
QY 301 CDNCQHTMGRNCEQCKPFYFQHPERDIRDNLCEPCTCDPAGSENGGICDGYTDFSVGL 360
DB 362 CDNCQHTMGRNCEQCKPFYFQHPERDIRDNLCEPCTCDPAGSENGGICDGYTDFSVGL 421
QY 361 IAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGGNPDSETGYCYC 420
DB 422 IAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGGNPDSETGYCYC 481
QY 421 KRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCDLGGALNNSCSEDSGQCSCLPHMIGRQCN 480
DB 482 KRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCDLGGALNNSCSEDSGQCSCLPHMIGRQCN 541

or send an email to license@isb-sib.ch).

CC
CC
DR EMBL; M61951; AAA59486.1; --
DR EMBL; M58147; AAA59486.1; JOINED.
DR EMBL; M61917; AAA59486.1; JOINED.
DR EMBL; M61918; AAA59486.1; JOINED.
DR EMBL; M61921; AAA59486.1; JOINED.
DR EMBL; M61922; AAA59486.1; JOINED.
DR EMBL; M61923; AAA59486.1; JOINED.
DR EMBL; M61924; AAA59486.1; JOINED.
DR EMBL; M61925; AAA59486.1; JOINED.
DR EMBL; M61926; AAA59486.1; JOINED.
DR EMBL; M61927; AAA59486.1; JOINED.
DR EMBL; M61928; AAA59486.1; JOINED.
DR EMBL; M61929; AAA59486.1; JOINED.
DR EMBL; M61930; AAA59486.1; JOINED.
DR EMBL; M61931; AAA59486.1; JOINED.
DR EMBL; M61932; AAA59486.1; JOINED.
DR EMBL; M61933; AAA59486.1; JOINED.
DR EMBL; M61934; AAA59486.1; JOINED.
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DR EMBL; M61941; AAA59486.1; JOINED.
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DR EMBL; M61943; AAA59486.1; JOINED.
DR EMBL; M61944; AAA59486.1; JOINED.
DR EMBL; M61945; AAA59486.1; JOINED.
DR EMBL; M61946; AAA59486.1; JOINED.
DR EMBL; M61947; AAA59486.1; JOINED.
DR EMBL; M61948; AAA59486.1; JOINED.
DR EMBL; M61949; AAA59486.1; JOINED.
DR EMBL; M61950; AAA59486.1; JOINED.
DR EMBL; M55370; AAA59485.1; --
DR EMBL; M55378; AAA59485.1; JOINED.
DR EMBL; M55365; AAA59485.1; JOINED.
DR EMBL; M55371; AAA59485.1; JOINED.
DR EMBL; M55372; AAA59485.1; JOINED.
DR EMBL; M55373; AAA59485.1; JOINED.
DR EMBL; M55374; AAA59485.1; JOINED.
DR EMBL; M55375; AAA59485.1; JOINED.
DR EMBL; M55376; AAA59485.1; JOINED.
DR EMBL; M55344; AAA59485.1; JOINED.
DR EMBL; M55345; AAA59485.1; JOINED.
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DR EMBL; M55347; AAA59485.1; JOINED.
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DR EMBL; M55352; AAA59485.1; JOINED.
DR EMBL; M55353; AAA59485.1; JOINED.
DR EMBL; M55355; AAA59485.1; JOINED.
DR EMBL; M55356; AAA59485.1; JOINED.
DR EMBL; M55357; AAA59485.1; JOINED.
DR EMBL; M55358; AAA59485.1; JOINED.
DR EMBL; M55359; AAA59485.1; JOINED.
DR EMBL; M55360; AAA59485.1; JOINED.
DR EMBL; M55361; AAA59485.1; JOINED.
DR EMBL; M55362; AAA59485.1; JOINED.
DR EMBL; M55363; AAA59485.1; JOINED.
DR EMBL; M55364; AAA59485.1; JOINED.
DR EMBL; M55366; AAA59485.1; JOINED.
DR EMBL; M55367; AAA59485.1; JOINED.
DR EMBL; M55368; AAA59485.1; JOINED.
DR EMBL; M55369; AAA59485.1; JOINED.
DR EMBL; M61916; AAA59482.1; --
DR EMBL; M20206; AAA59487.1; --
DR PIR; S13547; MMHUB1.
DR HSSP; P02468; 1KLO.
DR Genew; HGNC:6486; LAMB1.

DR MIM; 150240; --
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR008211; LamNT.
DR Pfam; PF00053; laminin_EGF; 13.
DR Pfam; PF00055; laminin_Nterm; 1.
DR PRINTS; PR00011; EGFLAMININ.
DR SMART; SM00180; EGF_Lam; 12.
DR SMART; SM00136; LamNT; 1.
DR PROSITE; PS00022; EGF_1; 9.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 11.
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal; Polymorphism.
FT SIGNAL 1 21
FT CHAIN 22 1786 LAMININ BETA-1 CHAIN.
FT DOMAIN 22 270 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 271 334 LAMININ EGF-LIKE 1.
FT DOMAIN 335 397 LAMININ EGF-LIKE 2.
FT DOMAIN 398 457 LAMININ EGF-LIKE 3.
FT DOMAIN 458 509 LAMININ EGF-LIKE 4.
FT DOMAIN 510 540 LAMININ EGF-LIKE 5 (INCOMPLETE).
FT DOMAIN 541 771 LAMININ DOMAIN IV.
FT DOMAIN 773 820 LAMININ EGF-LIKE 6.
FT DOMAIN 821 866 LAMININ EGF-LIKE 7.
FT DOMAIN 867 916 LAMININ EGF-LIKE 8.
FT DOMAIN 917 975 LAMININ EGF-LIKE 9.
FT DOMAIN 976 1027 LAMININ EGF-LIKE 10.
FT DOMAIN 1028 1083 LAMININ EGF-LIKE 11.
FT DOMAIN 1084 1131 LAMININ EGF-LIKE 12.
FT DOMAIN 1132 1178 LAMININ EGF-LIKE 13.
FT DOMAIN 1179 1397 DOMAIN II.
FT DOMAIN 1398 1430 DOMAIN ALPHA.
FT DOMAIN 1431 1786 DOMAIN I.
FT DOMAIN 1216 1315 COILED COIL (POTENTIAL).
FT DOMAIN 1353 1388 COILED COIL (POTENTIAL).
FT DOMAIN 1442 1781 COILED COIL (POTENTIAL).
FT DISULFID 271 280 BY SIMILARITY.
FT DISULFID 273 298 BY SIMILARITY.
FT DISULFID 300 309 BY SIMILARITY.
FT DISULFID 312 332 BY SIMILARITY.
FT DISULFID 335 344 BY SIMILARITY.
FT DISULFID 337 362 BY SIMILARITY.
FT DISULFID 365 374 BY SIMILARITY.
FT DISULFID 377 395 BY SIMILARITY.
FT DISULFID 398 411 BY SIMILARITY.
FT DISULFID 400 426 BY SIMILARITY.
FT DISULFID 428 437 BY SIMILARITY.
FT DISULFID 440 455 BY SIMILARITY.
FT DISULFID 458 472 BY SIMILARITY.
FT DISULFID 460 479 BY SIMILARITY.
FT DISULFID 481 490 BY SIMILARITY.
FT DISULFID 493 507 BY SIMILARITY.
FT DISULFID 773 785 BY SIMILARITY.
FT DISULFID 775 792 BY SIMILARITY.
FT DISULFID 794 803 BY SIMILARITY.
FT DISULFID 806 818 BY SIMILARITY.
FT DISULFID 821 833 BY SIMILARITY.
FT DISULFID 823 840 BY SIMILARITY.
FT DISULFID 842 851 BY SIMILARITY.
FT DISULFID 854 864 BY SIMILARITY.
FT DISULFID 867 876 BY SIMILARITY.
FT DISULFID 869 883 BY SIMILARITY.
FT DISULFID 886 895 BY SIMILARITY.
FT DISULFID 898 914 BY SIMILARITY.
FT DISULFID 917 933 BY SIMILARITY.
FT DISULFID 919 944 BY SIMILARITY.
FT DISULFID 946 955 BY SIMILARITY.

Query Match 94.1%; Score 8873; DB 1; Length 1786;
Best Local Similarity 92.9%; Pred. No. 0;
Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

QY 1 EPYCIIVSHLOEDKCKFCIDSRDPYHETLNPDSHLIENVVTTFAFNRLKIWWQSENGVENV 60
Db 62 EPYCIIVSHLOEDKCKFCICNSQDPYHETLNPDSHLIENVVTTFAFNRLKIWWQSENGVENV 121
QY 61 TIOLDLEAEHFHTHLIMTKFTRPAAMLIERSDDFGKTGWVYRFAYDCESFPFGISTGP 120
Db 122 TIOLDLEAEHFHTHLIMTKFTRPAAMLIERSDDFGKTGWVYRFAYDCESFPFGISTGP 181
QY 121 MKKVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPIQNLLKITNLRIFKFKLH 180
Db 182 MKKVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPIQNLLKITNLRIFKFKLH 241
QY 181 TLGDNLLDSRMEIREKYYYAYVDMVRGNCFCYGHASECAPVDGVNEEVEGMVHGHCRCR 240
Db 242 TLGDNLLDSRMEIREKYYYAYVDMVRGNCFCYGHASECAPVDGVNEEVEGMVHGHCRCR 301
QY 241 HNTKGLNCELMDPYHDLPRPAPAEGRNSNACKKCNKNEHSSSCHDFDPAVFLATGNVSGV 300
Db 302 HNTKGLNCELMDPYHDLPRPAPAEGRNSNACKKCNKNEHSISCHDFDPAVFLATGNVSGV 361
QY 301 CDNCQHNTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 360
Db 362 CDNCQHNTMGRNCEQCKPFYFQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTGL 421
QY 361 IAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGPNPCDSETGYCYC 420
Db 422 IAGQCRCKLHVEGEHCDVCKEGFYDLSSEDYFGCKSCACNPLGTIPGPNPCDSETGHYCYC 481
QY 421 KRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCLGGALNNSCSDSGQCSCLPHMIGROCN 480
Db 482 KRLVTGQHCDQCLPEHWGLSNDLDGCRPCDCLGGALNNSCFABSGQCSCRPHMIGROCN 541
QY 481 EVESGYFTTLDHYIYEAEANLGPVGVVERQYIQDRIPSWTGPFGFVRVPEGAYLEFFI 540
Db 542 EVEPGYYFATLDHYLYEAEANLGPVGSIVERQYIQDRIPSWTGAFFVRVPEGAYLEFFI 601
QY 541 DNIPYSMEYEILIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTPVDDDNQVVSLSPGS 600
Db 602 DNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPSTSSRCGNTPVDDDNQVVSLSPGS 661
QY 601 RYVVLPRPVCPEKGMNYYTVRLELPQYTAGSDVESPYYTFIDSLVMPYCKSLDIFTVGGS 660
Db 662 RYVVLPRPVCPEKGTNYTVRLELPQYTSDDSDVESPYTLIDSLVMPYCKSLDIFTVGGS 721
QY 661 GDGEVTNSAWETPQRYRCLENSRSVVKTPMTDVCRNIIIFSALIHQTLGACECDPQGS 720
Db 722 GDGVVTNSAWETPQRYRCLENSRSVVKTPMTDVCRNIIIFSALLHQTGLACECDPQGS 781
QY 721 SSVCDPNGGQCCOCPNWWGRTCNRCAPGTFFGPGNCKPCDCHLQGSASAFCDAITGOCH 780
Db 782 SSVCDPNGGQCCOCPNWWGRTCNRCAPGTFFGPGNCKPCDCHLQGSVAFNCPVPTGOCH 841
QY 781 CFQGIYARQCDRCLPGYWGFPSCQPCQCNCHALDCTVTGECILSCQDYTTGHNRCERCLAG 840
Db 842 CFQGVYARQCDRCLPGHWGFPSCQPCQCNCHADDCDPTVTECLNCQDYTMGHNRCERCLAG 901
QY 841 YYGDPPIIGSGDHCRPCPCPDGPDGSRQFARSCYQDPVTLQACVCDPBGYIGSRCDDCAGS 900
Db 902 YYGDPPIIGSGDHCRPCPCPDGPDGSRQFARSCYQDPVTLQACVCDPBGYIGSRCDDCAGS 961
QY 901 FFGNPSDFGSGCQPCQCHNIDTTDPEACDKDTGRCLKCLYHTEGDHCOLCQYGYGDAL 960
Db 962 YFGNPSDFGSGCQPCQCHNIDTTDPEACDKDTGRCLKCLYHTEGDHCOLCQYGYGDAL 1021
QY 961 RQDCRKVCVNYLGTVKEHCNGSDCHCDKATGQCSCLPNVIGQNCDRCAPNTWQLASGTGC 1020
Db 1022 RQDCRKVCVNYLGTVQEHCHNGSDCQCDKATGQCCLCLPNVIGQNCDRCAPNTWQLASGTGC 1081
QY 1021 GPCNCNAHSGFSPSCNEFTGQCQCMFPGGRTCTSECELFWGDVDDVECRACDCDPRGIET 1080
Db 1082 DPCNCNAHSGFSPSCNEFTGQCQCMFPGGRTCTSECELFWGDVDDVECRACDCDPRGIET 1141
QY 1081 PQCDQSTGQCVCVEGVEGPRCDKCTRGYSGVFPDCTPCHQCFAWDIAIIGELTNRTHKFL 1140

Db 1142 PQCDQSTGQCVCVEGVEGPRCDKCTRGYSGVFPDCTPCHQCFAWDIAIIGELTNRTHKFL 1201
QY 1141 EKAKALKISGVIGPYRETVDSEKKNVEIKDILAQSPAAEPLKNIGILFEEAEKLTKDVT 1200
Db 1202 EKAKALKISGVIGPYRETVDSEKKNVEIKDILAQSPAAEPLKNIGILFEEAEKLTKDVT 1261
QY 1201 EKMAQVEVKLTDTASQSNSTAGELGALQABAEASLDKTVKELAEQLEFIKNSDIOGALDSI 1260
Db 1262 EMMAQVEVKLSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSI 1321
QY 1261 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLERESPFKEQOEQARLLDEL 1320
Db 1322 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLERESPFKEQOEQARLLDEL 1381
QY 1321 AGKLQSLDLSAAQMTCTGTPPGADCESECGGPNCRCTDEGEKKCGGCGGLVTVAHSAW 1380
Db 1382 AGKLQSLDLSAAQMTCTGTPPGASCSCTECCGPNCRCTDEGERKCGGCGGLVTVAHNAW 1441
QY 1381 QKAMDFDRDVLALAEVEQSLKMSVSEAKVRADEAKQNAQDVLTKTNATKEKVDKSNEDLR 1440
Db 1442 QKAMDLDDQVLSALAEVEQSLKMSVSEAKVRADEAKQNAQDVLTKTNATKEKVDKSNEDLR 1501
QY 1441 NLIKQIRNFLTSDSADLDSIEAVANEVLKSGNASTPQQLQNLTERIRERVETLSQVEVIL 1500
Db 1502 NLIKQIRNFLTSDSADLDSIEAVANEVLKSGNASTPQQLQNLTERIRERVETLSQVEVIL 1561
QY 1501 QQSAADIAAEELLLEAEKRAKSKSATDVKTADVMVKEALEEAEKAAKQADEDIQ 1560
Db 1562 QHSAADIAAEMLLEAEKRAKSKSATDVKTADVMVKEALEEAEKAAKQADEDIQ 1621
QY 1561 GTQNLTSIESETAASEETLTNASQRIKSLERNVEELKRKAQNSGEAEYIEKVVSVKQ 1620
Db 1622 GTQNLTSIESETAASEETLTNASQRIKSLERNVEELKRKAQNSGEAEYIEKVVSVKQ 1681
QY 1621 NADDVKTLDGELDEKYYKVESLIAQKTESADARRKAELLQNEAKTLLAQANSKLQLE 1680
Db 1682 SAEDVKTLDGELDEKYYKVENLIAKTESADARRKAEMLQNEAKTLLAQANSKLQLE 1741
QY 1681 DLERKYEDNQYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1725
Db 1742 DLERKYEDNQYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1786

RESULT 3

LMB2_RAT

ID LMB2_RAT STANDARD; PRT; 1801 AA.
AC P15800;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Laminin beta-2 chain precursor (S-laminin) (Laminin chain B3).
GN LAMB2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89159410; PubMed=2922051;
RA Hunter D.D., Shah V., Merlie J.P., Sanes J.R.;
RT "A laminin-like adhesive protein concentrated in the synaptic cleft of the neuromuscular junction."
RL Nature 338:229-234(1989).
CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin is thought to mediate the attachment, migration and organization of cells into tissues during embryonic development by interacting with other extracellular matrix components.
CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three different polypeptide chains (alpha, beta, gamma), which are bound to each other by disulfide bonds into a cross-shaped molecule comprising one long and three short arms with globules at each

FT	DISULFID	475	494	BY SIMILARITY.
FT	DISULFID	496	505	BY SIMILARITY.
FT	DISULFID	508	522	BY SIMILARITY.
FT	DISULFID	786	798	BY SIMILARITY.
FT	DISULFID	788	805	BY SIMILARITY.
FT	DISULFID	807	816	BY SIMILARITY.
FT	DISULFID	819	831	BY SIMILARITY.
FT	DISULFID	834	846	BY SIMILARITY.
FT	DISULFID	836	853	BY SIMILARITY.
FT	DISULFID	855	864	BY SIMILARITY.
FT	DISULFID	867	877	BY SIMILARITY.
FT	DISULFID	880	889	BY SIMILARITY.
FT	DISULFID	882	896	BY SIMILARITY.
FT	DISULFID	899	908	BY SIMILARITY.
FT	DISULFID	911	927	BY SIMILARITY.
FT	DISULFID	930	946	BY SIMILARITY.
FT	DISULFID	932	957	BY SIMILARITY.
FT	DISULFID	959	968	BY SIMILARITY.
FT	DISULFID	971	986	BY SIMILARITY.
FT	DISULFID	989	1003	BY SIMILARITY.
FT	DISULFID	991	1010	BY SIMILARITY.
FT	DISULFID	1013	1022	BY SIMILARITY.
FT	DISULFID	1025	1038	BY SIMILARITY.
FT	DISULFID	1098	1110	BY SIMILARITY.
FT	DISULFID	1100	1117	BY SIMILARITY.
FT	DISULFID	1119	1128	BY SIMILARITY.
FT	DISULFID	1131	1143	BY SIMILARITY.
FT	DISULFID	1146	1158	BY SIMILARITY.
FT	DISULFID	1148	1165	BY SIMILARITY.
FT	DISULFID	1167	1176	BY SIMILARITY.
FT	DISULFID	1179	1190	BY SIMILARITY.
FT	DISULFID	1193	1193	INTERCHAIN (PROBABLE).
FT	DISULFID	1196	1196	INTERCHAIN (PROBABLE).
FT	DISULFID	1800	1800	INTERCHAIN (PROBABLE).
FT	CARBOHYD	251	251	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	371	371	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1088	1088	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1252	1252	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1311	1311	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1351	1351	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1502	1502	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	1801	AA; 196473 MW; 97AEF32F8F31FA75 CRC64;	

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:28 ; Search time 46.7946 Seconds
(without alignments)
11631.021 Million cell updates/sec

Title: US-10-037-182-12
Perfect score: 9429
Sequence: 1 EPGYCVSHLQEDKKCFICDS.....EVRSLDKISEKVAVYSTCL 1725

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	6600	70.0	1785	13 Q8JHV7	Q8jlv7 brachydanio
2	5434	57.6	1086	4 Q8TAS6	Q8tas6 homo sapien
3	5195	55.1	984	11 Q8K271	Q8k271 mus musculu
4	5162	54.7	1792	13 Q57484	Q57484 gallus gall
5	4934	52.3	1799	11 Q8R0Y0	Q8r0y0 mus musculu
6	4790	50.8	911	11 Q9CRX6	Q9crx6 mus musculu
7	3712.5	39.4	1761	4 Q86XN2	Q86xn2 homo sapien
8	3631.5	38.5	1827	13 Q8JHV6	Q8jlv6 brachydanio
9	3506.5	37.2	1631	4 Q9Y6U6	Q9y6u6 homo sapien
10	2741	29.1	1067	5 Q44565	Q44565 caenorhabdi
11	2271.5	24.1	1168	5 Q967S8	Q967s8 schistocerc
12	1936	20.5	1026	5 Q8SWY0	Q8swy0 drosophila
13	1914	20.3	761	4 Q9UHI2	Q9uhi2 homo sapien
14	1832	19.4	1069	5 Q9BPS2	Q9bps2 bombyx mori
15	1730	18.3	3704	5 P91904	P91904 caenorhabdi
16	1645	17.4	3712	5 Q9VRW0	Q9vrw0 drosophila

17	1623	17.2	1593	13 Q8JHV8	Q8jlv8 brachydanio
18	1615	17.1	1623	5 Q9U3U7	Q9u3u7 anopheles g
19	1558	16.5	3695	4 Q8TDF8	Q8tdf8 homo sapien
20	1402.5	14.9	1168	11 Q91V90	Q91v90 mus musculu
21	1342	14.2	1007	13 Q90ZN3	Q90zn3 gallus gall
22	1276.5	13.5	3102	5 Q45614	Q45614 caenorhabdi
23	1206.5	12.8	2731	5 Q9VJT5	Q9vjt5 drosophila
24	1206.5	12.8	3367	5 Q9XZC9	Q9xzc9 drosophila
25	1206.5	12.8	3375	5 Q8IP51	Q8ip51 drosophila
26	1101	11.7	1546	4 Q9NS27	Q9ns27 homo sapien
27	1099	11.7	1546	4 Q75445	Q75445 homo sapien
28	1064	11.3	1486	4 Q14637	Q14637 homo sapien
29	1041	11.0	1461	11 Q9JLP3	Q9jlp3 mus musculu
30	1032	10.9	750	4 Q86TP7	Q86tp7 homo sapien
31	978.5	10.4	616	4 Q15483	Q15483 homo sapien
32	964	10.2	1512	11 Q8K3K1	Q8k3k1 rattus norv
33	932	9.9	628	11 Q9JI33	Q9ji33 mus musculu
34	925	9.8	628	4 Q9HB63	Q9hb63 homo sapien
35	925	9.8	628	4 Q9BZP1	Q9bzip1 homo sapien
36	910	9.7	605	4 Q7Z5B6	Q7z5b6 homo sapien
37	875.5	9.3	1190	6 Q8HZI9	Q8hzi9 equus cabal
38	872.5	9.3	1196	6 Q867A2	Q867a2 canis famil
39	683.5	7.2	1664	5 Q9TVO2	Q9tvq2 caenorhabdi
40	680	7.2	1574	11 Q88281	Q88281 rattus norv
41	666	7.1	604	11 Q924Z9	Q924z9 rattus norv
42	664	7.0	1140	4 Q96KG7	Q96kg7 homo sapien
43	663.5	7.0	529	4 Q8N2D6	Q8n2d6 homo sapien
44	661.5	7.0	1045	5 Q8T3A6	Q8t3a6 caenorhabdi
45	661.5	7.0	1070	5 Q8T3A7	Q8t3a7 caenorhabdi

ALIGNMENTS

RESULT 1

Q8JHV7	Q8JHV7	PRELIMINARY;	PRT;	1785 AA.
AC	Q8JHV7;			
DT	01-OCT-2002 (Tremblrel. 22, Created)			
DT	01-OCT-2002 (Tremblrel. 22, Last sequence update)			
DT	01-JUN-2003 (Tremblrel. 24, Last annotation update)			
DE	Laminin beta 1.			
GN	LAMBI.			
OS	Brachydanio rerio (Zebrafish) (Danio rerio).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;			
OC	Cyprinidae; Danio.			
OX	NCBI_TaxID=7955;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22065263; PubMed=12070089;			
RA	Parsons M.J., Pollard S.M., Saude L., Feldman B., Coutinho P.,			
RA	Hirst E.M., Stemple D.L.;			
RT	"Zebrafish mutants identify an essential role for laminins in			
RT	notochord formation."			
RL	Development 129:3137-3146(2002).			
DR	EMBL; AF468049; AAM61767.1; -			
DR	GO; GO:0005578; C:extracellular matrix; IEA.			
DR	GO; GO:0005198; F:structural molecule activity; IEA.			
DR	InterPro; IPR006209; EGF like.			
DR	InterPro; IPR002049; Laminin_EGF.			
DR	InterPro; IPR008211; LamNT.			
DR	Pfam; PF00053; laminin_EGF; 13.			
DR	Pfam; PF00055; laminin_Nterm; 1.			
DR	PRINTS; PR00011; EGFLAMININ.			
DR	SMART; SM00180; EGF_Lam; 13.			
DR	SMART; SM00136; LamNT; 1.			
DR	PROSITE; PS00022; EGF_1; 10.			
DR	PROSITE; PS01186; EGF_2; 2.			
DR	PROSITE; PS01248; LAMININ_TYPE_EGF; 12.			
KW	Laminin EGF-like domain.			
SQ	SEQUENCE 1785 AA; 197279 MW; 1BD338A0B6AB9F26 CRC64;			

Query Match		70.0%;	Score 6600;	DB 13;	Length 1785;
Best Local Similarity		67.2%;	Pred. No. 1.9e-282;		
Matches 1162;		Conservative 242;	Mismatches 319;	Indels 6;	Gaps 6;
Qy	1	EPYCIIVSHLQEDKFCIDSRDPYHETLNP--DSHLIENVVTTTFAPNRLKIWQSENGVEN	59		
Db	58	EPFCIVSHLQEEKKCFVCDSRQAYNETAHQVTSIENVVTTTFAPNRLKTTWQSENGLEN	117		
Qy	60	VTIQLDLEAEFHFTHLIMTFKTRPAAMLIERSDDFGKTGWVRYPAYDCESFPFGISTG	119		
Db	118	VTIQLDLEAEFHFTHLIMTFKTRPAAMVIERADFGNTQVRYPAYDCESFPFSVSHG	177		
Qy	120	PMKKVDDIIICDSRYSDIEPSTEGEVIFRALDPFAFKIEDPYSPIQNLLKITNLRKFVKL	179		
Db	178	PMTKVDDVICDTRYSDIEPSTEGEVIFRVLDPAFRIEDPYSPIQNMLKITNLRVKFTKL	237		
Qy	180	HTLGDNLLDSRMEIREKYYAYVYDMVVRGNCFYGHASECAPVDGVNBEVEGMVHGCMC	239		
Db	238	HTLGDNLLDSRIEIKKYYAYIYDMVVRGNCFYGHASECAPVDGTGEAVEGMVHGCMC	297		
Qy	240	RHNTKGLNCELMDFYHDLWPRPAEGRNSNACKKCNKNEHSSSCHFDMAVFLATGNVSGG	299		
Db	298	NHNTIGLNCERCQDFYHDLWPRPAEGRNTNACKKCHCNHSHSCHFDMAVYRASGNVSGG	357		
Qy	300	VCDNCQHTMTGRNCEOCKPFYFQHPERDIRDNLCEPCTCDPAGSENGGICDGYTDFSVG	359		
Db	358	VCDNCQHTMTGNCEOCKPFYFQHPKDIRDNPICPCNDPVGSLNGVCDDPMTDVSIG	417		
Qy	360	LIAGQCRCKLHVEGERCDVCKEGFYDLSEAEDPYGCKSCACNPLGTIPGGNPCDSETGYCY	419		
Db	418	LISGQCRCKPNVEGERCDQCKQGHYGLS-EDPLGCPQCTCNALGTVPGGSPCDTDSGNCY	476		
Qy	420	CKRLVTGORCDQCLPQHGLSNDLDGCRPCDCDLDGALNNSCEDSDGQCSCLPHMIGRQC	479		
Db	477	CKRLVTGRNCDQCLPQHGLSNDMDGCRPCDCDHGGAINNCSPVSGCQCQREHMFGRRC	536		
Qy	480	NEVESGYFTTLDHYIYEABEANLPGVVVVERQYIQDRIPSWTGPVVRPEGAYLEFF	539		
Db	537	DQVESGYFIALDHYIYEABEAKFGPGVTVPNRNHPQDRSPTWTGIGFVNVPEGAFLFS	596		
Qy	540	IDNIPYSMEYEILIRYEPQLPDHWEKAVITVQRPCKIPASSRCGNVTDPDDNQVVSLSPG	599		
Db	597	IDNIPYSMEYDLIIRYEPQLPEQWEEVMTVIRPRVITADSRCANTPDDNQMVSLHPG	656		
Qy	600	SRYVVLPRPVCFEKGMNVTVRLELPQYTAGSDVESPYTFIDSLVLPYCKSLDIFTVGG	659		
Db	657	SRYVVLPRPVCFEGLNYTVRLSLYSAL-SDVQSPYTLIDSIVLMPHCKNLDIFS	715		
Qy	660	SGDGE-VTNSAWETFORYRCLENSRSVVXTMTDTCVCRNIIFSISALIHQTGLACECDPQG	718		
Db	716	TEGGNLVTNSAWENFORYRCLENSQAVVXTMTDTCVCRNIIFSVSALLHQGVKACQCDPQG	775		
Qy	719	SLSSVCDPNGGQCCQCRPNVVGRTCNRCAPGTGFGPNGCKPCDCHLQGSASAFCAITGQ	778		
Db	776	SLSTVCDPSGGQCCQCRPNVVGRTCNRCAPATFLFXPQGCRPCDCSPESVHSYCHEATGQ	835		
Qy	779	CHCFQGIYARQCRCPLPGYWGFPSPCQPCQCNHGLDCTVTGECCLSCODYTTGHNCCERCL	838		
Db	836	CECTAGAYGRQCRCPLPGYWGFPNCRPCTCNHGAHQCDPQTGQCLSCRDHHTGHNCCERCL	895		
Qy	839	AGYYGDPPIIGSGDHCRCPCPDGPDSDGRQFARSCYQDPVTLQLACVCDPGYIGSRCDDCA	898		
Db	896	GGYGDPPVLGSGDHCRCPCPDGPGSGRQFSGACYSKSPDSSQVFCVNCQYKRGARCECA	955		
Qy	899	SGFFGNPSDFGGSCQPCQCHHNIDTTDPEACDKDTGRCLKCLYHTEGHDHCLCQYGYGD	958		
Db	956	PGYGNPHEVGEGRPCQCNIDMDMPESCDARTGACVKCLYHTEGESNCRCLGYGN	1015		
Qy	959	ALRQDCRKCVCNVLGTVKEHC-NGSDCHCDKATGQCSCLPNVIGNQNCRCAPNTWQLASG	1017		
Db	1016	ALTQSCRKVCNQMGTVEEMCPSPGNCNCDLTSGQCLCLPNVVGHCDCQCAPDTWNMASG	1075		
Qy	1018	TGCGPCNCNAHSFGPSCNEFTGQCQCMFPGFGRTCSCEQLFWGDDPDVECRACDCDPRG	1077		

Db	1076	KCEDCDPDPNHSFGSSCNEIMGQCSCKPFGGRTCRECLFWGNPEVKHACDCDPRG	1135		
Qy	1078	IETPQCDQSTGCVCVEGVEGPRCDKCTRGYSGVFPDCTPCHQCPALWDAILGELTNRTH	1137		
Db	1136	IAEQCNKVTGHCVCVEGVSGRCDTCAAGTGEFFQPCRCHQCFAEWDIIVGDLTNQTH	1195		
Qy	1138	KFLEKAKALKISGIVGYPYRETVDVSVEKKVNEIKDILAQSPAAEPLKNIGILFEEAEKLT	1197		
Db	1196	RLVQKVNTIKATGTPYQATINNVSANSIRNILAQNPAQTPQPLTEIQGLEQATALMA	1255		
Qy	1198	DVTEKMAQVEVKLTDTASQSNSTAGELGALQAEAESLDKTVKELAEQLEFIKNSDIQAL	1257		
Db	1256	EMNSNLNLTETLSEISSDNNSTDTKLKSLKEEAQKLEQTVKDLREQVEFPVKNSDIRGAR	1315		
Qy	1258	DSITKYFQMSLEAEKRVNASTTDPNSTVQESALTRDRVEDLMLERESPFFKEQEEQARLL	1317		
Db	1316	ASVTRYEQSQNAEIRANASTTDPYNLVNQSATLRTETEELMNQTKKEEFNRQDEFSSKL	1375		
Qy	1318	DELAKLQSLDLSAAAQWTCGTPPGAD-CSESECGGPNCRDTEGEKCGGPGCGGLVTVA	1376		
Db	1376	DNLAQLETLDLSLSEKTCGSPAGSENCADSRGGLSCVDMQGSRKCGGEGCDGLTTLA	1435		
Qy	1377	HSAWQKAMDFDRDVLALAEVEQLSKMVSEAKVRADEAKQNAQDVLKTNATKEKVDKSN	1436		
Db	1436	HNAWQAKADFLEIISAMEEVDKLSKMVSEAKVKADEAKLNAQEVLAKTNETKKRVDSN	1495		
Qy	1437	EDLRNLKIQIRNFLTDSADLDSIEAVANEVLKSGNASTPQQLQNLTDIERERVETLSQV	1496		
Db	1496	BELRLIKIQIRDFLTQDGADLESIEAVANEVLQMQMPTTTPAQQLNLTEIERERVSLTDV	1555		
Qy	1497	EVILQCSAADIAEALLLEAKRASKSATDVKVTADMVKEALEEAEKAAQVAAEKAKQAD	1556		
Db	1556	EDILNQSAADILRAESLLEQARKARKEASDVKSTAEVMVKEALQHAEPRAQNSVAEALKQAA	1615		
Qy	1557	EDIQGTQNLTSISETAASEETLTNASQISKLERNVEELKRKAQNSGEAEYIEKVY	1616		
Db	1616	VDIKGTQDLLVSESETSDSELKLSNATRLKLESVDALLKEKALNTSISANSTEKEAE	1675		
Qy	1617	SVKQNAADDVKTLDCGELDEKYYKVESLIAQKTESADARRKAEALLQNEAKTLLAQANSKL	1676		
Db	1676	SINALAEQLKKDLDBSELKDKYSTVEELITQKAEGVAAEKKAELQBEARNLLQASEKL	1735		
Qy	1677	QLLEDLERYEDNQYLEDKAQELVRLGEVRSLLKIDISEKVAVYSTCL	1725		
Db	1736	QLLKNLEKNYDQNKLLDKANELVDLEKAVKELLQEISHKVTVYSTCL	1784		

RESULT 2

Q8TAS6		
ID	Q8TAS6	PRELIMINARY; PRT; 1086 AA.
AC	Q8TAS6;	
DT	01-JUN-2002 (TrEMBLrel. 21, Created)	
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)	
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)	
DE	Similar to laminin, beta 1 (Fragment).	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Muscle;	
RA	Strausberg R.;	
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; BC026018; AAH26018.1; -	
DR	GO; GO:0005198; F:structural molecule activity; IEA.	
DR	InterPro; IPR002049; EGF like.	
DR	InterPro; IPR002049; Laminin EGF.	
DR	Pfam; PF00053; laminin EGF; 8.	
DR	PRINTS; PRO011; EGFLAMININ.	
DR	SMART; SM00180; EGF_Lam; 8.	
DR	PROSITE; PS00022; EGF_1; 5.	

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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:25:32 ; Search time 43.6478 Seconds
(without alignments)
10415.614 Million cell updates/sec

Title: US-10-037-182-14
Perfect score: 8713
Sequence: 1 MRGSHRAAPALRGRRLWPV.....EDIRKTLPSGCFNTPSIEKP 1609

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8713	100.0	1609	3 AAB19801	Aab19801 Human lam
2	8713	100.0	1609	3 AAB48452	Aab48452 Human lam
3	8713	100.0	1609	5 ABB81594	Abb81594 Human lam
4	8713	100.0	1609	7 ADC01887	Adc01887 Human lam
5	8713	100.0	1617	3 AAB19803	Aab19803 Human lam
6	8709	100.0	1609	2 AAW50898	Aaw50898 Human lam
7	8544	98.1	1576	3 AAB19802	Aab19802 Human lam
8	8544	98.1	1576	3 AAB48453	Aab48453 Human lam
9	8544	98.1	1576	5 ABB81595	Abb81595 Human lam
10	8544	98.1	1584	3 AAB19804	Aab19804 Human lam
11	8148	93.5	1605	3 AAB19805	Aab19805 Mouse lam
12	8148	93.5	1605	3 AAB48454	Aab48454 Mouse lam
13	8148	93.5	1605	5 ABB81596	Abb81596 Mouse lam
14	8147	93.5	1607	2 AAW50897	Aaw50897 Mouse lam
15	8038	92.3	1572	3 AAB19806	Aab19806 Mouse lam
16	8038	92.3	1572	3 AAB48455	Aab48455 Mouse lam
17	8038	92.3	1572	5 ABB81597	Abb81597 Mouse lam
18	3613	41.5	1587	3 AAB40917	Aab40917 Human ORF
19	3611	41.4	1587	5 AAM50361	Aam50361 Mouse lam
20	3611	41.4	1587	6 ABR58467	Abr58467 Human NOV
21	3609	41.4	1575	6 ABR58468	Abr58468 Human NOV
22	3463.5	39.8	1524	2 AAY15458	Aay15458 Human lam
23	3440	39.5	1639	4 ABB59807	Abb59807 Drosophil
24	2637	30.3	1193	2 AAR91427	Aar91427 Kalinin/1
25	2637	30.3	1193	3 AAB48468	Aab48468 Human lam

26	2637	30.3	1193	5 AAE14712	Aae14712 Human lam
27	2637	30.3	1193	5 AAO14992	Aao14992 Laminin g
28	2637	30.3	1193	6 ABR48214	Abr48214 Human bla
29	2637	30.3	1193	6 ABUS6513	Abu56513 Lung canc
30	2637	30.3	1193	6 ABUS6696	Abu56696 Lung canc
31	2637	30.3	1193	6 ABR92103	Abr92103 Human cer
32	2637	30.3	1193	6 ADA74120	Ada74120 Human lam
33	2630	30.2	1172	3 AAB48469	Aab48469 Human lam
34	2629	30.2	1193	3 AAB48470	Aab48470 Human lam
35	2622	30.1	1172	3 AAB48471	Aab48471 Human lam
36	2612.5	30.0	1190	6 ADA74091	Ada74091 Equine la
37	2516.5	28.9	1111	2 AAR91428	Aar91428 Kalinin/1
38	2516.5	28.9	1111	5 AAE14713	Aae14713 Human lam
39	2516.5	28.9	1111	5 AAO14993	Aao14993 Laminin g
40	2454.5	28.2	1171	3 AAB48473	Aab48473 Mouse lam
41	2454.5	28.2	1192	3 AAB48472	Aab48472 Mouse lam
42	2454.5	28.2	1192	5 AAE14711	Aae14711 Mouse lam
43	2454.5	28.2	1192	6 ADA74121	Ada74121 Murine la
44	2355.5	27.0	1171	2 AAW26583	Aaw26583 Rat hemid
45	1783.5	20.5	3122	7 ADE61794	Ade61794 Human Pro

ALIGNMENTS

RESULT 1
AAB19801
ID AAB19801 standard; protein; 1609 AA.

AC AAB19801;

XX
DT 05-MAR-2001 (first entry)

XX Human laminin 2 gamma-1 chain.

KW Laminin 2; human; nerve regeneration; angiogenic; cell adhesion;
XX degenerative muscle disorder; muscular dystrophy; cell therapy.

OS Homo sapiens.

XX
FH Key Location/Qualifiers
FT Peptide 1..33
FT Protein 34..1609
FT /label= Signal_peptide
FT /label= Mature_protein

PN WO200065730-A2.

XX 09-NOV-2000.

XX 28-APR-2000; 2000WO-US011378.

XX 30-APR-1999; 99US-0131720P.

XX 15-JUN-1999; 99US-0139198P.

XX 12-JUL-1999; 99US-0143289P.

XX 24-SEP-1999; 99US-0155945P.

XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.

XX Yurchenco P;

XX WPI; 2000-687537/67.

XX N-PSDB; AAA88901.

XX Purified laminin 2 protein, useful for research and therapeutic purposes

XX including peripheral nerve regeneration, treatment of degenerative muscle

XX disorders, angiogenesis regulation, and ex vivo cell therapy.

XX Claim 5; Page 239-244; 305pp; English.

XX The present sequence is that of the gamma-1 chain of human laminin 2.

XX Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1

XX (100 kDa) chains. It is thought to be specifically required for

CC stabilizing myotubes during skeletal muscle development, and for
CC preventing apoptosis. Genetic defects in its structure or expression are
CC associated with a major type of congenital muscular dystrophy. Laminin 2
CC is also thought to be important in Schwann cell/basal lamina
CC interactions. The invention provides laminin 2, beta-1 and gamma-
CC 1 chain polypeptides (see AAB19791-806) and the polynucleotides encoding
CC them (see AAB8891-906), methods for making recombinant laminin 2, cells
CC that express recombinant laminin 2, and methods for using purified
CC laminin 2 for research and therapeutic purposes including peripheral
CC nerve regeneration, treatment of degenerative muscle disorders,
CC angiogenesis regulation, promoting cell attachment and migration, ex vivo
CC cell therapy, improving the take of grafts, improving the
CC biocompatibility of medical devices and preparing improved culture
CC devices and media
XX

SQ Sequence 1609 AA;

Query Match 100.0%; Score 8713; DB 3; Length 1609;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSHRAAPALRPRGRLWPVLAVLAAAAAGCAQAAMDECTDEGGRPQRCMPEFVNAAFN 60
DB 1 MRGSHRAAPALRPRGRLWPVLAVLAAAAAGCAQAAMDECTDEGGRPQRCMPEFVNAAFN 60
QY 61 VTWATNTCGTPPEEYCVQGTGVTGKTSCHLCDAGQPHLQHGAAFLTDYNNQADTTWQS 120
DB 61 VTWATNTCGTPPEEYCVQGTGVTGKTSCHLCDAGQPHLQHGAAFLTDYNNQADTTWQS 120
QY 121 QTMLAGVQYPPSSINLTLLHKGAFDITYVRLKFHTSRPESFAIYKRTREDGWPWIPYQYSG 180
DB 121 QTMLAGVQYPPSSINLTLLHKGAFDITYVRLKFHTSRPESFAIYKRTREDGWPWIPYQYSG 180
QY 181 SCENTYSKANRGFTRTGGDEQQAALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFNDSFVL 240
DB 181 SCENTYSKANRGFTRTGGDEQQAALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFNDSFVL 240
QY 241 QEWVTATDIRVTILNRLNTEGDEVFNDPKVLKSYYYAISDFAVGRCCKNGHASECMKNEF 300
DB 241 QEWVTATDIRVTILNRLNTEGDEVFNDPKVLKSYYYAISDFAVGRCCKNGHASECMKNEF 300
QY 301 DKLVNCCKHNTYGVDCCKLPLFFNDRPWRRTAESAASECLPCDCNGRSQECYFDPPELYRS 360
DB 301 DKLVNCCKHNTYGVDCCKLPLFFNDRPWRRTAESAASECLPCDCNGRSQECYFDPPELYRS 360
QY 361 TGHGGHCTNCQDNTDGAHCERCENFFRLGNNEACSSCHSPVSLSTQCDSYGRCSCKP 420
DB 361 TGHGGHCTNCQDNTDGAHCERCENFFRLGNNEACSSCHSPVSLSTQCDSYGRCSCKP 420
QY 421 GVMGDKCDRCQPGFHSLTEAGRCPCSDPSGSDIECNVETGRCVKCNVGEFNCERCKPG 480
DB 421 GVMGDKCDRCQPGFHSLTEAGRCPCSDPSGSDIECNVETGRCVKCNVGEFNCERCKPG 480
QY 481 FFNLESSNPRGCTPCFCFGHSSVCTNAVGYSVYISISSTFQIDEDGWRAEQRDGSEASLEW 540
DB 481 FFNLESSNPRGCTPCFCFGHSSVCTNAVGYSVYISISSTFQIDEDGWRAEQRDGSEASLEW 540
QY 541 SSERQDIAVISDSYFPRIYFIAPAKFLGKQVLSYGQNLSPFSFRVDRDRTRLSAEDLVLEGA 600
DB 541 SSERQDIAVISDSYFPRIYFIAPAKFLGKQVLSYGQNLSPFSFRVDRDRTRLSAEDLVLEGA 600
QY 601 GLRVSVPLIAQGNYSYPSSETTVKYVFRLEHATDYPWRPALTPPEFQKLLNNLTTSIKIRGTY 660
DB 601 GLRVSVPLIAQGNYSYPSSETTVKYVFRLEHATDYPWRPALTPPEFQKLLNNLTTSIKIRGTY 660
QY 661 SERSAGYLDVTLASARPGVPATWVESCTCPVGYGGQFCMCLSGYRRETNLGPYSP 720
DB 661 SERSAGYLDVTLASARPGVPATWVESCTCPVGYGGQFCMCLSGYRRETNLGPYSP 720
QY 721 CVLCACNGHSETCDPETGVCNCRDNTAGPHCBKCSGDYGYDSTAGTSSDCQPCPCGGSS 780
DB 721 CVLCACNGHSETCDPETGVCNCRDNTAGPHCBKCSGDYGYDSTAGTSSDCQPCPCGGSS 780

QY 781 CAVVPKTKXEVVCTNCPTGTTGKRCCLCDDGYFGDPLGRNGPVRLCRLCQCSDNIDPNAV 840
DB 781 CAVVPKTKXEVVCTNCPTGTTGKRCCLCDDGYFGDPLGRNGPVRLCRLCQCSDNIDPNAV 840
QY 841 NCNRLTGECLKCIYNTAGFYCDRCCKDGGFFGNPLAPNPADKCKACNCNYPYGTMKQSSCNP 900
DB 841 NCNRLTGECLKCIYNTAGFYCDRCCKDGGFFGNPLAPNPADKCKACNCNYPYGTMKQSSCNP 900
QY 901 VTGQCECLPHVTGQDCGACDPGFYNLQSGQGCRCDCCHALGSTNGQCDIRTGQCECQPGI 960
DB 901 VTGQCECLPHVTGQDCGACDPGFYNLQSGQGCRCDCCHALGSTNGQCDIRTGQCECQPGI 960
QY 961 TGOHCERCEVNHFGFGPEGCKPCDCHPEGSLSLQCKDDGRCRCREGFVGNRCDCQCEENYF 1020
DB 961 TGOHCERCEVNHFGFGPEGCKPCDCHPEGSLSLQCKDDGRCRCREGFVGNRCDCQCEENYF 1020
QY 1021 YNRSWPGCEPCACRYLVKQKVADHRVKLQELLESILANLGTGDEMVTDOAFEDRLKEAER 1080
DB 1021 YNRSWPGCEPCACRYLVKQKVADHRVKLQELLESILANLGTGDEMVTDOAFEDRLKEAER 1080
QY 1081 EVMDDLREAOQVDVQDQNLMDRLQRVNNTLSSQISRLQNIPTIETGNLAEQARAHVEN 1140
DB 1081 EVMDDLREAOQVDVQDQNLMDRLQRVNNTLSSQISRLQNIPTIETGNLAEQARAHVEN 1140
QY 1141 TERLIEIASRELEKAKVAAANVSVTQPESTGDPNNMTLLAEARKLAERHKQEAADDIVRV 1200
DB 1141 TERLIEIASRELEKAKVAAANVSVTQPESTGDPNNMTLLAEARKLAERHKQEAADDIVRV 1200
QY 1201 AKTANDTSTEAYNLLRLTAGENQTAFAIEELNRKYEQAKNISQDLEKQAAARVHEEAKRA 1260
DB 1201 AKTANDTSTEAYNLLRLTAGENQTAFAIEELNRKYEQAKNISQDLEKQAAARVHEEAKRA 1260
QY 1261 GDKAVEIYASVAQLSPDLSETLENEANNIKMEAEENLEQLIDOKLDYEDLREDMRGKELE 1320
DB 1261 GDKAVEIYASVAQLSPDLSETLENEANNIKMEAEENLEQLIDOKLDYEDLREDMRGKELE 1320
QY 1321 VKNLLEKKGTEQQTADQLLARADAALAEAAKKGRTDILQEBANDILNNLKDFDRRVNDN 1380
DB 1321 VKNLLEKKGTEQQTADQLLARADAALAEAAKKGRTDILQEBANDILNNLKDFDRRVNDN 1380
QY 1381 KTAEEALRKIPAINQITTEANEKTRAQALGSAADATEAKNKAHEAERIAASAVQKNA 1440
DB 1381 KTAEEALRKIPAINQITTEANEKTRAQALGSAADATEAKNKAHEAERIAASAVQKNA 1440
QY 1441 TSTKAEAEARTFAEVTDLNEVNNMLKQIQEAEKELKRKQDDADQDMMAGMASQAQAEAE 1500
DB 1441 TSTKAEAEARTFAEVTDLNEVNNMLKQIQEAEKELKRKQDDADQDMMAGMASQAQAEAE 1500
QY 1501 INARKAKNSVTSLLSIINDLLEQLGQDITVDLNLKNEIEGTILNKADEMKSVDLDRKVS 1560
DB 1501 INARKAKNSVTSLLSIINDLLEQLGQDITVDLNLKNEIEGTILNKADEMKSVDLDRKVS 1560
QY 1561 LENEAKKQEAALMDYNRDIEEIMKDIRNLEDIRKTLPSGCFNTPSIEKP 1609
DB 1561 LENEAKKQEAALMDYNRDIEEIMKDIRNLEDIRKTLPSGCFNTPSIEKP 1609
RESULT 2
AAB48452
ID AAB48452 standard; protein; 1609 AA.
XX
AC AAB48452;
XX
DT 02-MAR-2001 (first entry)
XX
DE Human laminin 8 polypeptide, SEQ ID NO: 22.
XX
KW Human; laminin 8; neuroprotective; angiogenic; osteopathic;
KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;
KW vascular tissue injury; neural injury; angiogenesis regulation.
XX
OS Homo sapiens.
XX

PN WO200065732-A2.
XX PD 09-NOV-2000.
XX 28-APR-2000; 2000WO-US011543.
XX 30-APR-1999; 99US-0131720P.
PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.
PR 11-FEB-2000; 2000US-0182012P.
XX (BIOS-) BIOSTRATUM INC.
PA Kortesmaa J, Tryggvason K;
XX WPI; 2000-687539/67.
XX N-PSDB; AAC83713.
DR
XX
PT Purified laminin 8 protein, useful for research and therapeutic purposes
PT including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.
XX
PS Claim 5; Page 202-207; 245pp; English.
XX
CC The present sequence is a laminin 8 polypeptide chain. Laminins are a
CC family of heterotrimeric glycoproteins that function via binding
CC interactions with neighbouring cell receptors and by forming laminin
CC networks. They are signalling molecules which influence cellular
CC function. Laminin 8 is useful for treating injuries to tissue of
CC mesenchymal origin, such as bone, cartilage, tendon, and ligament,
CC treating injuries to vascular tissue, promoting cell attachment and
CC migration, ex vivo cell therapy, improving the biocompatibility of
CC medical devices, and preparing improved cell culture devices and media.
CC Laminin 8 is also useful for promoting re-endothelialisation at the site
CC of vascular injuries, improving the take of grafts, improving the
CC biocompatibility of medical devices, treating neural injuries (neural
CC regeneration), regulating angiogenesis, and promoting cell attachment and
XX migration
SQ Sequence 1609 AA;
Query Match 100.0%; Score 8713; DB 3; Length 1609;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRGSHRAAPALRPRGRLWPVLAVLAAAAAGCAQAAMDECTDEGGRPQRCMPEFVNAAFN 60
Db 1 MRGSHRAAPALRPRGRLWPVLAVLAAAAAGCAQAAMDECTDEGGRPQRCMPEFVNAAFN 60
QY 61 VTVVAINTCGTPPEEYCVQGTGVTGKSKCHLDCAGQPHLQHGAAFLTDYNNQADTTWQS 120
Db 61 VTVVAINTCGTPPEEYCVQGTGVTGKSKCHLDCAGQPHLQHGAAFLTDYNNQADTTWQS 120
QY 121 QTMLAGVQYPSSINLTLLHKGAFDITYVRLKFTSRPESPAIYKRTREDGPNTPYQYYSG 180
Db 121 QTMLAGVQYPSSINLTLLHKGAFDITYVRLKFTSRPESPAIYKRTREDGPNTPYQYYSG 180
QY 181 SCENTYSKANRGFIRTTGGDEQQAALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFDNSPVL 240
Db 181 SCENTYSKANRGFIRTTGGDEQQAALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFDNSPVL 240
QY 241 QEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSYYYAISDFAVGGRCKCNGHASECMKNEF 300
Db 241 QEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSYYYAISDFAVGGRCKCNGHASECMKNEF 300
QY 301 DKLVCKNKHNTYGVDCCKLPPFNDRPWRRATAESASECLPCDCNCRSQECYFDPPELYRS 360
Db 301 DKLVCKNKHNTYGVDCCKLPPFNDRPWRRATAESASECLPCDCNCRSQECYFDPPELYRS 360
QY 361 TGHGCHTNCQDNTDGAHCERCENFFRLGNNEACSSCHCSFVGSLSLSTQCDSYGRCSCKP 420
Db 361 TGHGCHTNCQDNTDGAHCERCENFFRLGNNEACSSCHCSFVGSLSLSTQCDSYGRCSCKP 420

QY 421 GVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSDICNVETGRCVKDNVGFCNCRCKPG 480
Db 421 GVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSDICNVETGRCVKDNVGFCNCRCKPG 480
QY 481 FFNLESSNPRGCTPCFCFGHSSVCTNAVGYSVYSISSTFQIDEDGWRAEQRDSEASLEW 540
Db 481 FFNLESSNPRGCTPCFCFGHSSVCTNAVGYSVYSISSTFQIDEDGWRAEQRDSEASLEW 540
QY 541 SSERQDIAVISDSYFPRYFIAPAKFLGKQVLSYGQNLFSFSFRVDRDRTRLSAEDLVLEGA 600
Db 541 SSERQDIAVISDSYFPRYFIAPAKFLGKQVLSYGQNLFSFSFRVDRDRTRLSAEDLVLEGA 600
QY 601 GLRVSVPLIAQNSYPSSETVKYVFRHLHEATDYPWRPALTPFEFQKLLNLTSTKIRGTY 660
Db 601 GLRVSVPLIAQNSYPSSETVKYVFRHLHEATDYPWRPALTPFEFQKLLNLTSTKIRGTY 660
QY 661 SERSAGYLDVTLASARPGPGVPATWVESCTCPVGGGQFCMCLSGYRRRETNLGPYSP 720
Db 661 SERSAGYLDVTLASARPGPGVPATWVESCTCPVGGGQFCMCLSGYRRRETNLGPYSP 720
QY 721 CVLCACNGHSETCDPETGVCNCRDNTAGPHCEKCSGYYGDSSTAGTSSDCQPCPCPGSS 780
Db 721 CVLCACNGHSETCDPETGVCNCRDNTAGPHCEKCSGYYGDSSTAGTSSDCQPCPCPGSS 780
QY 781 CAVVPKTKEVVCTNCPTGTTGKRCCELDDGYFGDPLGRNGPVRCLRCQCSNDIDPNAVG 840
Db 781 CAVVPKTKEVVCTNCPTGTTGKRCCELDDGYFGDPLGRNGPVRCLRCQCSNDIDPNAVG 840
QY 841 NCNRLTGECLKCIYNTAGFYCDRCCKDGFNPLAPNADCKKACNCNPNYGTMKQOSSCNP 900
Db 841 NCNRLTGECLKCIYNTAGFYCDRCCKDGFNPLAPNADCKKACNCNPNYGTMKQOSSCNP 900
QY 901 VTGQCECLPHVTGQDCGACDPGFYNLQSGQGRCERCDCALGSTNGQCDIRTGQCECQPGI 960
Db 901 VTGQCECLPHVTGQDCGACDPGFYNLQSGQGRCERCDCALGSTNGQCDIRTGQCECQPGI 960
QY 961 TGQHCEVCEVNHFGFGPEGCKPCDCHPEGSLSLQCKDDGRCECREGVGNRCDCOEENYF 1020
Db 961 TGQHCEVCEVNHFGFGPEGCKPCDCHPEGSLSLQCKDDGRCECREGVGNRCDCOEENYF 1020
QY 1021 YNRSWPGCQECPCYRLVKDKVADHRVKLQELSLIANLGTGDEMVTDOAFEDRLKEAER 1080
Db 1021 YNRSWPGCQECPCYRLVKDKVADHRVKLQELSLIANLGTGDEMVTDOAFEDRLKEAER 1080
QY 1081 EVMDLLREAQDVKDQNLMDRLQRVNNTLSSQISRLQINRNTIETGNLAEQARAHVEN 1140
Db 1081 EVMDLLREAQDVKDQNLMDRLQRVNNTLSSQISRLQINRNTIETGNLAEQARAHVEN 1140
QY 1141 TERLIEIASRELEKAKVAAANVSVTQPESTGDPNNMTLLAEARKLAERHKQEAADDIVRV 1200
Db 1141 TERLIEIASRELEKAKVAAANVSVTQPESTGDPNNMTLLAEARKLAERHKQEAADDIVRV 1200
QY 1201 AKTANDTSTEAYNLLRLTLAGENQTAFIEBELNRKYEQAKNISQDLEKQAAARVHEEAKRA 1260
Db 1201 AKTANDTSTEAYNLLRLTLAGENQTAFIEBELNRKYEQAKNISQDLEKQAAARVHEEAKRA 1260
QY 1261 GDKAVEIYASVAQLSPLDSEITLENEANNIKMEAEENLEQLIDQKLKDYEDLREDMRGKELE 1320
Db 1261 GDKAVEIYASVAQLSPLDSEITLENEANNIKMEAEENLEQLIDQKLKDYEDLREDMRGKELE 1320
QY 1321 VKNLLKKGKTEQQTADQLLARADAAKALAEAAKKGKRDITLQEAANDILNNLKDFDRRVNDN 1380
Db 1321 VKNLLKKGKTEQQTADQLLARADAAKALAEAAKKGKRDITLQEAANDILNNLKDFDRRVNDN 1380
QY 1381 KTAEEELRKIPAINQTTITEANEKTRQAQALGSAADATEAKNKAHEAERIAASAVQKNA 1440
Db 1381 KTAEEELRKIPAINQTTITEANEKTRQAQALGSAADATEAKNKAHEAERIAASAVQKNA 1440
QY 1441 TSTKAEABERTFAEVTDLNEVNNMLKQLEAEKELKRKQDDADQDMMAGMASQAQAEAE 1500
Db 1441 TSTKAEABERTFAEVTDLNEVNNMLKQLEAEKELKRKQDDADQDMMAGMASQAQAEAE 1500
QY 1501 INARKAKNSVTSLLSIINDLLEQLGLQDLDVTLNKLNEIEGLTNKAKDEMKVSDLRKVSD 1560

Db 1501 INARKKNSVTSLSIINDLLEQLGQDVTVDLNLKNEIEGTINKAKDEMKVSDLDKRVSD 1560
QY 1561 LENEAKKQEAAIMDYNRDIEEIMKDIRNLEDIRKTLPSGCFNTPSIEKP 1609
Db 1561 LENEAKKQEAAIMDYNRDIEEIMKDIRNLEDIRKTLPSGCFNTPSIEKP 1609

RESULT 3
ABB81594
ID ABB81594 standard; protein; 1609 AA.
XX ABB81594;
AC ABB81594;
XX ABB81594;
DT 19-SEP-2002 (first entry)
XX Human laminin 10 third chain protein sequence SEQ ID NO:14.
DE Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;
XX tissue repair development; laminin; healing; vascular tissue;
KW re-endothelialisation; vascular injury; cell attachment; cell stasis;
KW proliferation; migration.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH Peptide 1..33
FT /label= signal
FT 34..1609
FT /label= laminin_10_third_chain
XX

WO200250111-A2.
27-JUN-2002.
21-DEC-2001; 2001WO-US051035.
21-DEC-2000; 2000US-0257449P.
28-MAR-2001; 2001US-0279282P.
13-NOV-2001; 2001US-00279282.
(BIOS-) BIOSTRATUM INC.
Tryggvason K, Doi M, Thyboll J;
WPI; 2002-557650/59.
N-PSDB; ABQ72912.

New human laminin-10 proteins, useful for accelerating the healing of
vascular tissue, improving the biocompatibility of grafts, or for
promoting re-endothelialization at the site of vascular injuries.
Claim 9; Page 165-170; 231pp; English.

The present invention describes human laminin alpha 5. Also described is
an isolated laminin 10. Laminin 10 has vulnery activity. Laminins are
useful in maintaining cell/tissue phenotype as well as promoting cell
growth and differentiation in tissue repair development. Specifically,
laminin 10 can be used for accelerating the healing injuries of vascular
tissue, improving the biocompatibility of grafts useful for treating such
injuries, for promoting re-endothelialisation at the site of vascular
injuries, and promote cell attachment and subsequent cell stasis,
proliferation, differentiation, and/or migration. The present sequence
represents a third chain protein of laminin 10, from the present
invention

Sequence 1609 AA;
Query Match 100.0%; Score 8713; DB 5; Length 1609;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MRGSHRAAPALRPRGRLLWFLVLAALAAAAAGCAQAMDECTDEGGRPQRCMPEFVNAAFN 60

1 MRGSHRAAPALRPRGRLLWFLVLAALAAAAAGCAQAMDECTDEGGRPQRCMPEFVNAAFN 60
61 VTVVATNTCTPPEEYCVQGTGVTGKSKCHLCLDAGQPHLQGAFLTDYNNQADTTWQSS 120
61 VTVVATNTCTPPEEYCVQGTGVTGKSKCHLCLDAGQPHLQGAFLTDYNNQADTTWQSS 120
121 QTMLAGVQPPSSINLTLHLGKAFDITYVRLKFHTSRPESFAIYKRTREDGPIPYQYYS 180
121 QTMLAGVQPPSSINLTLHLGKAFDITYVRLKFHTSRPESFAIYKRTREDGPIPYQYYS 180
181 SCENTYSKANRGFIIRTTGGDEQALCTDEFSDISPLTGNVAFSTLEGRPSAYNFDNSPVL 240
181 SCENTYSKANRGFIIRTTGGDEQALCTDEFSDISPLTGNVAFSTLEGRPSAYNFDNSPVL 240
241 QEWVTATDIRVTLNRLNLTGDEVFNDPKVLKSYVVAISDFAVGGRCCKNGHASECMKNEF 300
241 QEWVTATDIRVTLNRLNLTGDEVFNDPKVLKSYVVAISDFAVGGRCCKNGHASECMKNEF 300
301 DKLVCKNCKHNTYGVDCCKLCPFFNDRPWRRTAASASECLPCDCNGRSQECYFDPPELYRS 360
301 DKLVCKNCKHNTYGVDCCKLCPFFNDRPWRRTAASASECLPCDCNGRSQECYFDPPELYRS 360
361 TGHGHCNTCQDNTDGAHCERCRENFFRLGNNEACSSCHCSPVGLSTQCDSYGRCSCKP 420
361 TGHGHCNTCQDNTDGAHCERCRENFFRLGNNEACSSCHCSPVGLSTQCDSYGRCSCKP 420
421 GVMGDKCDRCQPGFHSLEAGRCPCSDPSGSDENETGRCVKDNVEGFNCERCKPG 480
421 GVMGDKCDRCQPGFHSLEAGRCPCSDPSGSDENETGRCVKDNVEGFNCERCKPG 480
481 FFNLESSNPRGCTPCFCFCHSSVCTNAVGYVYSISSTFOIDEDGWRAEQRDGSEASLEW 540
481 FFNLESSNPRGCTPCFCFCHSSVCTNAVGYVYSISSTFOIDEDGWRAEQRDGSEASLEW 540
541 SSERQDIAVISDSYFPFYFIAPAKFLGKQVLSYQNLFSFRVDRDRTRLSAEDLVLEGA 600
541 SSERQDIAVISDSYFPFYFIAPAKFLGKQVLSYQNLFSFRVDRDRTRLSAEDLVLEGA 600
601 GLRVSVPVLIAGNSYPSSETTKYVFRLEHATDYPWRPALTPFEFQKLLNLTSLIKIRGTY 660
601 GLRVSVPVLIAGNSYPSSETTKYVFRLEHATDYPWRPALTPFEFQKLLNLTSLIKIRGTY 660
661 SERSAGYLDVTLASARPFGVPATWVESCPCPVGYGGQFCMCLSGYRRETNPNGPSP 720
661 SERSAGYLDVTLASARPFGVPATWVESCPCPVGYGGQFCMCLSGYRRETNPNGPSP 720
721 CVLCACNGHSETCDPETGVNCRDNTAGHCEKCSDDGYGDSSTAGTSSDCPCPCGSS 780
721 CVLCACNGHSETCDPETGVNCRDNTAGHCEKCSDDGYGDSSTAGTSSDCPCPCGSS 780
781 CAVVPKTKEVVCTNCTTGTGKRCCELDDGYFGDPLGRNGPVLRLCQCSNIDPNVAVG 840
781 CAVVPKTKEVVCTNCTTGTGKRCCELDDGYFGDPLGRNGPVLRLCQCSNIDPNVAVG 840
841 NCNRLTGECLKCIYNTAGFYCDRCCKDGFNGPLAPNPADKCKACNPNPYGTMKQSSCNP 900
841 NCNRLTGECLKCIYNTAGFYCDRCCKDGFNGPLAPNPADKCKACNPNPYGTMKQSSCNP 900
901 VTGQCECLPHVTGQDGCACDPGFYNLQSGQGCERCDCCHALGSTNGQCDIRTGQCECQPGI 960
901 VTGQCECLPHVTGQDGCACDPGFYNLQSGQGCERCDCCHALGSTNGQCDIRTGQCECQPGI 960
961 TGOHCERCEVNHFGFPGEGCKPCDCHPEGLSLQCKDDGRCREGFVGNRCDCQCEENYF 1020
961 TGOHCERCEVNHFGFPGEGCKPCDCHPEGLSLQCKDDGRCREGFVGNRCDCQCEENYF 1020
1021 YNRSWPGQCECPACYRLVKDKVADHRVKLQLESILIANLGTGDMVTDQAFEDRLKEAER 1080
1021 YNRSWPGQCECPACYRLVKDKVADHRVKLQLESILIANLGTGDMVTDQAFEDRLKEAER 1080
1081 EWMDLLEAQDVKDVQNLMDRLQVNNLTSSQISRLQNTIRNTEETGNLAEQARAHEVN 1140

Db 841 NCNRLTGECLKCIYNTAGFYCDRCCKDGGFFGNPLAPNPADCKACNCNPYGTMKQOSSCNP 900
Qy 901 VTGQCECLPHVVTGQDCGACDPGFYNLQSGQGCERCDCCHALGSTNGQCDIRTGQCECQPGI 960
Db 901 VTGQCECLPHVVTGQDCGACDPGFYNLQSGQGCERCDCCHALGSTNGQCDIRTGQCECQPGI 960
Qy 961 TGQHCECEVNHFGFPGEGCKPCDCHPEGSLSLQCKDDGRCECREGVGNRCDQCEENYF 1020
Db 961 TGQHCECEVNHFGFPGEGCKPCDCHPEGSLSLQCKDDGRCECREGVGNRCDQCEENYF 1020
Qy 1021 YNRSWPGCQCECPACRYRLVKDVADHRVKLQLESLIANLGTGDEMVTDOAFEDRLKEAER 1080
Db 1021 YNRSWPGCQCECPACRYRLVKDVADHRVKLQLESLIANLGTGDEMVTDOAFEDRLKEAER 1080
Qy 1081 EVMDLLEAQQVDVQDQNLMDRLQRVNNTLSSQISRLQNIRNTIETGNLAEQARAHVEN 1140
Db 1081 EVMDLLEAQQVDVQDQNLMDRLQRVNNTLSSQISRLQNIRNTIETGNLAEQARAHVEN 1140
Qy 1141 TERLIEIASRELEKAKVAAANVSVTQPESTGDPNNMTLLAEAEARKLAERHKQEAADDIVRV 1200
Db 1141 TERLIEIASRELEKAKVAAANVSVTQPESTGDPNNMTLLAEAEARKLAERHKQEAADDIVRV 1200
Qy 1201 AKTANDTSTEAYNLLRTLAGEQTAFIEELNRKYEQAKNISQDLEKQAAARVHEEAKRA 1260
Db 1201 AKTANDTSTEAYNLLRTLAGEQTAFIEELNRKYEQAKNISQDLEKQAAARVHEEAKRA 1260
Qy 1261 GDKAVEIYASVAQLSPDSETLENEANNIKMEAEENLEQLIDQKLKDYEDLREDMRGKELE 1320
Db 1261 GDKAVEIYASVAQLSPDSETLENEANNIKMEAEENLEQLIDQKLKDYEDLREDMRGKELE 1320
Qy 1321 VKNLLEKGTQEQQTADQLLARADAALAEAAKKGRTDILQEAANDILNNLKDFDRRVNDN 1380
Db 1321 VKNLLEKGTQEQQTADQLLARADAALAEAAKKGRTDILQEAANDILNNLKDFDRRVNDN 1380
Qy 1381 KTAABEALRKIPAINQITITEANEKTREAAQALGSAADATEAKNKAHEAERIAASAVQKNA 1440
Db 1381 KTAABEALRKIPAINQITITEANEKTREAAQALGSAADATEAKNKAHEAERIAASAVQKNA 1440
Qy 1441 TSTKAEARTFAEVTDLNEVNNMLKQLQEAELKELKRKODDADQDMMAGMASQAAQEA 1500
Db 1441 TSTKAEARTFAEVTDLNEVNNMLKQLQEAELKELKRKODDADQDMMAGMASQAAQEA 1500
Qy 1501 INARKAKNSVTSLLSIINDLLEQLGQDQDVTDLNKLNEIEGTLNKAKDEMKVSDIDRKVSD 1560
Db 1501 INARKAKNSVTSLLSIINDLLEQLGQDQDVTDLNKLNEIEGTLNKAKDEMKVSDIDRKVSD 1560
Qy 1561 LENEAKQEAAIMDYNRDIEEIMKDINLEDIRKTLPSGCFNTPSIEKP 1609
Db 1561 LENEAKQEAAIMDYNRDIEEIMKDINLEDIRKTLPSGCFNTPSIEKP 1609
RESULT 5
AAB19803
ID AAB19803 standard; protein; 1617 AA.
XX AC AAB19803;
XX DT 05-MAR-2001 (first entry)
XX DE Human laminin 2 gamma-1 chain with C-terminal FLAG epitope.
XX KW Laminin 2; human; nerve regeneration; angiogenic; cell adhesion;
XX KW degenerative muscle disorder; muscular dystrophy; cell therapy.
XX OS Homo sapiens.
XX Key Location/Qualifiers
XX Peptide 1..33
XX FT /label= Signal_peptide
XX FT 34..1609
XX FT /label= Mature_protein
XX FT 1610..1617

FT XX /label= FLAG
PN WO200066730-A2.
XX 09-NOV-2000.
XX 28-APR-2000; 2000WO-US011378.
XX 30-APR-1999; 99US-0131720P.
XX 15-JUN-1999; 99US-0139198P.
XX 12-JUL-1999; 99US-0143289P.
XX 24-SEP-1999; 99US-0155945P.
XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX Yurchenco P;
XX WPI; 2000-687537/67.
XX N-PSDB; AAA88903.
XX Purified laminin 2 protein, useful for research and therapeutic purposes
XX including peripheral nerve regeneration, treatment of degenerative muscle
XX disorders, angiogenesis regulation, and ex vivo cell therapy.
XX Claim 5; Page 263-268; 305pp; English.
XX The present sequence is that of the gamma-1 chain of human laminin 2,
XX with an additional C-terminal FLAG epitope, resulting from expression in
XX transfected cells from mammalian expression vectors. Laminin 2 is
XX composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1 (100 kDa)
XX chains. It is thought to be specifically required for stabilizing
XX myotubes during skeletal muscle development, and for preventing
XX apoptosis. Genetic defects in its structure or expression are associated
XX with a major type of congenital muscular dystrophy. Laminin 2 is also
XX thought to be important in Schwann cell/basal lamina interactions. The
XX invention provides laminin 2 alpha-2, beta-1 and gamma-1 chain
XX polypeptides (see AAB19791-806) and the polynucleotides encoding them
XX (see AAA8891-906), methods for making recombinant laminin 2, cells that
XX express recombinant laminin 2, and methods for using purified laminin 2
XX for research and therapeutic purposes including peripheral nerve
XX regeneration, treatment of degenerative muscle disorders, angiogenesis
XX regulation, promoting cell attachment and migration, ex vivo cell
XX therapy, improving the take of grafts, improving the biocompatibility of
XX medical devices and preparing improved culture devices and media
XX Sequence 1617 AA;

Query Match 100.0%; Score 8713; DB 3; Length 1617;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MRGSHRAAPALRPRGLWPVLAVLAAAAAGCAQAAMDECTDEGGRPQRCMPEFVNAAFN 60
Db 1 MRGSHRAAPALRPRGLWPVLAVLAAAAAGCAQAAMDECTDEGGRPQRCMPEFVNAAFN 60
Qy 61 VTVVATNTCGTPPEEYCVQGTGVTGVTKSCHLCDAGQPHLQHGAFLTDYNNQADTTWQVS 120
Db 61 VTVVATNTCGTPPEEYCVQGTGVTGVTKSCHLCDAGQPHLQHGAFLTDYNNQADTTWQVS 120
Qy 121 QTMLAGVQYPPSSINLTLLHLGKAFDITYVRLKFHTSRPESFAIYKRTREDGWPWIPYQYSG 180
Db 121 QTMLAGVQYPPSSINLTLLHLGKAFDITYVRLKFHTSRPESFAIYKRTREDGWPWIPYQYSG 180
Qy 181 SCENTYSKANRGFIRTTGGDEQQALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFNDSFVL 240
Db 181 SCENTYSKANRGFIRTTGGDEQQALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFNDSFVL 240
Qy 241 QEWVTATDIRVTNLRLNTFGDEVNDPKVLKSYYYAISPAVGGRCCKNGHASECMKNEF 300
Db 241 QEWVTATDIRVTNLRLNTFGDEVNDPKVLKSYYYAISPAVGGRCCKNGHASECMKNEF 300
Qy 301 DKLVNCKHNTYGVDCCKLPFFNDRPWRRTAESASECLPCDCNGRSQECYFDPPELYRS 360
Db 301 DKLVNCKHNTYGVDCCKLPFFNDRPWRRTAESASECLPCDCNGRSQECYFDPPELYRS 360

Db 301 DKLVNCKHNTYGYDCEKCLPFFNDRPWRRATAESAECPLPCDCNGRSQECYFDPELYRS 360

QY 361 TGHGGHCTNCQNDTGAHCERCRENFFRLGNNEACSSCHCSPVGSLSLTCQDSYGRCSCKP 420

Db 361 TGHGGHCTNCQNDTGAHCERCRENFFRLGNNEACSSCHCSPVGSLSLTCQDSYGRCSCKP 420

QY 421 GVMGDKCDRCQPGFHSLTEAGCRPCSDPSGIDECNVETGRVCVKDNVEGFNCERCCKPG 480

Db 421 GVMGDKCDRCQPGFHSLTEAGCRPCSDPSGIDECNVETGRVCVKDNVEGFNCERCCKPG 480

QY 481 FFNLESSNPRGCTPCFCFGHSSVCTNAVGSYVSISSFTQIDEDGWRABQRDGSEASLEW 540

Db 481 FFNLESSNPRGCTPCFCFGHSSVCTNAVGSYVSISSFTQIDEDGWRABQRDGSEASLEW 540

QY 541 SSERQDIAVISDSYFPFYFIAPAKFLGKQVLSYQGNLSFSFRVDRDRTRLSAEDLVLEGA 600

Db 541 SSERQDIAVISDSYFPFYFIAPAKFLGKQVLSYQGNLSFSFRVDRDRTRLSAEDLVLEGA 600

QY 601 GLRVSVPLIAQGNVPSETTVKYVFRLHEATDYPWRPALTPFEFQKLLNNLTSIKIRGTY 660

Db 601 GLRVSVPLIAQGNVPSETTVKYVFRLHEATDYPWRPALTPFEFQKLLNNLTSIKIRGTY 660

QY 661 SERSAGYLDVTLASARPGPGVPATWVESCTCPVYGGQFCFEMCLSGYRRETPLNGPYSP 720

Db 661 SERSAGYLDVTLASARPGPGVPATWVESCTCPVYGGQFCFEMCLSGYRRETPLNGPYSP 720

QY 721 CVLCACNGHSETCDPETGVNCRDNTAGPHCEKSDGYGDSGTAGTSSDCQPCPCPGSS 780

Db 721 CVLCACNGHSETCDPETGVNCRDNTAGPHCEKSDGYGDSGTAGTSSDCQPCPCPGSS 780

QY 781 CAVVPKTKEVVCTNCPTGTGKRCCELDDGYFGDPLGRNGPVLRLCQCSDNIDPNAVG 840

Db 781 CAVVPKTKEVVCTNCPTGTGKRCCELDDGYFGDPLGRNGPVLRLCQCSDNIDPNAVG 840

QY 841 NCNRLTGECLKCIYNTAGFYCDRCCKDGFNGNPLAPNPADCKACNCNPYGTMKQSSCNP 900

Db 841 NCNRLTGECLKCIYNTAGFYCDRCCKDGFNGNPLAPNPADCKACNCNPYGTMKQSSCNP 900

QY 901 VTGQCECLPHVTGQDCGACDPGFYNLQSGQGCERCDCCHALGSTNGQCDIRTGQCECQPGI 960

Db 901 VTGQCECLPHVTGQDCGACDPGFYNLQSGQGCERCDCCHALGSTNGQCDIRTGQCECQPGI 960

QY 961 TQGHCECEVNHFGFPGEGCKPCDCHPEGSLSLQCKDDGRCECREGVGNRCDQCEENYF 1020

Db 961 TQGHCECEVNHFGFPGEGCKPCDCHPEGSLSLQCKDDGRCECREGVGNRCDQCEENYF 1020

QY 1021 YNRSWPGCQECPCYRLVKDQVADHRVKLQELSLIANLGTGDEMVTDAQFEDRLKEAER 1080

Db 1021 YNRSWPGCQECPCYRLVKDQVADHRVKLQELSLIANLGTGDEMVTDAQFEDRLKEAER 1080

QY 1081 EYMDLLREAQDVKDQVNDQNLMDRLQRVNNTLSSQISRLQNRNTIETGNLAEQARAHVEN 1140

Db 1081 EYMDLLREAQDVKDQVNDQNLMDRLQRVNNTLSSQISRLQNRNTIETGNLAEQARAHVEN 1140

QY 1141 TERLIEIASRELEKAKVAANVSVTQPESTGDPNNTLLAEAEARKLAERHKQEAADDIVRV 1200

Db 1141 TERLIEIASRELEKAKVAANVSVTQPESTGDPNNTLLAEAEARKLAERHKQEAADDIVRV 1200

QY 1201 AKTANDTSTEAYNLLRLTAGENQTAFEIEELNRKYEQAKNISQDLEKQAARVHEEAKRA 1260

Db 1201 AKTANDTSTEAYNLLRLTAGENQTAFEIEELNRKYEQAKNISQDLEKQAARVHEEAKRA 1260

QY 1261 GDKAVEIYASVAQLSPLDSETLENEANNIKMEAEENLEQLIDQKLKOYEDLREDMRGKELE 1320

Db 1261 GDKAVEIYASVAQLSPLDSETLENEANNIKMEAEENLEQLIDQKLKOYEDLREDMRGKELE 1320

QY 1321 VKNLLKKGKTEQQTADQLLARADAATAKALAEAAKGRDTLQEANDILNLLKDFDRRVNDN 1380

Db 1321 VKNLLKKGKTEQQTADQLLARADAATAKALAEAAKGRDTLQEANDILNLLKDFDRRVNDN 1380

QY 1381 KTAABEALRKIPAINQITIETANEKTREAAQALGSAADATEAKNKAHEABERIAASAVQKNA 1440

Db 1381 KTAABEALRKIPAINQITIETANEKTREAAQALGSAADATEAKNKAHEABERIAASAVQKNA 1440

QY 1441 TSTKABAERTFAEVTDLNEVNNMLKQLOEAEKELKRKQDDADQDMMAGMASQAAQEA 1500

Db 1441 TSTKABAERTFAEVTDLNEVNNMLKQLOEAEKELKRKQDDADQDMMAGMASQAAQEA 1500

QY 1501 INARKAKNSVTSLLSIINDLLEQLGQDQDVTDLNKLNEIEGTLNKADEMKSVDLDRKVSD 1560

Db 1501 INARKAKNSVTSLLSIINDLLEQLGQDQDVTDLNKLNEIEGTLNKADEMKSVDLDRKVSD 1560

QY 1561 LENEAKKQEAAIMDYNRDIEEIMKDIRNLEDIRKTLPSGCFNTPSIEKP 1609

Db 1561 LENEAKKQEAAIMDYNRDIEEIMKDIRNLEDIRKTLPSGCFNTPSIEKP 1609

RESULT 6

AAW50898

ID AAW50898 standard; protein; 1609 AA.

XX

AC AAW50898;

XX

DT 07-DEC-1998 (first entry)

XX

DE Human laminin G1 chain.

XX

KW Laminin; human; beta-amyloid; amyloidosis; Alzheimer's disease; Down's syndrome; hereditary cerebral haemorrhage; inflammation; malignancy; Familial Mediterranean Fever; multiple myeloma; type II diabetes; prion disease; Creutzfeldt-Jacob disease; CJD; Gertsmann-Straussler syndrome; kuru; scrapie; haemodialysis; carpal tunnel syndrome; senile cardiac amyloid polynuropathy; Familial Amyloidotic Polynuropathy; thyroid carcinoma; diagnosis; therapy.

XX

OS Homo sapiens.

XX

FN WO9815179-A1.

XX

PD 16-APR-1998.

XX

PF 08-OCT-1997; 97WO-US018145.

XX

PR 08-OCT-1996; 96US-0027981P.

XX

PA (UNIW) UNIV WASHINGTON.

XX

PI Castillo G, Snow AD;

XX

DR WPI; 1998-240534/21.

XX

PT Use of laminin and fragments - for developing products for use in the diagnosis and treatment of amyloid disease, e.g. Alzheimer's disease or CJD.

XX

PS Claim 15; Page 106-109; 132pp; English.

XX

CC This is the amino acid sequence of the human laminin G1 chain. The primary object of the invention is to use laminin, laminin-derived protein fragments and/or laminin-derived polypeptides as potent inhibitors of amyloid formation, deposition, accumulation and/or persistence in Alzheimer's disease and other amyloidoses. The laminin products (see AAW50888-98) may include mouse or human laminin A or A1 chain, laminin B1 or B2 chain, laminin A2 chain (merosin), laminin G1 chain, the globular repeats of the laminin A1 chain and the beta-amyloid binding domain of the laminin A chain. A claimed method for treating an amyloid disease comprises administering a polypeptide having a conformational similarity to a fragment of a laminin protein. A method for diagnosing an amyloid disease involves determining levels of laminin in a sample. Production of laminin or its fourth globular repeat in vivo provides a method for in vivo inhibition of beta-amyloid amyloidosis. The products and methods can be used for the diagnosis, prognosis, monitoring and treatment of amyloidoses such as Alzheimer's disease, Down's syndrome and hereditary cerebral haemorrhage with amyloidosis of the Dutch type (where the specific amyloid is the beta-amyloid protein), the amyloidosis

associated with chronic inflammation, various forms of malignancy and Familial Mediterranean Fever (AA amyloid or inflammation-association amyloidosis), the amyloidosis associated with multiple myeloma and other B-cell abnormalities (AL amyloid), the amyloidosis associated with type II diabetes (amylin or islet amyloid), the amyloidosis associated with prion diseases including Creutzfeldt-Jacob disease, Gertsmann-Straussler syndrome, kuru and animal scrapie (PrP amyloid), the amyloidosis associated with long-term haemodialysis and carpal tunnel syndrome (beta 2-microglobulin amyloid), the amyloidosis associated with senile cardiac amyloid and Familial Amyloidotic Polyneuropathy (prealbumin or transthyretin amyloid), and the amyloidosis associated with endocrine tumours such as medullary carcinoma of the thyroid (variant of procalcitonin)

XX SQ Sequence 1609 AA;

Query Match 100.0%; Score 8709; DB 2; Length 1609;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MRGSHRAAPALRPRGRLLWPVLAVLAAAAAGCAQAAMDECTDEGGRPQRCMPPEFVNAAFN	60
Db	1	MRGSHRAAPALRPRGRLLWPVLAVLAAAAAGCAQAAMDECTDEGGRPQRCMPPEFVNAAFN	60
QY	61	VTVAATNTCGTPPEEYCVQGTGVTGVTKSCHLCDAGQPHLQHGAFLTDYNNQADTTWQS	120
Db	61	VTVAATNTCGTPPEEYCVQGTGVTGVTKSCHLCDAGQPHLQHGAFLTDYNNQADTTWQS	120
QY	121	QTMLAGVQYPSSINLTLLHLGKAFDITYVRLKFHTSRPESFALYKRTREDGWPWIPYQYISG	180
Db	121	QTMLAGVQYPSSINLTLLHLGKAFDITYVRLKFHTSRPESFALYKRTREDGWPWIPYQYISG	180
QY	181	SCENTYSKANRGFIRTGDEQQALCTDEPDSISPLTGNVAFSTLEGRPSAYNFDNSPVL	240
Db	181	SCENTYSKANRGFIRTGDEQQALCTDEPDSISPLTGNVAFSTLEGRPSAYNFDNSPVL	240
QY	241	QEWVTATDIRVTNRLNTFGDEVFNDPKVLKSYYYAISDFAVGRCCKNGHASECMKNEF	300
Db	241	QEWVTATDIRVTNRLNTFGDEVFNDPKVLKSYYYAISDFAVGRCCKNGHASECMKNEF	300
QY	301	DKLVCKNHTYGVDCCKLPFFNDRPWRATAESASECLPCDNGRSQECYFDPPELYRS	360
Db	301	DKLVCKNHTYGVDCCKLPFFNDRPWRATAESASECLPCDNGRSQECYFDPPELYRS	360
QY	361	TGHGGHCTNCQNTDGAHCERCENFFRLGNNEACSSCHSPVGSLSLTCDSYGRCSCKP	420
Db	361	TGHGGHCTNCQNTDGAHCERCENFFRLGNNEACSSCHSPVGSLSLTCDSYGRCSCKP	420
QY	421	GVMDKCDRCQPGFHSLTEAGRCPCSDPSGSDIECNVETGRCVKCDNVEGFNCERCCKPG	480
Db	421	GVMDKCDRCQPGFHSLTEAGRCPCSDPSGSDIECNVETGRCVKCDNVEGFNCERCCKPG	480
QY	481	FFNLESSNPRGCTPCFCFGHSSVCTNAVGYSVYSISSTFQIDEDGWRAEQRDGSEASLEW	540
Db	481	FFNLESSNPRGCTPCFCFGHSSVCTNAVGYSVYSISSTFQIDEDGWRAEQRDGSEASLEW	540
QY	541	SSERQDIAVISDSYFPRYFIAPAKFLGKQVLSYGQNLSEFSFRVDRDTRLAEDLVLEGA	600
Db	541	SSERQDIAVISDSYFPRYFIAPAKFLGKQVLSYGQNLSEFSFRVDRDTRLAEDLVLEGA	600
QY	601	GLRVSVPLIAQGNSTPSETTVKYVFRLHEATDYPWRPALTPPEFOKLNNLTISIKIRGTY	660
Db	601	GLRVSVPLIAQGNSTPSETTVKYVFRLHEATDYPWRPALTPPEFOKLNNLTISIKIRGTY	660
QY	661	SERSAGYLDVTLASARPGVPATWVESCTCPVGYGGQFCMCLSGYRRETNPNGPYSP	720
Db	661	SERSAGYLDVTLASARPGVPATWVESCTCPVGYGGQFCMCLSGYRRETNPNGPYSP	720
QY	721	CVLCACNGHSETCDPETGVCNCRDNTAGPHCEKCSGDYGYGDSTAGTSSDCQPCPCGGSS	780
Db	721	CVLCACNGHSETCDPETGVCNCRDNTAGPHCEKCSGDYGYGDSTAGTSSDCQPCPCGGSS	780
QY	781	CAVVPKTKEVVCTNCPTGTTGKRCCLCDDGYFGDPLGRNGPVRCLRCQCSDNIDPNAVG	840

Db	781	CAVVPKTKEVVCTNCPTGTTGKRCCLCDDGYFGDPLGRNGPVRCLRCQCSDNIDPNAVG	840
QY	841	NCNRLTGECLKCIYNTAGFYCDRCCKDGFFGNPLAPNPADKCKACNCNYPYGTMKQOSSCNP	900
Db	841	NCNRLTGECLKCIYNTAGFYCDRCCKDGFFGNPLAPNPADKCKACNCNYPYGTMKQOSSCNP	900
QY	901	VTGQCECLPHVTGQDCGACDPGFYNLQSGQGCERCDCCHALGSTNGQCDIRTGQCECQPGI	960
Db	901	VTGQCECLPHVTGQDCGACDPGFYNLQSGQGCERCDCCHALGSTNGQCDIRTGQCECQPGI	960
QY	961	TGQHCECERCEVNHFGFPGCKPCDCHPEGSLSLQCKDDGRCECREGVGNRCDCQCEENYF	1020
Db	961	TGQHCECERCEVNHFGFPGCKPCDCHPEGSLSLQCKDDGRCECREGVGNRCDCQCEENYF	1020
QY	1021	YNRSWPGCQCECPACYRLVKQKVADHRVKLQELLESILANLGTGDEMVTDOAFEDRLKEAER	1080
Db	1021	YNRSWPGCQCECPACYRLVKQKVADHRVKLQELLESILANLGTGDEMVTDOAFEDRLKEAER	1080
QY	1081	EVMDLLREAQDVQKVDQNLMDRLQRVNNTLSSQISRLQNIIRNTIETGNLAEQARAHVEN	1140
Db	1081	EVMDLLREAQDVQKVDQNLMDRLQRVNNTLSSQISRLQNIIRNTIETGNLAEQARAHVEN	1140
QY	1141	TERLIEIASRELEKAKVAAANVSVTQPESTGDPNNMTLLAEARKLAERHKQEAADDIVRV	1200
Db	1141	TERLIEIASRELEKAKVAAANVSVTQPESTGDPNNMTLLAEARKLAERHKQEAADDIVRV	1200
QY	1201	AKTANDTSTEAYNLLRLTLAGENQTAFAIEELNRKYEQAQKNIQDLEKQAARVHEEAKRA	1260
Db	1201	AKTANDTSTEAYNLLRLTLAGENQTAFAIEELNRKYEQAQKNIQDLEKQAARVHEEAKRA	1260
QY	1261	GDKAVEIYASVAQLSPLDSETLENEANNIKWEAENLEQLIDQKLKDYEDLREDMRGKELE	1320
Db	1261	GDKAVEIYASVAQLSPLDSETLENEANNIKWEAENLEQLIDQKLKDYEDLREDMRGKELE	1320
QY	1321	VKNLLEKGKTEQQTADQLLARADAAKALAEAAKGRDTLQEQANDILNNLKOFDRRVNDN	1380
Db	1321	VKNLLEKGKTEQQTADQLLARADAAKALAEAAKGRDTLQEQANDILNNLKOFDRRVNDN	1380
QY	1381	KTAAEEALRKIPAINQITTEANEKTRQAQALGSAADAAATEAKNKAHEAERIAASAVQKNA	1440
Db	1381	KTAAEEALRKIPAINQITTEANEKTRQAQALGSAADAAATEAKNKAHEAERIAASAVQKNA	1440
QY	1441	TSTKAAEAERTFAEVTDLNEVNNMLKQIQEAELKELKRKQDDADQDMMAGMASQAAQAEAE	1500
Db	1441	TSTKAAEAERTFAEVTDLNEVNNMLKQIQEAELKELKRKQDDADQDMMAGMASQAAQAEAE	1500
QY	1501	INARKAKNSVTSLSIINDLLEQLGLDVTDLNKLNEIEGTNLKAKDEMVKVSDLDLRKVSD	1560
Db	1501	INARKAKNSVTSLSIINDLLEQLGLDVTDLNKLNEIEGTNLKAKDEMVKVSDLDLRKVSD	1560
QY	1561	LENEAKKQEAAIMDYNRDIEEIMKDINLEDIRKTLPSGCFNTPSIEKP	1609
Db	1561	LENEAKKQEAAIMDYNRDIEEIMKDINLEDIRKTLPSGCFNTPSIEKP	1609

RESULT 7

AAB19802
ID AAB19802 standard; protein; 1576 AA.

XX AC AAB19802;

XX DT 05-MAR-2001 (first entry)

XX DE Human laminin 2 mature gamma-1 chain.

XX KW Laminin 2; human; nerve regeneration; angiogenic; cell adhesion; degenerative muscle disorder; muscular dystrophy; cell therapy.

XX OS Homo sapiens.

XX PN WO200066730-A2.

XX

PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US011378.
XX
PR 30-APR-1999; 99US-0131720P.
PR 15-JUN-1999; 99US-0139198P.
PR 12-JUL-1999; 99US-0143289P.
PR 24-SEP-1999; 99US-0155945P.
XX
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
PI Yurchenco P;
XX
XX WPI; 2000-687537/67.
DR N-PSDB; AAA88902.
XX
PT Purified laminin 2 protein, useful for research and therapeutic purposes
PT including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.
XX
PS Claim 5; Page 251-256; 305pp; English.
XX
CC The present sequence is that of human laminin 2 gamma-1 chain mature
CC protein. Laminin-2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and
CC gamma-1 (100 kDa) chains. It is thought to be specifically required for
CC stabilizing myotubes during skeletal muscle development, and for
CC preventing apoptosis. Genetic defects in its structure or expression are
CC associated with a major type of congenital muscular dystrophy. Laminin 2
CC is also thought to be important in Schwann cell/basal lamina
CC interactions. The invention provides laminin 2 alpha-2, beta-1 and gamma-
CC 1 chain polypeptides (see AAB19791-806) and the polynucleotides encoding
CC them (see AAA8891-906), methods for making recombinant laminin 2, cells
CC that express recombinant laminin 2, and methods for using purified
CC laminin 2 for research and therapeutic purposes including peripheral
CC nerve regeneration, treatment of degenerative muscle disorders,
CC angiogenesis regulation, promoting cell attachment and migration, ex vivo
CC cell therapy, improving the take of grafts, improving the
CC biocompatibility of medical devices and preparing improved culture
CC devices and media
XX
SQ Sequence 1576 AA;

Query Match 98.1%; Score 8544; DB 3; Length 1576;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 QAAMDECTDEGGRPQRCMPEFVNAFNTVVAATNTCGTPPEEYCVQTGVTGKTSCHLCD 93
Db 1 QAAMDECTDEGGRPQRCMPEFVNAFNTVVAATNTCGTPPEEYCVQTGVTGKTSCHLCD 60

QY 94 AGQPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYPPSSINLTLLHKGAFDITYVRLKFH 153
Db 61 AGQPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYPPSSINLTLLHKGAFDITYVRLKFH 120

QY 154 TSRPESFAIYKRTREDGPMIPYQYYSGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDIS 213
Db 121 TSRPESFAIYKRTREDGPMIPYQYYSGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDIS 180

QY 214 PLTGGNVAFSTLEGPRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSY 273
Db 181 PLTGGNVAFSTLEGPRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSY 240

QY 274 YYAISDFAVGGRCKNGHASECMKNEFDKLVCKNKHNTYGVDCCKLPFFNDRPWRATA 333
Db 241 YYAISDFAVGGRCKNGHASECMKNEFDKLVCKNKHNTYGVDCCKLPFFNDRPWRATA 300

QY 334 ESASECLPCDCNGRSQECYFDPPELYRSTGHGHCNTCQDNTDGAHCERCRCENFFRLGNNE 393
Db 301 ESASECLPCDCNGRSQECYFDPPELYRSTGHGHCNTCQDNTDGAHCERCRCENFFRLGNNE 360

QY 394 ACSSCHCSPVGSLSSTQCDSDYGRCSCKPGVMGDKCDRCQPGFHSLSLTAAGCRPCSCDPSGSI 453
Db 361 ACSSCHCSPVGSLSSTQCDSDYGRCSCKPGVMGDKCDRCQPGFHSLSLTAAGCRPCSCDPSGSI 420

QY 454 DECNVETGRCVCKDNVEGFNCERCKPGFFNLESSNPRGCTPCFCFHHSSVCTNAVGYSVY 513
Db 421 DECNVETGRCVCKDNVEGFNCERCKPGFFNLESSNPRGCTPCFCFHHSSVCTNAVGYSVY 480

QY 514 SISSTFQIDEDGWAEQORDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY 573
Db 481 SISSTFQIDEDGWAEQORDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY 540

QY 574 GQNLFSFRVDRRDLRLSAEDLVLEGAGLRVSVPLIAQGNISYPSSETTVKYVFRLEHATDY 633
Db 541 GQNLFSFRVDRRDLRLSAEDLVLEGAGLRVSVPLIAQGNISYPSSETTVKYVFRLEHATDY 600

QY 634 PWRPALTPPEFQKLLNLTSLIKIRGTYSERSAGYLDVTLASARPGPGVPATWVESCTCP 693
Db 601 PWRPALTPPEFQKLLNLTSLIKIRGTYSERSAGYLDVTLASARPGPGVPATWVESCTCP 660

QY 694 VGYGGQFCMCLSGYRRETPNLGPYSPCVLCAHGHSETCDPETGVNCNRDNTAGPHCEK 753
Db 661 VGYGGQFCMCLSGYRRETPNLGPYSPCVLCAHGHSETCDPETGVNCNRDNTAGPHCEK 720

QY 754 CSDGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKVVTNCPTGTTGKRCCLDDGYFG 813
Db 721 CSDGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKVVTNCPTGTTGKRCCLDDGYFG 780

QY 814 DPLGRNGPVRLCRLCQCSNIDPNAVGNLRTGECILKCIYNTAGFYCDRCCKDGFPGNPL 873
Db 781 DPLGRNGPVRLCRLCQCSNIDPNAVGNLRTGECILKCIYNTAGFYCDRCCKDGFPGNPL 840

QY 874 AENPADKCKACNPNPYGTWKQSSCNFVTGQCECLPHVTGQDCGACDPPGFYNLQSGQCE 933
Db 841 AENPADKCKACNPNPYGTWKQSSCNFVTGQCECLPHVTGQDCGACDPPGFYNLQSGQCE 900

QY 934 RCDHALGSTNGQCDIRTGQCECQPGITGOHCERCERNHFGFEGEGCKPCDCHPEGSLSL 993
Db 901 RCDHALGSTNGQCDIRTGQCECQPGITGOHCERCERNHFGFEGEGCKPCDCHPEGSLSL 960

QY 994 QCKDDGRCECREGFGVGNRCDCQCEENYFYNRSWPGCQPCACRYLVKDKVADHRVKLQELE 1053
Db 961 QCKDDGRCECREGFGVGNRCDCQCEENYFYNRSWPGCQPCACRYLVKDKVADHRVKLQELE 1020

QY 1054 SLIANLGTGDEMVTDOAFEDRLKEAREVMDLLREAQDKVDQONLMDRLQRVNNTLSSQ 1113
Db 1021 SLIANLGTGDEMVTDOAFEDRLKEAREVMDLLREAQDKVDQONLMDRLQRVNNTLSSQ 1080

QY 1114 ISRLQNIIRNTIETGNLAEOARAHVENTERLIEIASRELEKAKAAANVSVTQPESTGDP 1173
Db 1081 ISRLQNIIRNTIETGNLAEOARAHVENTERLIEIASRELEKAKAAANVSVTQPESTGDP 1140

QY 1174 NNMTLLAEAEARKLAERHKQAEADDIVRVAKTANDTSTEAYNLLRLTLAGEQTAFIEELN 1233
Db 1141 NNMTLLAEAEARKLAERHKQAEADDIVRVAKTANDTSTEAYNLLRLTLAGEQTAFIEELN 1200

QY 1234 RKYEOAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPLDSETLENEANNIKMEA 1293
Db 1201 RKYEOAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPLDSETLENEANNIKMEA 1260

QY 1294 ENLEQLIDQKLKDYEDLREDVRGKELEVKNLLEKGTQQTADQLLARADAALAEAA 1353
Db 1261 ENLEQLIDQKLKDYEDLREDVRGKELEVKNLLEKGTQQTADQLLARADAALAEAA 1320

QY 1354 KKGRDITLQEAANDILNLLKDFRRVNDNKTAAEEALRKIPAINQTIITEANEKTRAQOALG 1413
Db 1321 KKGRDITLQEAANDILNLLKDFRRVNDNKTAAEEALRKIPAINQTIITEANEKTRAQOALG 1380

QY 1414 SAAADATEAKNKAHEARIASAVQKNATSTKAEARTFAEVTDLDNEVNNMLKQLQAEK 1473
Db 1381 SAAADATEAKNKAHEARIASAVQKNATSTKAEARTFAEVTDLDNEVNNMLKQLQAEK 1440

QY 1474 ELKRRQDDADQDMMAGMASQAAQAEAEINARKAKNSVTSLLSIINDLLEQLGOLDTVDLN 1533
Db 1441 ELKRRQDDADQDMMAGMASQAAQAEAEINARKAKNSVTSLLSIINDLLEQLGOLDTVDLN 1500

QY 1534 KLINEIEGTLNKADEMKSVDLDRKVSLENEAKQBAAIMDYNRDIEEIMKDIRNLEDIR 1593
Db 1501 KLINEIEGTLNKADEMKSVDLDRKVSLENEAKQBAAIMDYNRDIEEIMKDIRNLEDIR 1560
QY 1594 KTLPSGCFNTPSIEKP 1609
Db 1561 KTLPSGCFNTPSIEKP 1576

RESULT 8
AAB48453
ID AAB48453 standard; protein; 1576 AA.
XX AAB48453;
XX AC
XX DT 02-MAR-2001 (first entry)
XX Human laminin 8 polypeptide, SEQ ID NO: 24.
XX Human; laminin 8; neuroprotective; angiogenic; osteopathic;
KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;
KW vascular tissue injury; neural injury; angiogenesis regulation.
XX Homo sapiens.

XX WO200066732-A2.
XX 09-NOV-2000.
XX 28-APR-2000; 2000WO-US011543.
XX 30-APR-1999; 99US-0131720P.
XX 21-AUG-1999; 99US-0149738P.
XX 24-SEP-1999; 99US-0155945P.
XX 11-FEB-2000; 2000US-0182012P.

PA (BIOS-) BIOSTRATUM INC.
XX Kortessmaa J, Tryggvason K;
PI WPI; 2000-687539/67.
XX N-PSDB; AAC83714.
DR Purified laminin 8 protein, useful for research and therapeutic purposes
PT including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.
XX Claim 5; Page 214-218; 245pp; English.

XX The present sequence is a laminin 8 polypeptide chain. Laminins are a
CC family of heterotrimeric glycoproteins that function via binding
CC interactions with neighbouring cell receptors and by forming laminin
CC networks. They are signalling molecules which influence cellular
CC function. Laminin 8 is useful for treating injuries to tissue of
CC mesenchymal origin, such as bone, cartilage, tendon, and ligament,
CC treating injuries to vascular tissue, promoting cell attachment and
CC migration, ex vivo cell therapy, improving the biocompatibility of
CC medical devices, and preparing improved cell culture devices and media.
CC Laminin 8 is also useful for promoting re-endothelialisation at the site
CC of vascular injuries, improving the take of grafts, improving the
CC biocompatibility of medical devices, treating neural injuries (neural
CC regeneration), regulating angiogenesis, and promoting cell attachment and
XX migration

SQ Sequence 1576 AA;

Query Match 98.1%; Score 8544; DB 3; Length 1576;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 QAAMDECTDEGRPQRCMPEFVNAAFNVTVATNTCGTPPEEYCVQGTGVTKSCHLCD 93
Db 1 QAAMDECTDEGRPQRCMPEFVNAAFNVTVATNTCGTPPEEYCVQGTGVTKSCHLCD 60

QY 94 ACQPHLOHGAFLTDYNNQADTTWQSQTMLAGVQYFSSINLTLLHLGKAFDITYVRLKEH 153
Db 61 ACQPHLOHGAFLTDYNNQADTTWQSQTMLAGVQYFSSINLTLLHLGKAFDITYVRLKEH 120
QY 154 TSRPESFAIYKRTREDEGPWIPYQYYSGCCENTYSKANRGFIRTTGGDEQQALCTDEFSDIS 213
Db 121 TSRPESFAIYKRTREDEGPWIPYQYYSGCCENTYSKANRGFIRTTGGDEQQALCTDEFSDIS 180
QY 214 PLTGGNVAFSTLEGRPSAYNFNDNSPVLQEWVTATDIRVTNLRLNTFGDEVNDPKVLKSY 273
Db 181 PLTGGNVAFSTLEGRPSAYNFNDNSPVLQEWVTATDIRVTNLRLNTFGDEVNDPKVLKSY 240
QY 274 YYAISDFAVGGRCKCNHGHASECMKNEFDKLVCNCKHNTYGVDCCKLCPFFNDRPWRATA 333
Db 241 YYAISDFAVGGRCKCNHGHASECMKNEFDKLVCNCKHNTYGVDCCKLCPFFNDRPWRATA 300
QY 334 ESASECLPCDCNGRSQECYFDPPELYRSTGHGHCTNCQDNTDGAHCRCRENFRLGNNE 393
Db 301 ESASECLPCDCNGRSQECYFDPPELYRSTGHGHCTNCQDNTDGAHCRCRENFRLGNNE 360
QY 394 ACSSCHCSPVGSLSSTQCDSYGRCSCKPGVMGDKDRCQPGFHSLTEAGCRPCSCDPSGSI 453
Db 361 ACSSCHCSPVGSLSSTQCDSYGRCSCKPGVMGDKDRCQPGFHSLTEAGCRPCSCDPSGSI 420
QY 454 DECNVETGRCVCKONVEGFNCERCKPGFFNFLESNPRGCTPCFCFHHSSVCTNAVGYSVY 513
Db 421 DECNVETGRCVCKONVEGFNCERCKPGFFNFLESNPRGCTPCFCFHHSSVCTNAVGYSVY 480
QY 514 SISSTFQIDEDGWAEQRDCSEASLEWSSERQDIAVISDSYFPFYFIAPAKFLGKQVLSY 573
Db 481 SISSTFQIDEDGWAEQRDCSEASLEWSSERQDIAVISDSYFPFYFIAPAKFLGKQVLSY 540
QY 574 GQNLSPFRVDRRDLRLSAEDLVLEGAGLRVSVPLIAQNSYPSSETTVKYVFRLHEATDY 633
Db 541 GQNLSPFRVDRRDLRLSAEDLVLEGAGLRVSVPLIAQNSYPSSETTVKYVFRLHEATDY 600
QY 634 PWRPALTPEFEQKLLNLTSIKIRGTYSERSAGYLDVTLASARPGPGVPATWVESCTCP 693
Db 601 PWRPALTPEFEQKLLNLTSIKIRGTYSERSAGYLDVTLASARPGPGVPATWVESCTCP 660
QY 694 VGYGQFCMCLSGYRRETNLGPYSPCVLCACNGHSETCDPETGVNCNRDNTAGPHCEK 753
Db 661 VGYGQFCMCLSGYRRETNLGPYSPCVLCACNGHSETCDPETGVNCNRDNTAGPHCEK 720
QY 754 CSDGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKVVTNCPTGTTGKRCCLDDGYFG 813
Db 721 CSDGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKVVTNCPTGTTGKRCCLDDGYFG 780
QY 814 DPLGRNGPVLRLCQCSDNIDPNAVGNLRTGECLKCIYNTAGFYCDRCCKDGFNPL 873
Db 781 DPLGRNGPVLRLCQCSDNIDPNAVGNLRTGECLKCIYNTAGFYCDRCCKDGFNPL 840
QY 874 APNPADKCKACNPNFYGTMKQSSCNPNVTGQCECLPHVTGQDCGACDPGFYNLQSGQCE 933
Db 841 APNPADKCKACNPNFYGTMKQSSCNPNVTGQCECLPHVTGQDCGACDPGFYNLQSGQCE 900
QY 934 RCDCHALGSTNGQCDIRTGQCECQPGITGOHCERCEVNHFGFEGCKPCDCHPEGSLSL 993
Db 901 RCDCHALGSTNGQCDIRTGQCECQPGITGOHCERCEVNHFGFEGCKPCDCHPEGSLSL 960
QY 994 QCKDDGRCECREGFGVGNRCDQCEENYFYNRSWPGCQCECPACYRLVKDKVADHRVKLQBLE 1053
Db 961 QCKDDGRCECREGFGVGNRCDQCEENYFYNRSWPGCQCECPACYRLVKDKVADHRVKLQBLE 1020
QY 1054 SLIANLTGDEMVTDOAFEDRLKEAREVMDLLREAOQVKDQVQDQNLMDRLQVRNNTLSQ 1113
Db 1021 SLIANLTGDEMVTDOAFEDRLKEAREVMDLLREAOQVKDQVQDQNLMDRLQVRNNTLSQ 1080
QY 1114 ISRLQNIIRNTIETGNLAEOQRAHVENTERLIEIASRELEKAKAAANVSVTQPESTGDP 1173
Db 1081 ISRLQNIIRNTIETGNLAEOQRAHVENTERLIEIASRELEKAKAAANVSVTQPESTGDP 1140

QY 1174 NMWLLAEARKLAERHKEADDDIVRVAKTANDTSTAYNLLRLTLAGENQTAFAIEELN 1233
Db 1141 NMWLLAEARKLAERHKEADDDIVRVAKTANDTSTAYNLLRLTLAGENQTAFAIEELN 1200
QY 1234 RKYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDSELENEANNIKMEA 1293
Db 1201 RKYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDSELENEANNIKMEA 1260
QY 1294 ENLEQLIDQKLKDYEDLREDMRGKELEVKNLLEKKGTEQQTADQLLARADAAKALAEAA 1353
Db 1261 ENLEQLIDQKLKDYEDLREDMRGKELEVKNLLEKKGTEQQTADQLLARADAAKALAEAA 1320
QY 1354 KKGRTDLOEANDILNNLKDFDRRVNDNKTAAEBEALRKIPAINQTTITEANEKTRAQQALG 1413
Db 1321 KKGRTDLOEANDILNNLKDFDRRVNDNKTAAEBEALRKIPAINQTTITEANEKTRAQQALG 1380
QY 1414 SAAADATEAKNKAHEAERIAASAVQKNATSTKAEAEARTFAEVTDLNEVNNMLKQLOEAEK 1473
Db 1381 SAAADATEAKNKAHEAERIAASAVQKNATSTKAEAEARTFAEVTDLNEVNNMLKQLOEAEK 1440
QY 1474 ELKRKQDDADQDMMAGMASQAAQAEAEINAKKAKNSVTSLLSIINDLLEQLGQLDTVDLN 1533
Db 1441 ELKRKQDDADQDMMAGMASQAAQAEAEINAKKAKNSVTSLLSIINDLLEQLGQLDTVDLN 1500
QY 1534 KLNEIEGTNLKAKDEMKSVDLDRKVSQDLENAKQAEAAIMDYNRDIIEIMKDORNLEDIR 1593
Db 1501 KLNEIEGTNLKAKDEMKSVDLDRKVSQDLENAKQAEAAIMDYNRDIIEIMKDORNLEDIR 1560
QY 1594 KTLPSGCFNTPSIEKP 1609
Db 1561 KTLPSGCFNTPSIEKP 1576

RESULT 9

ABB81595
ID ABB81595 standard; protein; 1576 AA.

AC ABB81595;

XX 19-SEP-2002 (first entry)

XX Human laminin 10 third chain protein sequence SEQ ID NO:16.

XX Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;
KW tissue repair development; laminin; healing; vascular tissue;
KW re-endothelialisation; vascular injury; cell attachment; cell stasis;
KW proliferation; migration.

XX Homo sapiens.

PN WO200250111-A2.

XX 27-JUN-2002.

PF 21-DEC-2001; 2001WO-US051035.

XX 21-DEC-2000; 2000US-0257449P.

PR 28-MAR-2001; 2001US-0279282P.

PR 13-NOV-2001; 2001US-00279282.

XX (BIOS-) BIOSTRATUM INC.

XX Tryggvason K, Doi M, Thyboll J;

PI WPI; 2002-557650/59.

XX N-PSDB; ABQ72913.

XX New human laminin-10 proteins, useful for accelerating the healing of
PT vascular tissue, improving the biocompatibility of grafts, or for
PT promoting re-endothelialization at the site of vascular injuries.

XX Claim 9; Page 177-182; 231pp; English.

PS

CC The present invention describes human laminin alpha 5. Also described is
CC an isolated laminin 10. Laminin 10 has vulnery activity. Laminins are
CC useful in maintaining cell/tissue phenotype as well as promoting cell
CC growth and differentiation in tissue repair development. Specifically,
CC laminin 10 can be used for accelerating the healing injuries of vascular
CC tissue, improving the biocompatibility of grafts useful for treating such
CC injuries, for promoting re-endothelialisation at the site of vascular
CC injuries, and promote cell attachment and subsequent cell stasis,
CC proliferation, differentiation, and/or migration. The present sequence
CC represents a third chain protein of laminin 10, from the present
CC invention

XX
SQ Sequence 1576 AA;

Query Match 98.1%; Score 8544; DB 5; Length 1576;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 QAAMDECTDEGGRPQRCMPEFVNAFNTVVAINTCGTPPEYCVQGTGVTGTSCHLCD 93
Db 1 QAAMDECTDEGGRPQRCMPEFVNAFNTVVAINTCGTPPEYCVQGTGVTGTSCHLCD 60
QY 94 AGQPHLQHGAFLTDYNNQADTTWQSQTMLAGVQYPPSSINLTHLGKAFDITYVRLKFH 153
Db 61 AGQPHLQHGAFLTDYNNQADTTWQSQTMLAGVQYPPSSINLTHLGKAFDITYVRLKFH 120
QY 154 TSRPESFAIYKRTREDGPWIPYQYYSGSCENTYSKANRGFIRTGDEQALCTDEFSDIS 213
Db 121 TSRPESFAIYKRTREDGPWIPYQYYSGSCENTYSKANRGFIRTGDEQALCTDEFSDIS 180
QY 214 PLTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVENDPKVLKSY 273
Db 181 PLTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVENDPKVLKSY 240
QY 274 YYAISDFAVGGRCCKNGHASECMKNEFDKLVCKNCKHNTYGVDCCKLPFFNDRPWRATA 333
Db 241 YYAISDFAVGGRCCKNGHASECMKNEFDKLVCKNCKHNTYGVDCCKLPFFNDRPWRATA 300
QY 334 ESASECLPCDCNGRSQECYFDPELYRSTGHGHCNTCQDNTDGAHCERENFFRLGNNE 393
Db 301 ESASECLPCDCNGRSQECYFDPELYRSTGHGHCNTCQDNTDGAHCERENFFRLGNNE 360
QY 394 ACSSCHCSPVGSLSQCDSSYGRCSCKPGVMGDKDCRCQPGFHSLTEAGRPCSCDPSGSI 453
Db 361 ACSSCHCSPVGSLSQCDSSYGRCSCKPGVMGDKDCRCQPGFHSLTEAGRPCSCDPSGSI 420
QY 454 DECNVETGRCVCCKDNVEGFNCERCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGYSVY 513
Db 421 DECNVETGRCVCCKDNVEGFNCERCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGYSVY 480
QY 514 SISSTFQIDEDGWAEQRDSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY 573
Db 481 SISSTFQIDEDGWAEQRDSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY 540
QY 574 GQNLSPSFRVDRRTRLAEDLVLEGAGLEVSVPLIAQGNYSYPSETTVKYVFRLHEATDY 633
Db 541 GQNLSPSFRVDRRTRLAEDLVLEGAGLEVSVPLIAQGNYSYPSETTVKYVFRLHEATDY 600
QY 634 PWRPALTPEFFQKLLNNLTSTIKIRGTYSERSAGYLDVTLASARPGVGPATWVESCTCP 693
Db 601 PWRPALTPEFFQKLLNNLTSTIKIRGTYSERSAGYLDVTLASARPGVGPATWVESCTCP 660
QY 694 VGYGGQFCMCLSGYRRETPNLGPYSPCVLCAACNGHSETCDPETGVCNCRDNTAGPHCEK 753
Db 661 VGYGGQFCMCLSGYRRETPNLGPYSPCVLCAACNGHSETCDPETGVCNCRDNTAGPHCEK 720
QY 754 CSDGYGDDSTAGTSSDCCQPCPCGGSSCAVVPKTKEVVCTNCPTGTTGKRCCELCDGDFG 813
Db 721 CSDGYGDDSTAGTSSDCCQPCPCGGSSCAVVPKTKEVVCTNCPTGTTGKRCCELCDGDFG 780
QY 814 DPLGRNGVPVRLCRLCQCSNDIDPNVAGNCRNLTGECCLKCIYNTAGFYCDRCKDGGFFGNPL 873
Db 781 DPLGRNGVPVRLCRLCQCSNDIDPNVAGNCRNLTGECCLKCIYNTAGFYCDRCKDGGFFGNPL 840

QY 874 APNPADKCKACNCNPYGTMTKQSSCNPNVPTGQCECLPHVTGQDCGACDPGFYNLQSGQGCE 933
Db 841 APNPADKCKACNCNPYGTMTKQSSCNPNVPTGQCECLPHVTGQDCGACDPGFYNLQSGQGCE 900
QY 934 RCDCHALGSTNGQCDIRTGQCECOPGITGQHCHERCCEVNHFGFEGCKPCDCHPEGSLSL 993
Db 901 RCDCHALGSTNGQCDIRTGQCECOPGITGQHCHERCCEVNHFGFEGCKPCDCHPEGSLSL 960
QY 994 QCKDDGRCCEGREGVGNRCDOCEENYFYNRSWPGCECPACRYLVKDKVADHRVKLQELE 1053
Db 961 QCKDDGRCCEGREGVGNRCDOCEENYFYNRSWPGCECPACRYLVKDKVADHRVKLQELE 1020
QY 1054 SLIANLGTGDEMVTDOAFEDRLKEAREVMDLLREAOQVXDQVNDQNLMDRLQRVNNTLSSQ 1113
Db 1021 SLIANLGTGDEMVTDOAFEDRLKEAREVMDLLREAOQVXDQVNDQNLMDRLQRVNNTLSSQ 1080
QY 1114 ISRLQNRNTIETGTLAEQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1173
Db 1081 ISRLQNRNTIETGTLAEQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1140
QY 1174 NNMNTLLAEARKLAERHKQEAADDIVRVAKTANDTSTEAYNLLRLTLAGENQTAFFIEELN 1233
Db 1141 NNMNTLLAEARKLAERHKQEAADDIVRVAKTANDTSTEAYNLLRLTLAGENQTAFFIEELN 1200
QY 1234 RKYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQISPLDSETLENEANNIKMEA 1293
Db 1201 RKYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQISPLDSETLENEANNIKMEA 1260
QY 1294 ENLEQLIDQKLDYEDLREDMRGKELEVKNLLEKKGTEQQTADQLLARADAAKALAEAA 1353
Db 1261 ENLEQLIDQKLDYEDLREDMRGKELEVKNLLEKKGTEQQTADQLLARADAAKALAEAA 1320
QY 1354 KKGRTDLOEANDILNNLKDFDRRVNDNKTAAEEALRKIPAINQITITEANEKTRAQQAALG 1413
Db 1321 KKGRTDLOEANDILNNLKDFDRRVNDNKTAAEEALRKIPAINQITITEANEKTRAQQAALG 1380
QY 1414 SAAADATEAKNKAHEAERIAASAVQKNATSTKAEARTFAEVTDLDDNEVNNMLKQLQEAKE 1473
Db 1381 SAAADATEAKNKAHEAERIAASAVQKNATSTKAEARTFAEVTDLDDNEVNNMLKQLQEAKE 1440
QY 1474 ELKRKQDDADQDMMAGMASQAAQAEAINARKAKNSVTSLLSIINDLLEQLGLDVTVDLN 1533
Db 1441 ELKRKQDDADQDMMAGMASQAAQAEAINARKAKNSVTSLLSIINDLLEQLGLDVTVDLN 1500
QY 1534 KLNEIEGTLNKAKDEMKVSDLRKVSDDLNEAKKQEAALMDYNRDIEEIMKDIRNLEDIR 1593
Db 1501 KLNEIEGTLNKAKDEMKVSDLRKVSDDLNEAKKQEAALMDYNRDIEEIMKDIRNLEDIR 1560
QY 1594 KTLPSGCFNTPSIEKP 1609
Db 1561 KTLPSGCFNTPSIEKP 1576

RESULT 10
AAB19804
ID AAB19804 standard; protein; 1584 AA.

XX AC AAB19804;
XX 05-MAR-2001 (first entry)
DT Human laminin 2 gamma-1 chain with C-terminal FLAG epitope.
DE Laminin 2; human; nerve regeneration; angiogenic; cell adhesion;
XX KW degenerative muscle disorder; muscular dystrophy; cell therapy.
XX OS Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 1..33
FT /label= Signal_peptide
FT Protein 34..1609

FT Peptide /label= Mature_protein
FT 1610..1617
XX /label= FLAG
PN WO200066730-A2.
XX 09-NOV-2000.
XX 28-APR-2000; 2000WO-US011378.
XX 30-APR-1999; 99US-0131720P.
PR 15-JUN-1999; 99US-0139198P.
PR 12-JUL-1999; 99US-0143289P.
PR 24-SEP-1999; 99US-0155945P.
XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX Yurchenco P;
XX WPI; 2000-687537/67.
XX N-PSDB; AAA88904.

Purified laminin 2 protein, useful for research and therapeutic purposes including peripheral nerve regeneration, treatment of degenerative muscle disorders, angiogenesis regulation, and ex vivo cell therapy.
Claim 5; Page 275-280; 305pp; English.

The present sequence is that of the mature gamma-1 chain of human laminin 2, with an additional C-terminal FLAG epitope, resulting from expression in transfected cells from mammalian expression vectors. Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1 (100 kDa) chains. It is thought to be specifically required for stabilizing myotubes during skeletal muscle development, and for preventing apoptosis. Genetic defects in its structure or expression are associated with a major type of congenital muscular dystrophy. Laminin 2 is also thought to be important in Schwann cell/basal lamina interactions. The invention provides laminin 2 alpha-2, beta-1 and gamma-1 chain polypeptides (see AAB19791-806) and the polynucleotides encoding them (see AAA8891-906), methods for making recombinant laminin 2, cells that express recombinant laminin 2, and methods for using purified laminin 2 for research and therapeutic purposes including peripheral nerve regeneration, treatment of degenerative muscle disorders, angiogenesis regulation, promoting cell attachment and migration, ex vivo cell therapy, improving the take of grafts, improving the biocompatibility of medical devices and preparing improved culture devices and media

Sequence 1584 AA;

Query Match 98.1%; Score 8544; DB 3; Length 1584;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 QAAMDECTDEGGRPQRCMPEFVNAAFNVTVAATNTCGTPPEEYCVQGTGVTGTSCHLCD 93
Db 1 QAAMDECTDEGGRPQRCMPEFVNAAFNVTVAATNTCGTPPEEYCVQGTGVTGTSCHLCD 60
QY 94 AGQPHLQHGAFLTDYNNQADTTWQSQTMLAGVQYPPSSINLTLLHKGAFDITYVRLKEH 153
Db 61 AGQPHLQHGAFLTDYNNQADTTWQSQTMLAGVQYPPSSINLTLLHKGAFDITYVRLKEH 120
QY 154 TSRPESFAIYKRTREDGWPWIPYQYSGSCENTYSKANRGFTRTGGDEQQAALCTDEFSDIS 213
Db 121 TSRPESFAIYKRTREDGWPWIPYQYSGSCENTYSKANRGFTRTGGDEQQAALCTDEFSDIS 180
QY 214 PLTGGNVAFSTLEGRPSAYNFNDSVPLQEWVTATDIRVTNLRLNTFGDEVNDPKVLKSY 273
Db 181 PLTGGNVAFSTLEGRPSAYNFNDSVPLQEWVTATDIRVTNLRLNTFGDEVNDPKVLKSY 240
QY 274 YYAISDFAVGGRCKCNGHASECMKNEFDKLVNCCKHNTYGVDCCKLPPFNDRPWRATA 333
Db 241 YYAISDFAVGGRCKCNGHASECMKNEFDKLVNCCKHNTYGVDCCKLPPFNDRPWRATA 300

QY 334 ESASECLPCDNGRSQECYFDPELYRSTGHGHCTNCQDNTDGAHCERENFFRLGNNE 393
Db 301 ESASECLPCDNGRSQECYFDPELYRSTGHGHCTNCQDNTDGAHCERENFFRLGNNE 360
QY 394 ACSSCHCSPVGSLSLTCDSYGRCSCKPGVMDKCDRCQPGFHSILTEAGCRPCSCDPSGSI 453
Db 361 ACSSCHCSPVGSLSLTCDSYGRCSCKPGVMDKCDRCQPGFHSILTEAGCRPCSCDPSGSI 420
QY 454 DECNVETGRCVKDNVEGFNCERCKPGFPNLESSNPRGCTPCFCGHSSVCTNAVGVSY 513
Db 421 DECNVETGRCVKDNVEGFNCERCKPGFPNLESSNPRGCTPCFCGHSSVCTNAVGVSY 480
QY 514 SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY 573
Db 481 SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY 540
QY 574 QNLSFSFRVDRDTRLSEAEDLVLEGAGLRVSVPLIAQGNSYPSETTVKYVFLRHEATDY 633
Db 541 QNLSFSFRVDRDTRLSEAEDLVLEGAGLRVSVPLIAQGNSYPSETTVKYVFLRHEATDY 600
QY 634 PWRPALTPFEFQKLLNNLTSIKIRGTYSERSAGYLDVTLASARPGVPATWVESCCTCP 693
Db 601 PWRPALTPFEFQKLLNNLTSIKIRGTYSERSAGYLDVTLASARPGVPATWVESCCTCP 660
QY 694 VYGGQFCFEMCLSGYRRETPLNPGYSPCVLCACNGHSETCDPETGVCNCRDNTAGPHCEK 753
Db 661 VYGGQFCFEMCLSGYRRETPLNPGYSPCVLCACNGHSETCDPETGVCNCRDNTAGPHCEK 720
QY 754 CSDGYGDSGTAGTSSDCQPCPCPGSSCAVVPKTEKVVCTNCPTGTGKRCCELCDGDFYFG 813
Db 721 CSDGYGDSGTAGTSSDCQPCPCPGSSCAVVPKTEKVVCTNCPTGTGKRCCELCDGDFYFG 780
QY 814 DPLGRNGPVRRLCRLCQSDNIDPNAVGNCRNLTGECLKCIYNTAGFYCDRCCKDGGFFGNPL 873
Db 781 DPLGRNGPVRRLCRLCQSDNIDPNAVGNCRNLTGECLKCIYNTAGFYCDRCCKDGGFFGNPL 840
QY 874 APNPADKCKACNCPYGTMKQOSSCNPTVGTQCECLPHVTGQDCGACDPGFYNLQSGQGCE 933
Db 841 APNPADKCKACNCPYGTMKQOSSCNPTVGTQCECLPHVTGQDCGACDPGFYNLQSGQGCE 900
QY 934 RCDCHALGSTNGQCDIRTGQCECQPGITGQHGERCEVNHFGFPEGCKPCDCHPEGSLSL 993
Db 901 RCDCHALGSTNGQCDIRTGQCECQPGITGQHGERCEVNHFGFPEGCKPCDCHPEGSLSL 960
QY 994 QCKDDGRCECREGFVGNRCDQCEENYFYNRSPGCGCEPCACYRLVKDVADHRVKLQLE 1053
Db 961 QCKDDGRCECREGFVGNRCDQCEENYFYNRSPGCGCEPCACYRLVKDVADHRVKLQLE 1020
QY 1054 SLIANLGTGDEMVTDOAFEDRLKEAEREVMDLLREAOQDVQDQNLMDRLQRVNNTLSSQ 1113
Db 1021 SLIANLGTGDEMVTDOAFEDRLKEAEREVMDLLREAOQDVQDQNLMDRLQRVNNTLSSQ 1080
QY 1114 ISRLQIRNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1173
Db 1081 ISRLQIRNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1140
QY 1174 NNMVLLAEARKLAERHKQEAADDIVRVAKTANDTSTEAYNLLRLTAGENQTAFAIEELN 1233
Db 1141 NNMVLLAEARKLAERHKQEAADDIVRVAKTANDTSTEAYNLLRLTAGENQTAFAIEELN 1200
QY 1234 RKVEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPLDSETLENEANNIKMEA 1293
Db 1201 RKVEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPLDSETLENEANNIKMEA 1260
QY 1294 ENLEQLIDQKLKOYEDLREDMRGKELEVKNLLEKGTQEQQTADQLLARADAAKALAEAAA 1353
Db 1261 ENLEQLIDQKLKOYEDLREDMRGKELEVKNLLEKGTQEQQTADQLLARADAAKALAEAAA 1320
QY 1354 KKGRDTLQEANDILNLLKDFRRVNDNKTAAEEALRKIPAINQTTITEANEKTRAAQALG 1413
Db 1321 KKGRDTLQEANDILNLLKDFRRVNDNKTAAEEALRKIPAINQTTITEANEKTRAAQALG 1380
QY 1414 SAAADATEAKNKAHEAERIAASAVQKNATSTKAEARTFAEVTDLDNVNNMLKQLQEA 1473

Db 1381 SAAADATEAKNKAHEAERIAASAVQKNATSTKAEARTFAEVTDLDNVNNMLKQLQEA 1440
QY 1474 ELKRKQDDADQDMMAGMASQAAQAEINARKAKNSVTSLSIINDLLEQLGQLDTVDLN 1533
Db 1441 ELKRKQDDADQDMMAGMASQAAQAEINARKAKNSVTSLSIINDLLEQLGQLDTVDLN 1500
QY 1534 KLNEIEGTLNKADEMKSVDLDRKVSLENEAKKQEAAMVYNRDIEEIMKDINLEDIR 1593
Db 1501 KLNEIEGTLNKADEMKSVDLDRKVSLENEAKKQEAAMVYNRDIEEIMKDINLEDIR 1560
QY 1594 KTLPSGCFNTPSIEKP 1609
Db 1561 KTLPSGCFNTPSIEKP 1576
RESULT 11
AAB19805
ID AAB19805 standard; protein; 1605 AA.
XX
AC AAB19805;
XX
DT 05-MAR-2001 (first entry)
XX
DE Mouse laminin 2 gamma-1 chain.
XX
KW Laminin 2; mouse; nerve regeneration; angiogenic; cell adhesion; degenerative muscle disorder; muscular dystrophy; cell therapy.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Peptide 1..33
FT Protein /label= Signal_peptide
FT /label= Mature_protein 34..1605
XX
PN WO200066730-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US011378.
XX
PR 30-APR-1999; 99US-0131720P.
PR 15-JUN-1999; 99US-0139198P.
PR 12-JUL-1999; 99US-0143289P.
PR 24-SEP-1999; 99US-0155945P.
XX
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
PI Yurchenco P;
XX
DR WPI; 2000-687537/67.
XX N-PSDB; AAA88905.
PT Purified laminin 2 protein, useful for research and therapeutic purposes including peripheral nerve regeneration, treatment of degenerative muscle disorders, angiogenesis regulation, and ex vivo cell therapy.
XX
PS Claim 5; Page 288-294; 305pp; English.
XX
CC The present sequence is that of the gamma-1 chain of mouse laminin 2. Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1 (100 kDa) chains. It is thought to be specifically required for stabilizing myotubes during skeletal muscle development, and for preventing apoptosis. Genetic defects in human laminin 2 structure or expression are associated with a major type of congenital muscular dystrophy. Laminin 2 is also thought to be important in Schwann cell/basal lamina interactions. The invention provides laminin 2 alpha-2, beta-1 and gamma-1 chain polypeptides (see AAB19791-806) and the polynucleotides encoding them (see AAA8891-906); methods for making recombinant laminin 2, cells that express recombinant laminin 2, and methods for using purified laminin 2 for research and therapeutic

CC purposes including peripheral nerve regeneration, treatment of
CC degenerative muscle disorders, angiogenesis regulation, promoting cell
CC attachment and migration, ex vivo cell therapy, improving the take of
CC grafts, improving the biocompatibility of medical devices and preparing
CC improved culture devices and media
XX
SQ Sequence 1605 AA;
Query Match 93.5%; Score 8148; DB 3; Length 1605;
Best Local Similarity 92.8%; Pred. No. 0;
Matches 1493; Conservative 59; Mismatches 53; Indels 4; Gaps 3;
QY 1 MRGSHRAAPALRPRGRLLWPVLAVLAAAAAGCAQAAMDECTDEGGRPQRCMPEFVNAAFN 60
Db 1 MTGGRAALALQPRGRLLWPLLAVL--AAVAGCVRAAMDECADEGGRPQRCMPEFVNAAFN 58
QY 61 VTVVATNTCGTPPEEYCVQGTGVTGSKSCHLCDAGQPHLQHGAAFLTDYNNQADTTWQOS 120
Db 59 VTVVATNTCGTPPEEYCVQGTGVTGSKSCHLCDAGQPHLQHGAAFLTDYNNQADTTWQOS 118
QY 121 QTMLAGVQYSSINLTILHLGKAFDITYVRLKFHTSRPESFAIYKRTREDGPWIPYQYYSG 180
Db 119 QTMLAGVQYSPNSINLTILHLGKAFDITYVRLKFHTSRPESFAIYKRTREDGPWIPYQYYSG 178
QY 181 SCENTYSKANRGFIRTTGGDEQQALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFDSNPSVL 240
Db 179 SCENTYSKANRGFIRTTGGDEQQALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFDSNPSVL 238
QY 241 QEWVTATDIRVTNLRLNTFGDEVNDPKVLKSYYYAISDFAVGGRCKCNGHASECMKNEF 300
Db 239 QEWVTATDIRVTNLRLNTFGDEVNDPKVLKSYYYAISDFAVGGRCKCNGHASECMKNEF 298
QY 301 DKLVCNCKNTYGVDCCKLPPFNDRPWRRTAESAASECLPCDCNGRSQECYFDELRYRS 360
Db 299 DKLVCNCKNTYGVDCCKLPPFNDRPWRRTAESAASECLPCDCNGRSQECYFDELRYRS 358
QY 361 TGHGGHCTNCDNTDGAHCERCENEFRLGNNEACSSCHSPVGSLSLTCQDSYGRCSCKP 420
Db 359 TGHGGHCTNCDNTDGAHCERCENEFRLGNTEACSPCHSPVGSLSLTCQDSYGRCSCKP 418
QY 421 GVMGDKCDRCQPGFHSLTEAGRCPCSDPSGSIDECNVTETRCVKDNVEGFNCERCKPG 480
Db 419 GVMGDKCDRCQPGFHSLTEAGRCPCSDPSGSTDECNVTETRCVKDNVEGFNCERCKPG 478
QY 481 FFNLESSNPRGCTPCFCFGHSSVCTNAVGSYVSISSSTFQIDEDGWRAEQRDGSEASLEW 540
Db 479 FFNLESSNPKGCTPCFCFGHSSVCTNAVGSYVDIISSTFQIDEDGWRVEQRDGSEASLEW 538
QY 541 SSERQDIAVISDSYPPRYFIAPAKFLGKQVLSYGONLSFSFRVDRDRTRLSEADLVLEGA 600
Db 539 SSDRQYIAVISDSYPPRYFIAPVKFLGNQVLSYGONLSFSFRVDRDRTRLSEADLVLEGA 598
QY 601 GLRVSVPPLIAQNSYSPSETTVKYVFRHLHEATDYPWRPALTPPEFQKLLNLTISIIRGTY 660
Db 599 GLRVSVPPLIAQNSYSPSETTVKYIFRLHEATDYPWRPALSPPEFQKLLNLTISIIRGTY 658
QY 661 SERSAGYLDVTLASARPGVPATWVESCTCPVGYGGQFCBMCCLSGYRRETNPGLPYSP 720
Db 659 SERSAGYLDVTLQASARPGVPATWVESCTCPVGYGGQFCETCLPGYRRETNPGLPYSP 718
QY 721 CVLCAACNGHSETCDPETGVCNCRDNTAGPHCEKCSGDYGYGDSFAGTSSDCQPCPCPGSS 780
Db 719 CVLCTCNGHSETCDPETGVCDCRDNTAGPHCEKCSGDYGYGDSFAGTSSDCQPCPCPGSS 778
QY 781 CAVVPKTKEVVCTNCPTGTTGKRCCLCDGDFGDPGLGRNGPVRILCRQCSDNIDPNNAV 840
Db 779 CAIVPKTKEVVCTHCPTGTAGKRCCLCDGDFGDPGLGNSGVPVRLCRPCQCNIDPNNAV 838
QY 841 NCNRLTGECLKCIYNTAGFYCDRCCKDGFEGNPLAPNPADKCKACNCPYGTMKQQSSCNP 900
Db 839 NCNRLTGECLKCIYNTAGFYCDRCCKEGFEGNPLAPNPADKCKACACN-YGTVQQQSSCNP 897
QY 901 VTGQCECLPHVTGQDCGACDPGFYNLQSGQCERCDCHALGSTNGQCDIRTGQCECQPGI 960

Db 898 VTGQCQLPHVSGRDCGTCDFYNNLQSGQCERCDCCHALGSTNGQCDIRTGQCECQPGI 957
QY 961 TQHCERCEVNHFGFEGPEGCKPCDCHPEGSLQCKDDGRCCEGREGVGNRCDCQCENYF 1020
Db 958 TQHCERCEVNHFGFEGPEGCKPCDCHHEGSLQCKDDGRCCEGREGVGNRCDCQCENYF 1017
QY 1021 YNRSWPGCQCECPACRYLVKDVADHRVKLQLESILIANLGTGDEMVTDOAFEDRLKEAER 1080
Db 1018 YNRSWPGCQCECPACRYLVKDKAAEHRVKLQLESILIANLGTGDDMVTDOAFEDRLKEAER 1077
QY 1081 EVMDLLEBAQDVKDQNDLMDRLQVRVNTLSSQISRLQNTIRNTIETGNLAEQARAHEVN 1140
Db 1078 EVTDLLEBAQEVKDQNDLMDRLQVRVNTLSSQISRLQNTIRNTIETGILAEARARSVES 1137
QY 1141 TERLIEIASRELEKAKVAAANVSVTQPESTGDPNNMTLLAEBAARKLAERHKQEAADDIVRV 1200
Db 1138 TEQLIEIASRELEKAKM-AANVSITQPESTGEPNNMTLLAEBAARKLAERHKQEAADDIVRV 1196
QY 1201 AKTANDTSTEAYNLLLRLTAGENQTAFAIEEELNRKYEQAKNISQDLEKQAAARVHEEAkra 1260
Db 1197 AKTANEISAEAYNLLLRLTAGENQTAFAIEEELNRKYEQAKNISQDLEKQAAARVHEEAkra 1256
QY 1261 GDKAVEIYASVAQLSPDLSETLENEANNIKMEAEENLEQLIDOKLKDYEDLREDMRGKELE 1320
Db 1257 GDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLRLIDOKLKDYEDLREDMRGKEHE 1316
QY 1321 VKNLLEKGTQEQOTADQLLARADAAKALAEBAKKGRTDLOEANDILNLLKDFDRRVNDN 1380
Db 1317 VKNLLEKGAEQOTADQLLARADAAKALAEBAKKGRTDLOEANDILNLLKDFDRRVNDN 1376
QY 1381 KTAEEALRKIPAINQITITEANEKTREAAQALGSAADATEAKNKAHEAEERIASAVQKNA 1440
Db 1377 KTAEEALRRIPAINRTIAEANEKTREAAQALGNAADATEAKNKAHEAEERIASAAQKNA 1436
QY 1441 TSTKAEARTFAEVTDLNNEVNNMLKQLOEAEKELKRKQDDADQDMMAGMASQAQAEAE 1500
Db 1437 TSTKADARTFGEVTDLDNEVNGMLRQLEEAENELKRKQDDADQDMMAGMASQAQAEAE 1496
QY 1501 INARKAKNSVTSLLSIINDLLEQLGQDQTDVLDNKLNEIEGTLNKAKDEMKVSDLDKVS 1560
Db 1497 LNARKAKNSVSSLLSQLNLLDQQLDQTDVLDNKLNEIEGSLNKAKDEMKASDLDKVS 1556
QY 1561 LENEAKQEAAIMDYNRDIEEIMKDIRNLEDIRKTLPSGCFNTPSIEKP 1609
Db 1557 LESEARKQEAAIMDYNRDIAEIIKDIHNLEDIKKTLPTGCFNTPSIEKP 1605

RESULT 12

AAB48454
ID AAB48454 standard; protein; 1605 AA.

XX AAB48454;

AC AAB48454;

DT 02-MAR-2001 (first entry)

XX Mouse laminin 8 polypeptide, SEQ ID NO: 26.

DE Mouse; laminin 8; neuroprotective; angiogenic; osteopathic;

KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;

KW vascular tissue injury; neural injury; angiogenesis regulation.

OS Mus musculus.

XX WO200066732-A2.

XX 09-NOV-2000.

XX 28-APR-2000; 2000WO-US011543.

XX 30-APR-1999; 99US-0131720P.

PR 21-AUG-1999; 99US-0149738P.

PR 24-SEP-1999; 99US-0155945P.

ABB81596
ID ABB81596 standard; protein; 1605 AA.
XX
AC ABB81596;
XX
DT 19-SEP-2002 (first entry)
DE Mouse laminin 10 third chain protein sequence SEQ ID NO:18.
XX
KW Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;
KW tissue repair development; laminin; healing; vascular tissue;
KW re-endothelialisation; vascular injury; cell attachment; cell stasis;
KW proliferation; migration.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Peptide 1..33
FT /label= signal
FT Protein 34..1605
FT /label= laminin_10_third_chain
XX
XX WO200250111-A2.
XX
XX 27-JUN-2002.
XX
XX 21-DEC-2001; 2001WO-US051035.
XX
XX 21-DEC-2000; 2000US-0257449P.
XX
XX 28-MAR-2001; 2001US-0279282P.
XX
XX 13-NOV-2001; 2001US-00279282.
XX
XX (BIOS-) BIOSTRATUM INC.
XX
XX Tryggvason K, Doi M, Thyboll J;
XX
XX WPI; 2002-557650/59.
XX
XX N-PSDB; ABQ72914.
XX
XX New human laminin-10 proteins, useful for accelerating the healing of
XX
XX PT vascular tissue, improving the biocompatibility of grafts, or for
XX
XX PT promoting re-endothelialization at the site of vascular injuries.
XX
XX Claim 9; Page 191-195; 231pp; English.
XX
XX The present invention describes human laminin alpha 5. Also described is
XX
XX CC an isolated laminin 10. Laminin 10 has vulnery activity. Laminins are
XX
XX CC useful in maintaining cell/tissue phenotype as well as promoting cell
XX
XX CC growth and differentiation in tissue repair development. Specifically,
XX
XX CC laminin 10 can be used for accelerating the healing injuries of vascular
XX
XX CC tissue, improving the biocompatibility of grafts useful for treating such
XX
XX CC injuries, for promoting re-endothelialisation at the site of vascular
XX
XX CC injuries, and promote cell attachment and subsequent cell stasis,
XX
XX CC proliferation, differentiation, and/or migration. The present sequence
XX
XX CC represents a third chain protein of laminin 10, from the present
XX
XX CC invention
XX
SQ Sequence 1605 AA;
Query Match 93.5%; Score 8148; DB 5; Length 1605;
Best Local Similarity 92.8%; Pred. NO. 0;
Matches 1493; Conservative 59; Mismatches 53; Indels 4; Gaps 3;
QY 1 MRGSHRAAPALRPRGRLLPVLAVLAAAAAGCAQAAMDECTDEGGRPQRCMPEFVNAFN 60
DB 1 MTGGGRAALALQPRGRLLPVLAVL--AAVAGCVRAAMDECADEGGRPQRCMPEFVNAFN 58
QY 61 VTWVATNTCGTPPEYCVQGTGVTGKTSCHLQDAGQPHLQHGAAFLTDYNNQADTTWQS 120
DB 59 VTWVATNTCGTPPEYCVQGTGVTGKTSCHLQDAGQPHLQHGAAFLTDYNNQADTTWQS 118
QY 121 QTMLAGVQYPSSINLTLHLGKAFDITYVRLKFHTSRPESFAIYKRTREDGPWIPYQYSG 180

Db 119 QTMLAGVQYPNSINLTLHLGKAFDITYVRLKFHTSRPESFAIYKRTREDGPWIPYQYSG 178
QY 181 SCENTYSKANRGFIRTTGGDEQQAALCTDEFSDISPLTGGNVAFTLEGRPSAYNFDNSPVL 240
Db 179 SCENTYSKANRGFIRTTGGDEQQAALCTDEFSDISPLTGGNVAFTLEGRPSAYNFDNSPVL 238
QY 241 QEWVTATDIRVTNRLNTFGDEVFNDPKVLKSYYYAISDFAVGGRCKCNGHASECKNEF 300
Db 239 QEWVTATDIRVTNRLNTFGDEVFNDPKVLKSYYYAISDFAVGGRCKCNGHASECKNEF 298
QY 301 DKLVCNCKHNTYGVDCCKLPFFNDRPWRRTAESASECLPDCDCNRSQECYFDPPELYRS 360
Db 299 DKLVCNCKHNTYGVDCCKLPFFNDRPWRRTAESASECLPDCDCNRSQECYFDPPELYRS 358
QY 361 TGHGGHCTNCQDNTDGAHCERCRENFFRLGNNEACSSCHSPVGSLSLTCDSYGRCSCKP 420
Db 359 TGHGGHCTNCQDNTDGAHCERCRENFFRLGNTEACSPCHSPVGSLSLTCDSYGRCSCKP 418
QY 421 GVMGDKCDRCQPGFHSLTEAGRCPCSDPSGSDIDECNVEGRVCCKDNVEGFNCERCKPG 480
Db 419 GVMGDKCDRCQPGFHSLTEAGRCPCSDPSGSDIDECNVEGRVCCKDNVEGFNCERCKPG 478
QY 481 FFNLESSNPRGCTPCFCFGHSSVCTNAVGSYVYSISSTFQIDEDGWRAEQRDGSEASLEW 540
Db 479 FFNLESSNPRGCTPCFCFGHSSVCTNAVGSYVYDISTSFTQIDEDGWRAEQRDGSEASLEW 538
QY 541 SSERQDIAVISDSYFPRYFIAPAKFLGKQVLSYQNLSTFSFVDRDRDTRLSEAEDLVLEGA 600
Db 539 SSDROYIAVISDSYFPRYFIAPVKFLGNQVLSYQNLSTFSFVDRDRDTRLSEAEDLVLEGA 598
QY 601 GLRVSVPLIAQNSYPSSETTVKYVFRLEHATDYPRPALTPPEFQKLLNLTSLKIRGTY 660
Db 599 GLRVSVPLIAQNSYPSSETTVKYVFRLEHATDYPRPALTPPEFQKLLNLTSLKIRGTY 658
QY 661 SERSAGYLDVTLASARPGVGPATWVESCTCPVGYGGQFCQEMCLSGYRRETPLNLPYSP 720
Db 659 SERSAGYLDVTLASARPGVGPATWVESCTCPVGYGGQFCQETCLPGYRRETPLNLPYSP 718
QY 721 CVLCAACNGHSETCDPETGVNCRDNTAGPHCEKCSDDGYGSDTAGTSSDCCPCPGSSS 780
Db 719 CVLCTCNGHSETCDPETGVNCRDNTAGPHCEKCSDDGYGSDTAGTSSDCCPCPGSSS 778
QY 781 CAVPKTKVVTCTNCPTGTTGKRCCLCDDGYFGDPLGRNGVRLCRLCQCSNDIDPNAVG 840
Db 779 CAIVPKTKVVTCTNCPTGTTGKRCCLCDDGYFGDPLGRNGVRLCRLCQCSNDIDPNAVG 838
QY 841 NCNRLTGECLKCIYNTAGFYCDRCCKDGFNPLAPNPADKCAKNCNYPYGTMKQSSCNP 900
Db 839 NCNRLTGECLKCIYNTAGFYCDRCCKDGFNPLAPNPADKCAKNCNYPYGTMKQSSCNP 897
QY 901 VTGQCECLPHVTGQDCGACDPGFYNLQSGQGCERCDCCHALGSTNGQCDIRTGQCECQPGI 950
Db 898 VTGQCECLPHVTGQDCGACDPGFYNLQSGQGCERCDCCHALGSTNGQCDIRTGQCECQPGI 957
QY 961 TGQHCERCEVNHFGFGECKPCDCHHEGSLSLQCKDDGRCEGREGVGNRCDOCEENYF 1020
Db 958 TGQHCERCEVNHFGFGECKPCDCHHEGSLSLQCKDDGRCEGREGVGNRCDOCEENYF 1017
QY 1021 YNRSWPGCQCECPACRYRLVKOVADHRVKLQLESLIANLGTGDEMVTDOAFEDRLKEAER 1080
Db 1018 YNRSWPGCQCECPACRYRLVKOVADHRVKLQLESLIANLGTGDEMVTDOAFEDRLKEAER 1077
QY 1081 EWMDDLREAOQVVDQNLMDRLQNVNLTSSQISRLQINRNTIETGNLAEOARAHVEN 1140
Db 1078 EMTDLLREAOQVVDQNLMDRLQNVNLTSSQISRLQINRNTIETGNLAEOARAHVEN 1137
QY 1141 TERLIEIASRELEKAKVAAANVSVTQPESTGDPNNMTLLAEARKLAERHKKQEAADDIVRV 1200
Db 1138 TEQLIEIASRELEKAKVAAANVSITQPESTGDPNNMTLLAEARKLAERHKKQEAADDIVRV 1196
QY 1201 AKTANDTSTEAAYNLLRLTLAGENOTAFIEELNRKYEQAKNISQDLEKQAAARVHEEKRA 1260
Db 1197 AKTANETSABAYNLLRLTLAGENOTAFIEELNRKYEQAKNISQDLEKQAAARVHEEKRA 1256

QY 1261 GDKAVEIYASVAQISPLDSETLENEANNIKMEAEENLEQLIDQKLKDYEDLREDMRGKELE 1320
Db 1257 GDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLRLIDQKLKDYEDLREDMRGKEHE 1316
QY 1321 VKNLLEKKGTEQQTADQLLARADAAKALAEBAKKGRTDLOEANDILNKLKDFDRRVNDN 1380
Db 1317 VKNLLEKKGAEQQTADQLLARADAAKALAEBAKKGRTDLOEANDILNKLKDFDRRVNDN 1376
QY 1381 KTAABEALRKIPAINOTITEANEKTRTAAQALGSAADATEAKNKAHEAERIASAVQKNA 1440
Db 1377 KTAABEALRRIPAINRTIAEANEKTRTAAQALGNAADATEAKNKAHEAERIASAAQKNA 1436
QY 1441 TSTKAEAEARTFAEVTDLNEVNNMLKQLEAEKELKRKQDDADQDMNMAGMASQAAQAE 1500
Db 1437 TSTKADAERTFGEVTDLDNEVNGMLRQLEAEENELKRKQDDADQDMNMAGMASQAAQAE 1496
QY 1501 INARKAKNSVTSLLSINDLLEQLGQDQDQDQDQDQDQDQDQDQDQDQDQDQDQDQDQD 1560
Db 1497 INARKAKNSVSSLSQNLNLLDQLGQDQDQDQDQDQDQDQDQDQDQDQDQDQDQDQDQD 1556
QY 1561 LENEAKKQEAAMVDYNDIEEIMKDIRNLEDIRKTLPSGCFNTPSIEKP 1609
Db 1557 LESEARKQEAAMVDYNRDIAEIIKDIHNLEDIKKTLPTGCFNTPSIEKP 1605

RESULT 14
AAW50897
ID AAW50897 standard; protein; 1607 AA.
XX
AC AAW50897;

XX 07-DEC-1998 (first entry)
DT
XX
DE Mouse laminin G1 chain.

XX Laminin; mouse; beta-amyloid; amyloidosis; Alzheimer's disease;
KW Down's syndrome; hereditary cerebral haemorrhage; inflammation;
KW malignancy; Familial Mediterranean Fever; multiple myeloma;
KW type II diabetes; prion disease; Creutzfeldt-Jacob disease; CJD;
KW Gertsmann-Straussler syndrome; kuru; scrapie; haemodialysis;
KW carpal tunnel syndrome; senile cardiac amyloid polynuropathy;
KW Familial Amyloidotic Polynuropathy; thyroid carcinoma; diagnosis;
KW therapy.

XX Mus sp.
XX
XX WO9815179-A1.
XX
PD 16-APR-1998.
XX

PF 08-OCT-1997; 97WO-US018145.
XX
XX
PR 08-OCT-1996; 96US-0027981P.
XX

XX (UNIW) UNIV WASHINGTON.

XX Castillo G, Snow AD;

DR WPI; 1998-240534/21.

XX
XX
PT Use of laminin and fragments - for developing products for use in the
PT diagnosis and treatment of amyloid disease, e.g. Alzheimer's disease or
PT CJD.

XX Claim 15; Page 102-105; 132pp; English.

XX This is the amino acid sequence of the mouse laminin G1 chain. The
CC primary object of the invention is to use laminin, laminin-derived
CC protein fragments and/or laminin-derived polypeptides as potent
CC inhibitors of amyloid formation, deposition, accumulation and/or
CC persistence in Alzheimer's disease and other amyloidoses. The laminin
CC products (see AAW50888-98) may include mouse or human laminin A or A1

CC chain, laminin B1 or B2 chain, laminin A2 chain (merosin), laminin G1
CC chain, the globular repeats of the laminin A1 chain and the beta-amyloid
CC binding domain of the laminin A chain. A claimed method for treating an
CC amyloid disease comprises administering a polypeptide having a
CC conformational similarity to a fragment of a laminin protein. A method
CC for diagnosing an amyloid disease involves determining levels of laminin
CC in a sample. Production of laminin or its fourth globular repeat in vivo
CC provides a method for in vivo inhibition of beta-amyloid amyloidosis. The
CC products and methods can be used for the diagnosis, prognosis, monitoring
CC and treatment of amyloidoses such as Alzheimer's disease, Down's syndrome
CC and hereditary cerebral haemorrhage with amyloidosis of the Dutch type
CC (where the specific amyloid is the beta-amyloid protein), the amyloidosis
CC associated with chronic inflammation, various forms of malignancy and
CC Familial Mediterranean Fever (AA amyloid or inflammation-association
CC amyloidosis), the amyloidosis associated with multiple myeloma and other
CC B-cell abnormalities (AL amyloid), the amyloidosis associated with type
CC II diabetes (amylin or islet amyloid), the amyloidosis associated with
CC prion diseases including Creutzfeldt-Jacob disease, Gertsmann-Straussler
CC syndrome, kuru and animal scrapie (prp amyloid), the amyloidosis
CC associated with long-term haemodialysis and carpal tunnel syndrome (beta
CC 2-microglobulin amyloid), the amyloidosis associated with senile cardiac
CC amyloid and Familial Amyloidotic Polynuropathy (prealbumin or
CC transthyretin amyloid), and the amyloidosis associated with endocrine
CC tumours such as medullary carcinoma of the thyroid (variant of
CC procalsitonin)

XX
SQ Sequence 1607 AA;

Query Match 93.5%; Score 8147; DB 2; Length 1607;
Best Local Similarity 92.6%; Pred. No. 0;
Matches 1490; Conservative 61; Mismatches 56; Indels 2; Gaps 1;

QY 1 MEGSHRAAPALPRGRMLPVLAVLAAAGCAQAAMDECTDEGGRPQRCMPEFVNAAFN 60
Db 1 MTGGRAALALQPRGRMLPVLAVL--AAVAGCVRAAMDECADEGGRPQRCMPEFVNAAFN 58
QY 61 VTVVATNTCGTPPEEYCVQTVGTGVTKSKLCLDCAQPHLOHGAFLTDYNNQADTTWQS 120
Db 59 VTVVATNTCGTPPEEYCVQTVGTGVTKSKLCLDCAQPHLOHGAFLTDYNNQADTTWQS 118
QY 121 QTMLAGVOYQPSINLTLHLGKAFDITYVRLKFHTSRPSPFAIYKRTREDGPNWYQYYSG 180
Db 119 QTMLAGVOYQPSINLTLHLGKAFDITYVRLKFHTSRPSPFAIYKRTREDGPNWYQYYSG 178
QY 181 SCENTYSKANRGFI RTGGDEQQAALCTDEFSDISLITGGNVAFSTLEGRPSAYNFDNSPVL 240
Db 179 SCENTYSKANRGFI RTGGDEQQAALCTDEFSDISLITGGNVAFSTLEGRPSAYNFDNSPVL 238
QY 241 QEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSYYYAISDFAVGGRCKCNGHASECMKNEF 300
Db 239 QEWVTATDIRVTNLRLNTFGDEVFNEPKVLKSYYYAISDFAVGGRCKCNGHASECMKNEF 298
QY 301 DKLVCNCKHNTYGVDCCKCLPFFNDRPWRRATAESASECLPCDCNGRSQECYFDPPELYRS 360
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QY 361 TGHGGHTNCQDNTDGAHCRCRENFFRLGNNEACSSCHCSPVGSLSLTCQDSYGRCSCKP 420
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QY 421 GVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSDIBCNVETGRCVCKONVEGFNCERCKPG 480
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QY 481 FENLESSNPRGCTPCFCFGHSSVCTNAVGYSVYISSTFQIDEDGWRAEQRDGSEASLEW 540
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QY 541 SSERQDIAVISDSYFPRYFIAPAKFLGKQVLSYQNLFSFRVDRDRDRLSAEDLVLEGA 600
Db 539 SSERQDIAVISDSYFPRYFIAPVKFLGNQVLSYQNLFSFRVDRDRDRLSAEDLVLEGA 598
QY 601 GLRVSVPLIAQGNSSYPSETTVKYVFRHLHEATDVPWRPALTPFEFQKLLNLTLSIKIRGTY 660

Db 599 GLRVSVELIAQNSYPSSETTVKYIFRLHEATDYPWRPALSPFEQKLLNLTSLIKIRGTY 658
QY 661 SERSAGYLDVTLASARPGVGPATWVESCTCPVGYGGQFCMCLSGYRRRTPNLGPYPSP 720
Db 659 SERTAGYLDVTLQ SARPGVGPATWVESCTCPVGYGGQFCETCLPGYRRRTPSLGPYPSP 718
QY 721 CVLCAENGHSETCDPETGVNCBNDNTAGPHCEKCSGDYVGDSTAGTSSDCQPCPCPGSS 780
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QY 781 CAVPKTKEVVCTNCTGTTGKRCCLCDDGYFGDPLGRNGPVRLCRLCQCSNDIDPNAVG 840
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Db 839 NCNRLTGECLKCIYNTAGFYCDRCCKEGFFGNPLAPNPADCKACACNPGYTVQOSSCNP 898
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Db 899 VTGQCCQLPHVSGRDCGTCDPGYYNLQSGQGCERCDCCHALGSTNGQCDIRTGQCECQPGI 958
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RESULT 15
AAB19806
ID AAB19806 standard; protein; 1572 AA.
XX
AC AAB19806;

XX 05-MAR-2001 (first entry)
XX Mouse laminin 2 mature gamma-1 chain.
DE Laminin 2; mouse; nerve regeneration; angiogenic; cell adhesion;
XX degenerative muscle disorder; muscular dystrophy; cell therapy.
KW Mus musculus.
XX WO200066730-A2.
OS 09-NOV-2000.
XX 28-APR-2000; 2000WO-US011378.
XX 30-APR-1999; 99US-0131720P.
PR 15-JUN-1999; 99US-0139198P.
PR 12-JUL-1999; 99US-0143289P.
PR 24-SEP-1999; 99US-0155945P.
XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
PA Yurchenco P;
XX WPI; 2000-687537/67.
DR N-PSDB; AAA88906.
XX Purified laminin 2 protein, useful for research and therapeutic purposes
PT including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.
XX Claim 5; Page 302-306; 305pp; English.
PS The present sequence is that of mouse laminin 2 gamma-1 chain mature
XX protein. Laminin-2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and
CC gamma-1 (100 kDa) chains. It is thought to be specifically required for
CC stabilizing myotubes during skeletal muscle development, and for
CC preventing apoptosis. Genetic defects in human laminin 2 structure or
CC expression are associated with a major type of congenital muscular
CC dystrophy. Laminin 2 is also thought to be important in Schwann
CC cell/basal lamina interactions. The invention provides laminin 2 alpha-2,
CC beta-1 and gamma-1 chain polypeptides (see AAB19791-806) and the
CC polynucleotides encoding them (see AAA8891-906), methods for making
CC recombinant laminin 2, cells that express recombinant laminin 2, and
CC methods for using purified laminin 2 for research and therapeutic
CC purposes including peripheral nerve regeneration, treatment of
CC degenerative muscle disorders, angiogenesis regulation, promoting cell
CC attachment and migration, ex vivo cell therapy, improving the take of
CC grafts, improving the biocompatibility of medical devices and preparing
CC improved culture devices and media
XX Sequence 1572 AA;
SQ

Query Match 92.3%; Score 8038; DB 3; Length 1572;
Best Local Similarity 93.3%; Pred. NO. 0;
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;

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Db 61 QCHLQHGAFLTDYNNQADTTWQSQTMLAGVQYPNSINLTLLHKGAFDITYVRLKFHTS 120
QY 156 RPESFAIYKRTREDGPWIPYQYYSGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDISPL 215
Db 121 RPESFAIYKRTREDGPWIPYQYYSGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDISPL 180
QY 216 TGGNVAFTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVNDPKVLKSYYY 275
Db 181 TGGNVAFTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVNDPKVLKSYYY 240

OM protein - protein search, using sw model

Run on: May 18, 2004, 14:30:58 ; Search time 12.1718 Seconds
(without alignments)
6824.493 Million cell updates/sec

Title: US-10-037-182-14
Perfect score: 8713
Sequence: 1 MRGSHRAAPALRPRGRLWPV.....EDIRKTLPSGCFNTPSIEKP 1609

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8713	100.0	1609	4	US-09-562-702A-22
2	8713	100.0	1609	4	US-09-561-818A-22
3	8713	100.0	1617	4	US-09-562-702A-26
4	8544	98.1	1576	4	US-09-562-702A-24
5	8544	98.1	1576	4	US-09-561-818A-24
6	8544	98.1	1584	4	US-09-562-702A-28
7	8148	93.5	1605	4	US-09-562-702A-30
8	8148	93.5	1605	4	US-09-561-818A-26
9	8038	92.3	1572	4	US-09-562-702A-32
10	8038	92.3	1572	4	US-09-561-818A-28
11	3611	41.4	1587	4	US-09-845-583A-10
12	3611	41.4	1587	4	US-09-561-709B-3
13	2637	30.3	1193	1	US-08-317-450B-13
14	2637	30.3	1193	3	US-08-800-593-13
15	2516.5	28.9	1111	1	US-08-317-450B-15
16	2516.5	28.9	1111	3	US-08-800-593-15
17	2355.5	27.0	1171	1	US-08-445-135-1
18	1782.5	20.5	3110	4	US-09-562-702A-2
19	1782.5	20.5	3110	4	US-09-562-702A-6
20	1782.5	20.5	3110	4	US-09-561-709B-7
21	1782	20.5	3111	2	US-08-460-309-4
22	1782	20.5	3111	2	US-08-125-077-4
23	1776	20.4	3088	4	US-09-562-702A-8
24	1776	20.4	3089	4	US-09-562-702A-4
25	1774.5	20.4	3106	4	US-09-562-702A-10
26	1768.5	20.3	3084	4	US-09-562-702A-12
27	1717.5	19.7	3075	2	US-08-460-309-5

28	1717.5	19.7	3075	2	US-08-125-077-5	Sequence 5, Appli
29	1680.5	19.3	1765	4	US-09-562-702A-16	Sequence 16, Appl
30	1680.5	19.3	1765	4	US-09-561-818A-16	Sequence 16, Appl
31	1680.5	19.3	1786	4	US-09-562-702A-14	Sequence 14, Appl
32	1680.5	19.3	1786	4	US-09-561-818A-14	Sequence 14, Appl
33	1680.5	19.3	1786	4	US-09-561-709B-9	Sequence 9, Appli
34	1652	19.0	1761	4	US-09-561-709B-1	Sequence 1, Appli
35	1651	18.9	1786	4	US-09-562-702A-18	Sequence 18, Appl
36	1651	18.9	1786	4	US-09-561-818A-18	Sequence 18, Appl
37	1622.5	18.6	1725	4	US-09-562-702A-20	Sequence 20, Appl
38	1622.5	18.6	1725	4	US-09-561-818A-20	Sequence 20, Appl
39	1572	18.0	1799	4	US-09-845-583A-6	Sequence 6, Appli
40	1510.5	17.3	1798	4	US-09-561-709B-11	Sequence 11, Appl
41	1508.5	17.3	1798	4	US-09-845-583A-8	Sequence 8, Appli
42	1371	15.7	252	2	US-08-460-309-12	Sequence 12, Appl
43	1371	15.7	252	2	US-08-125-077-12	Sequence 12, Appl
44	1367	15.7	252	1	US-08-152-019A-38	Sequence 38, Appl
45	1346	15.4	251	1	US-08-152-019A-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1

US-09-562-702A-22

; Sequence 22, Application US/09562702A

; Patent No. 6632790

; GENERAL INFORMATION:

; APPLICANT: Yurchenco, Peter

; TITLE OF INVENTION: Laminin 2 and Methods for Its Use

; FILE REFERENCE: 99-274-B

; CURRENT APPLICATION NUMBER: US/09/562,702A

; CURRENT FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: 60/155,945

; PRIOR FILING DATE: 1999-09-24

; PRIOR APPLICATION NUMBER: 60/143,289

; PRIOR FILING DATE: 1999-07-12

; PRIOR APPLICATION NUMBER: 60/139,198

; PRIOR FILING DATE: 1999-06-15

; PRIOR APPLICATION NUMBER: 60/131,720

; PRIOR FILING DATE: 1999-04-30

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 22

; LENGTH: 1609

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-562-702A-22

Query Match 100.0%; Score 8713; DB 4; Length 1609;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGSHRAAPALRPRGRLWPVLAVLAAAAAGCAQAAMDECTDEGGRPQRCMPEFVNAAFN 60

Db 1 MRGSHRAAPALRPRGRLWPVLAVLAAAAAGCAQAAMDECTDEGGRPQRCMPEFVNAAFN 60

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Db 61 VTVVATNTCGTPPEEYCVQGTGVTGVTKSchLCDAGOPHLQHGAFLTDYNNQADTTWQs 120

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Db 121 QTMLAGVQYPSSINLTlHLGKAFDITYVRLKFHTSRPESFAIYKRTREDGPIPYQYSG 180

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RESULT 2

US-09-561-818A-22
; Sequence 22, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortessmaa, Jarrko
; APPLICANT: Tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 1609
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-818A-22

Query Match 100.0%; Score 8713; DB 4; Length 1609;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 541 SSERQDIAVISDSYFPRYFIAPAKFLGKQVLSYQNLFSFRVDRDRTRLSAEDLVLEGA 600
Db 541 SSERQDIAVISDSYFPRYFIAPAKFLGKQVLSYQNLFSFRVDRDRTRLSAEDLVLEGA 600
QY 601 GLRVSVPLIAQGNVSPSETTVKYVFRHLHEATDYPWRPALTPFEFQKLLNNLTSIKIRGTY 660
Db 601 GLRVSVPLIAQGNVSPSETTVKYVFRHLHEATDYPWRPALTPFEFQKLLNNLTSIKIRGTY 660
QY 661 SERSAGYLDVTLASARPGVPATWVESCTCPVGYGGQFCFEMCLSGYRRETPNLGPYSP 720
Db 661 SERSAGYLDVTLASARPGVPATWVESCTCPVGYGGQFCFEMCLSGYRRETPNLGPYSP 720
QY 721 CVLCAACNGHSETCDPETGVNCNRDNTAGPHCEKSDGYGSDTAGTSSDQPCPCPGGSS 780
Db 721 CVLCAACNGHSETCDPETGVNCNRDNTAGPHCEKSDGYGSDTAGTSSDQPCPCPGGSS 780
QY 781 CAVVPKTKEVVCTNCTGTGKRCCELDDGYFGDPLGRNGPVRRLCRLCQSDNIDPNAVG 840
Db 781 CAVVPKTKEVVCTNCTGTGKRCCELDDGYFGDPLGRNGPVRRLCRLCQSDNIDPNAVG 840
QY 841 NCNRLTGECLKCIYNTAGFYCDRCKDGFNGPLAPNPADCKACNCNPYGTMKQOSSCNP 900
Db 841 NCNRLTGECLKCIYNTAGFYCDRCKDGFNGPLAPNPADCKACNCNPYGTMKQOSSCNP 900
QY 901 VTGQCECLPHVTGDCGACDPGFYNLQSGQGGERCDCHALGSTNGQCDIRTGQCECQPGI 960
Db 901 VTGQCECLPHVTGDCGACDPGFYNLQSGQGGERCDCHALGSTNGQCDIRTGQCECQPGI 960
QY 961 TGQHCECEVNHFGFEGGCKPCDCHPEGSLSQCKDDGRCECREGFGVGNRCDQCEENYF 1020
Db 961 TGQHCECEVNHFGFEGGCKPCDCHPEGSLSQCKDDGRCECREGFGVGNRCDQCEENYF 1020
QY 1021 YNRSWPGCQCEPACVRLVKDVADHRVKLQELLESILANLGTGDEMVTQAFEDRLKEAER 1080
Db 1021 YNRSWPGCQCEPACVRLVKDVADHRVKLQELLESILANLGTGDEMVTQAFEDRLKEAER 1080
QY 1081 EWMDDLREAQDVKDQNLMDRLQRVNNTLSSQISRLQNRNTIETGNLAEQARAHVEN 1140
Db 1081 EWMDDLREAQDVKDQNLMDRLQRVNNTLSSQISRLQNRNTIETGNLAEQARAHVEN 1140
QY 1141 TERLIEIASRELEKAKVAAANVSVTQPESTGDPNNMTLLAEARKLAERHKQEAADDIVRV 1200
Db 1141 TERLIEIASRELEKAKVAAANVSVTQPESTGDPNNMTLLAEARKLAERHKQEAADDIVRV 1200
QY 1201 AKTANDTSTEAYNLLRTLAGEQTAFIEIIEELNRKVEQAKNISQDLEKQAAARVHEEKRA 1260
Db 1201 AKTANDTSTEAYNLLRTLAGEQTAFIEIIEELNRKVEQAKNISQDLEKQAAARVHEEKRA 1260
QY 1261 GDKAVEIYASVAQLSPDSETLENEANNIKMEAEENLEQLIDQKLKDYEDLREDMRGKELE 1320
Db 1261 GDKAVEIYASVAQLSPDSETLENEANNIKMEAEENLEQLIDQKLKDYEDLREDMRGKELE 1320
QY 1321 VKNLLEKGTQEQQTADQILLARADAAKALAEAEAAKKGRTDLOEANDILNMLKDFDRRVNDN 1380
Db 1321 VKNLLEKGTQEQQTADQILLARADAAKALAEAEAAKKGRTDLOEANDILNMLKDFDRRVNDN 1380
QY 1381 KTAABEALRKIPAINQTI TEANEKTR EAQQAALGSAADATEAKNKAHEAERIA SAVOKNA 1440
Db 1381 KTAABEALRKIPAINQTI TEANEKTR EAQQAALGSAADATEAKNKAHEAERIA SAVOKNA 1440
QY 1441 TSTKAEARTFAEVTDLDNVNNMLKQLEAEKELKRKQDDADQDMMAGMASQAAQAEAE 1500
Db 1441 TSTKAEARTFAEVTDLDNVNNMLKQLEAEKELKRKQDDADQDMMAGMASQAAQAEAE 1500
QY 1501 INARKAKNSVTSLLSIINDLLEQLGQDQDLDNKLNEIEGTLNKADEMKSVDLDRKVS 1560
Db 1501 INARKAKNSVTSLLSIINDLLEQLGQDQDLDNKLNEIEGTLNKADEMKSVDLDRKVS 1560
QY 1561 LENEAKKQEAAIMDYNRDIEEIMKDIRNLEDIRKTLPSGCFNTPSIEKP 1609
Db 1561 LENEAKKQEAAIMDYNRDIEEIMKDIRNLEDIRKTLPSGCFNTPSIEKP 1609

RESULT 3

US-09-562-702A-26
; Sequence 26, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 1617
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-26

Query Match 100.0%; Score 8713; DB 4; Length 1617;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGSHRAAPALRPRGRLPVLA LAAAAAGCAQAAMDECTDEGGRPQRCMPFVNAAFN 60
Db 1 MEGSHRAAPALRPRGRLPVLA LAAAAAGCAQAAMDECTDEGGRPQRCMPFVNAAFN 60
QY 61 VTVVATNTCGTPPEEYCVQTGVTGVT KSCHL CDAGQPHLQHGAFLTDYNNQADTTWQ 120
Db 61 VTVVATNTCGTPPEEYCVQTGVTGVT KSCHL CDAGQPHLQHGAFLTDYNNQADTTWQ 120
QY 121 QTMLAGVQYPSSINLT LHLGKAFDITYVRLKFTSRPESFAIYKRTREDGPWIPYQYSG 180
Db 121 QTMLAGVQYPSSINLT LHLGKAFDITYVRLKFTSRPESFAIYKRTREDGPWIPYQYSG 180
QY 181 SCENTYSKANRGFIRTGDEQQA LCTDEFSDISPLTGGNVAFTLEGPSAYNFDNSPVL 240
Db 181 SCENTYSKANRGFIRTGDEQQA LCTDEFSDISPLTGGNVAFTLEGPSAYNFDNSPVL 240
QY 241 QEWVTATDIRVT LRLNTFGDEVNDPKVLKSYVYAI SDFAVGGRCKNCNGHASECMKNEF 300
Db 241 QEWVTATDIRVT LRLNTFGDEVNDPKVLKSYVYAI SDFAVGGRCKNCNGHASECMKNEF 300
QY 301 DKLVCNCKHNTYGVDCBKCLPFFNDRPWRRATAESASECLPCDCNGRSQECYFDPPELYRS 360
Db 301 DKLVCNCKHNTYGVDCBKCLPFFNDRPWRRATAESASECLPCDCNGRSQECYFDPPELYRS 360
QY 361 TGHGGHCTNCQDNTDGAHCE RCNFFRLGNNEACSSCHCSPVGSLSSTQCDSYGRCSCKP 420
Db 361 TGHGGHCTNCQDNTDGAHCE RCNFFRLGNNEACSSCHCSPVGSLSSTQCDSYGRCSCKP 420
QY 421 GVMGDKCDRCQPGFHSILTEAGCRPCSCDPSGSDIECNVETGRCVCKDNVEGFNCERCKPG 480
Db 421 GVMGDKCDRCQPGFHSILTEAGCRPCSCDPSGSDIECNVETGRCVCKDNVEGFNCERCKPG 480
QY 481 FPNLESSNPRGCTPCFCFGHSSVCTNAVGYSVYSISSTFQIDEDGWAEQRDGSEASLEW 540
Db 481 FPNLESSNPRGCTPCFCFGHSSVCTNAVGYSVYSISSTFQIDEDGWAEQRDGSEASLEW 540
QY 541 SSERQDIAVISDSYFPRYFIAPAKFLGKQVLSYQNLFSFRVDRDRTRLSAEDLVLEGA 600
Db 541 SSERQDIAVISDSYFPRYFIAPAKFLGKQVLSYQNLFSFRVDRDRTRLSAEDLVLEGA 600
QY 601 GLRVSVPLIAQGNVSPSETTVKYVFRHLHEATDYPWRPALTPFEFQKLLNNLTSIKIRGTY 660

Db 601 GLRVSPLIAQNSYSPSETTVKYVFLHEATDYPWRPALTPFEFKLLNLSIKIRGTY 660
QY 661 SERSAGYLDVTLASARPGVGPATWVESCTCPVGYGGQFCMCLSGYRRETPLNLPYSP 720
Db 661 SERSAGYLDVTLASARPGVGPATWVESCTCPVGYGGQFCMCLSGYRRETPLNLPYSP 720
QY 721 CVLCAHSHSETCDPETGVNCNCRDNTAGPHCEKSCDGYGDSGTAGTSSDCQCPGSS 780
Db 721 CVLCAHSHSETCDPETGVNCNCRDNTAGPHCEKSCDGYGDSGTAGTSSDCQCPGSS 780
QY 781 CAVPKTXEVVTCNPTGTTGKRCCLDDGYFGDPLGRNGPVRRLCRLCQCSNIDPNAVG 840
Db 781 CAVPKTXEVVTCNPTGTTGKRCCLDDGYFGDPLGRNGPVRRLCRLCQCSNIDPNAVG 840
QY 841 NCNRLTGECLKCIYNTAGFYCDRCCKDGGFFGNPLAPNADKCKACNCPYGTMKQQSSCNP 900
Db 841 NCNRLTGECLKCIYNTAGFYCDRCCKDGGFFGNPLAPNADKCKACNCPYGTMKQQSSCNP 900
QY 901 VTGQCECLPHVTGQDCGACDPGFYNLQSGQGCRCDCCHALGSTNGQCDINTGQCECQPGI 960
Db 901 VTGQCECLPHVTGQDCGACDPGFYNLQSGQGCRCDCCHALGSTNGQCDINTGQCECQPGI 960
QY 961 TQHCERCEVNHFGFEGPEGCKPCDCHPEGSLSLQCKDDGRCECREGFVGNRCDCQCEENYF 1020
Db 961 TQHCERCEVNHFGFEGPEGCKPCDCHPEGSLSLQCKDDGRCECREGFVGNRCDCQCEENYF 1020
QY 1021 YNRSWPGQCECPACRYLVKDVADHRVKLQELSLIANLGTGDEMVTDOAFEDRLKEAER 1080
Db 1021 YNRSWPGQCECPACRYLVKDVADHRVKLQELSLIANLGTGDEMVTDOAFEDRLKEAER 1080
QY 1081 EVMDDLREAOQVQDVQDQNLMDRLQVRNLTSSQISRLQIRNTIETGNLAEOARAHVEN 1140
Db 1081 EVMDDLREAOQVQDVQDQNLMDRLQVRNLTSSQISRLQIRNTIETGNLAEOARAHVEN 1140
QY 1141 TERLIEIASRELEKAKVAAANVSVTQPESTGDPNNMTLLAEBARKLAERHKEADDDIVRV 1200
Db 1141 TERLIEIASRELEKAKVAAANVSVTQPESTGDPNNMTLLAEBARKLAERHKEADDDIVRV 1200
QY 1201 AKTANDTSTEAYNLLRLTAGENQTAPEIEELNRYEQAKNISQDLEKQAAVHEEAKRA 1260
Db 1201 AKTANDTSTEAYNLLRLTAGENQTAPEIEELNRYEQAKNISQDLEKQAAVHEEAKRA 1260
QY 1261 GDKAVEIYASVAQLSPDSELTENEANNIKMEAEENLEQLIDQKLKYEDLREDMRGKELE 1320
Db 1261 GDKAVEIYASVAQLSPDSELTENEANNIKMEAEENLEQLIDQKLKYEDLREDMRGKELE 1320
QY 1321 VKNLLEKGTQEQQTADQLLARADAALAEAAKKGRTDLOEANDILNLLKDFDRRVNDN 1380
Db 1321 VKNLLEKGTQEQQTADQLLARADAALAEAAKKGRTDLOEANDILNLLKDFDRRVNDN 1380
QY 1381 KTAEEALRKIPAINQTIITANEKTRTAAQALGSAADATEAKNKAHEABERIASAVQKNA 1440
Db 1381 KTAEEALRKIPAINQTIITANEKTRTAAQALGSAADATEAKNKAHEABERIASAVQKNA 1440
QY 1441 TSTKABERTFAEVTDLNNEVNNMLKQLOEAEKELKRRKQDDADQDMVMAGMASQAAQAE 1500
Db 1441 TSTKABERTFAEVTDLNNEVNNMLKQLOEAEKELKRRKQDDADQDMVMAGMASQAAQAE 1500
QY 1501 INARKAKNSVTSLLSIINDLLEQLGQDVTVDLNLKNEIEGTNLKAKDEMKSVDLDRKVS 1560
Db 1501 INARKAKNSVTSLLSIINDLLEQLGQDVTVDLNLKNEIEGTNLKAKDEMKSVDLDRKVS 1560
QY 1561 LENEAKKQEAAIMDYNRDIIEIMKDINLEDIRKTLPSGCFNTPSIEKP 1609
Db 1561 LENEAKKQEAAIMDYNRDIIEIMKDINLEDIRKTLPSGCFNTPSIEKP 1609

RESULT 4

US-09-562-702A-24
; Sequence 24, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:

; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 1576
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-24

Query Match 98.1%; Score 8544; DB 4; Length 1576;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 QAAMDECTDEGRPQRCMPFVNAAFNVTVATNTCGTPPEEYCVQTVGTGVTGTSCHLCD 93
Db 1 QAAMDECTDEGRPQRCMPFVNAAFNVTVATNTCGTPPEEYCVQTVGTGVTGTSCHLCD 60
QY 94 AGQPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYFSSINLTLLHKGAFDITYVRLKFH 153
Db 61 AGQPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYFSSINLTLLHKGAFDITYVRLKFH 120
QY 154 TSRPESFAIYKRTREDGPWPVPIQYYSGCCENTYSKANRGFIRTTGGDEQALCTDEFSDIS 213
Db 121 TSRPESFAIYKRTREDGPWPVPIQYYSGCCENTYSKANRGFIRTTGGDEQALCTDEFSDIS 180
QY 214 PLTGGNVAFSTLEGPRPSAYNFNSPVLQEWVTATDIRVTLNRLNTFGDEVNDPKVLKSY 273
Db 181 PLTGGNVAFSTLEGPRPSAYNFNSPVLQEWVTATDIRVTLNRLNTFGDEVNDPKVLKSY 240
QY 274 YYAISDFAVGGRCKCNGHASECMKNEFDKLVNCKHNTYGVDCCKLPFFNDRPWRATA 333
Db 241 YYAISDFAVGGRCKCNGHASECMKNEFDKLVNCKHNTYGVDCCKLPFFNDRPWRATA 300
QY 334 ESASECLPCDCNCRSQECYFDELYRSTGHGGHCTNCQDNTDGAHCERCRENFFRLGNNE 393
Db 301 ESASECLPCDCNCRSQECYFDELYRSTGHGGHCTNCQDNTDGAHCERCRENFFRLGNNE 360
QY 394 ACSSCHCSPVGSLSLSTQCDYSYGRCSCKPGVMGDKCDRCQPGFHSLSLTAAGRCPSCDPSGI 453
Db 361 ACSSCHCSPVGSLSLSTQCDYSYGRCSCKPGVMGDKCDRCQPGFHSLSLTAAGRCPSCDPSGI 420
QY 454 DECNVETGRVCVKDNVEGFNCERCKPGFFNLESNNRPGCTPCFCFGHSSVCTNAVGSYV 513
Db 421 DECNVETGRVCVKDNVEGFNCERCKPGFFNLESNNRPGCTPCFCFGHSSVCTNAVGSYV 480
QY 514 SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPFYFIAPAKFLGKQVLSY 573
Db 481 SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPFYFIAPAKFLGKQVLSY 540
QY 574 GQNLFSFVRVDRDRLSADLVLEGAGLRVSVPLIAQGNNSYPSSETTVKYVFRLHEATDY 633
Db 541 GQNLFSFVRVDRDRLSADLVLEGAGLRVSVPLIAQGNNSYPSSETTVKYVFRLHEATDY 600
QY 634 PWRPALTPFEFKLLNLSIKIRGTYSERSAGVLDVTLASARPGVGPATWVESCTCP 693
Db 601 PWRPALTPFEFKLLNLSIKIRGTYSERSAGVLDVTLASARPGVGPATWVESCTCP 660
QY 694 VGYGGQFCMCLSGYRRETPLNLPYSPCVLCAHSHSETCDPETGVNCNCRDNTAGPHCEK 753
Db 661 VGYGGQFCMCLSGYRRETPLNLPYSPCVLCAHSHSETCDPETGVNCNCRDNTAGPHCEK 720

QY 754 CSDGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKVEVCTNCPTGTTGKRCBLCDDGYFG 813
Db 721 CSDGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKVEVCTNCPTGTTGKRCBLCDDGYFG 780
QY 814 DPLGRNGPVRCLRCQCSDNIDPNAVGNCRNLGTGECILKCIYNTAGFYCDRCCKDGFNPL 873
Db 781 DPLGRNGPVRCLRCQCSDNIDPNAVGNCRNLGTGECILKCIYNTAGFYCDRCCKDGFNPL 840
QY 874 APNPADKCKACNPNPYGTMKQSSCNPTVGTQCECLPHVTGQDCGACDPGFYNLQSGQGE 933
Db 841 APNPADKCKACNPNPYGTMKQSSCNPTVGTQCECLPHVTGQDCGACDPGFYNLQSGQGE 900
QY 934 RCDCHALGSTNGQCDIRTGQCECOPGITGOHCERCEVNHFGFPGCKPCDCHPEGSLSL 993
Db 901 RCDCHALGSTNGQCDIRTGQCECOPGITGOHCERCEVNHFGFPGCKPCDCHPEGSLSL 960
QY 994 QKDDGRCECREGVGNRCDCQCEENFYNRSWPGCCQCEPCACYRLVKDKVADHRVKLQELE 1053
Db 961 QKDDGRCECREGVGNRCDCQCEENFYNRSWPGCCQCEPCACYRLVKDKVADHRVKLQELE 1020
QY 1054 SLIANLGTGDEMVTDOAFEDRLKEAREVMDLLREAOQVVDQNLMDRLQRVNNTLSSQ 1113
Db 1021 SLIANLGTGDEMVTDOAFEDRLKEAREVMDLLREAOQVVDQNLMDRLQRVNNTLSSQ 1080
QY 1114 ISRLQNIIRNTIETGNLAERHKEADIVRVAKTANDTSTEAVNLLRLTLAGENQTAFEIIEELN 1173
Db 1081 ISRLQNIIRNTIETGNLAERHKEADIVRVAKTANDTSTEAVNLLRLTLAGENQTAFEIIEELN 1140
QY 1174 NMWTLAEBARKLAERHKEADIVRVAKTANDTSTEAVNLLRLTLAGENQTAFEIIEELN 1233
Db 1141 NMWTLAEBARKLAERHKEADIVRVAKTANDTSTEAVNLLRLTLAGENQTAFEIIEELN 1200
QY 1234 RKYEQAKNISQDLEKQAAARVHEEAKGAGDKAVEIYASVAQLSPDLSETLENEANNIKMEA 1293
Db 1201 RKYEQAKNISQDLEKQAAARVHEEAKGAGDKAVEIYASVAQLSPDLSETLENEANNIKMEA 1260
QY 1294 ENLEQLIDOKLKDYEDLREDMRGKELEVKNLLEKKGTEQQTADQLLARADAALKALAEAAA 1353
Db 1261 ENLEQLIDOKLKDYEDLREDMRGKELEVKNLLEKKGTEQQTADQLLARADAALKALAEAAA 1320
QY 1354 KKGRTDLOEANDILNNLKDFDRRVNDNKTAAEEALRKIPAINQITTEANEKTRTAAQALG 1413
Db 1321 KKGRTDLOEANDILNNLKDFDRRVNDNKTAAEEALRKIPAINQITTEANEKTRTAAQALG 1380
QY 1414 SAAADATEAKNKAHEAERIAASAVQKNATSTKAEARTFAEVTDLNNEVNNMLKQLOEAEK 1473
Db 1381 SAAADATEAKNKAHEAERIAASAVQKNATSTKAEARTFAEVTDLNNEVNNMLKQLOEAEK 1440
QY 1474 ELKRKQDDADQDMMAGMASQAAQAEINARKAKNSVTSLLSINDLLEQLGQDITVDLN 1533
Db 1441 ELKRKQDDADQDMMAGMASQAAQAEINARKAKNSVTSLLSINDLLEQLGQDITVDLN 1500
QY 1534 KLNEIEGTLNKADEMKSVDLDRKVSLENEAKKQEAAMDVNDRDIEEIMKDIRNLEDIR 1593
Db 1501 KLNEIEGTLNKADEMKSVDLDRKVSLENEAKKQEAAMDVNDRDIEEIMKDIRNLEDIR 1560
QY 1594 KTLPSGCFNTPSIEKP 1609
Db 1561 KTLPSGCFNTPSIEKP 1576

RESULT 5
US-09-561-818A-24
; Sequence 24, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Korttesmaa, Jarrko
; APPLICANT: Tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 1576
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-818A-24

Query Match 98.1%; Score 8544; DB 4; Length 1576;
Best local Similarity 100.0%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 QAAAMDECTDEGGRPQRCMPPEFVNAAFNVTVATNTCGTPPEYCVQTVGTGVTKSCHLCD 93
Db 1 QAAAMDECTDEGGRPQRCMPPEFVNAAFNVTVATNTCGTPPEYCVQTVGTGVTKSCHLCD 60
QY 94 AGQPHLQHGAFLTDYNNQADTTWQSQTMLAGVQYPSINLTLHLGKAFDITYVRLKFX 153
Db 61 AGQPHLQHGAFLTDYNNQADTTWQSQTMLAGVQYPSINLTLHLGKAFDITYVRLKFX 120
QY 154 TSRPESFAIYKRTREDGWPWIPYQYISGSCENTYSKANRGFIRTTGGDEQQAALCTDEFSDIS 213
Db 121 TSRPESFAIYKRTREDGWPWIPYQYISGSCENTYSKANRGFIRTTGGDEQQAALCTDEFSDIS 180
QY 214 PLTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTLNRLNTFGDEVFNDPKVLKSY 273
Db 181 PLTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTLNRLNTFGDEVFNDPKVLKSY 240
QY 274 YYAISDFAVGGRCKCNHGHASECMKNEFDKLVCKNKNHTYGVDCCKCLPFFNDRPWRRTA 333
Db 241 YYAISDFAVGGRCKCNHGHASECMKNEFDKLVCKNKNHTYGVDCCKCLPFFNDRPWRRTA 300
QY 334 ESASECLPCDCNGRSQECYFDPPELYSTGGHCHCTNCQDNTDGAHCRCRENFRLGNNE 393
Db 301 ESASECLPCDCNGRSQECYFDPPELYSTGGHCHCTNCQDNTDGAHCRCRENFRLGNNE 360
QY 394 ACSSCHCSPVGSLSLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSI 453
Db 361 ACSSCHCSPVGSLSLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSI 420
QY 454 DECNVETGRCVCKDNVEGFNCERCCKPGFFNLESSNPRGCTPCFCFHHSSVCTNAVGSYVY 513
Db 421 DECNVETGRCVCKDNVEGFNCERCCKPGFFNLESSNPRGCTPCFCFHHSSVCTNAVGSYVY 480
QY 514 SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFFRYFIAPAKFLGKQVLSY 573
Db 481 SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFFRYFIAPAKFLGKQVLSY 540
QY 574 GQNLFSFRVDRDTRLAEDLVLEGAGLRVSVPVLIQAQNSYPSSETTVKYVFRLEHATDY 633
Db 541 GQNLFSFRVDRDTRLAEDLVLEGAGLRVSVPVLIQAQNSYPSSETTVKYVFRLEHATDY 600
QY 634 PWRPALTPFEFQKLNNLTSIKIRGTYSERSAGYLDVTLASARPGVPATWVESCTCP 693
Db 601 PWRPALTPFEFQKLNNLTSIKIRGTYSERSAGYLDVTLASARPGVPATWVESCTCP 660
QY 694 VGYGGQFCMCLSGYRRETPNLGPYSPCVLCACNGHSETCDPETGVCNCRDNTAGPHCEK 753
Db 661 VGYGGQFCMCLSGYRRETPNLGPYSPCVLCACNGHSETCDPETGVCNCRDNTAGPHCEK 720
QY 754 CSDGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKVEVCTNCPTGTTGKRCBLCDDGYFG 813
Db 721 CSDGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKVEVCTNCPTGTTGKRCBLCDDGYFG 780
QY 814 DPLGRNGPVRCLRCQCSDNIDPNAVGNCRNLGTGECILKCIYNTAGFYCDRCCKDGFNPL 873
Db 781 DPLGRNGPVRCLRCQCSDNIDPNAVGNCRNLGTGECILKCIYNTAGFYCDRCCKDGFNPL 840
QY 874 APNPADKCKACNPNPYGTMKQSSCNPTVGTQCECLPHVTGQDCGACDPGFYNLQSGQGE 933
Db 841 APNPADKCKACNPNPYGTMKQSSCNPTVGTQCECLPHVTGQDCGACDPGFYNLQSGQGE 900
QY 934 RCDCHALGSTNGQCDIRTGQCECOPGITGOHCERCEVNHFGFPGCKPCDCHPEGSLSL 993

Db 901 RCDHALGSTNGQCDIRGTGQCECQPGITGQHCHCERCEVNHFGFEGCKPCDCHPEGSLSL 960
Qy 994 QCKDDGRCECREGFGVGNRCDCQCEENFYNRSWPGCQCEPACVRLVKOKVADHRVKLQELE 1053
Db 961 QCKODGRCECREGFGVGNRCDCQCEENFYNRSWPGCQCEPACVRLVKDKVADHRVKLQELE 1020
Qy 1054 SLIANLGTGDMVTDQAFEDRLKEAEREVMDLLRREAQDVVDQNLMDRLQRVNNTLSSQ 1113
Db 1021 SLIANLGTGDMVTDQAFEDRLKEAEREVMDLLRREAQDVVDQNLMDRLQRVNNTLSSQ 1080
Qy 1114 ISRLQNRNTEETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1173
Db 1081 ISRLQNRNTEETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1140
Qy 1174 NNMVTLAEEARKLAERHKEQEAADDIVRVAKTANDTSTEAYNLLRRTLAGENQTAFEIEELN 1233
Db 1141 NNMVTLAEEARKLAERHKEQEAADDIVRVAKTANDTSTEAYNLLRRTLAGENQTAFEIEELN 1200
Qy 1234 RKYEQAKNISQLEKQAARVHEEAKRAGDKAVEIYASVAQLSPDLSETLENEANNIKMEA 1293
Db 1201 RKYEQAKNISQLEKQAARVHEEAKRAGDKAVEIYASVAQLSPDLSETLENEANNIKMEA 1260
Qy 1294 ENLEQLIDQKLDYEDLREDMRGKELEVKNLLEKKGTEQQTADQLLARADAAKALAEAA 1353
Db 1261 ENLEQLIDQKLDYEDLREDMRGKELEVKNLLEKKGTEQQTADQLLARADAAKALAEAA 1320
Qy 1354 KKGRTDLOEANDILNNLKDFDRRVNDNKTAAEEALRKIPAINQITTEANEKTRTAAQALG 1413
Db 1321 KKGRTDLOEANDILNNLKDFDRRVNDNKTAAEEALRKIPAINQITTEANEKTRTAAQALG 1380
Qy 1414 SAAADATEAKNAKHAHEAERIAASAVQKNATSTKAEAEARTFAEVTDLNNEVNNMLKQLEAEK 1473
Db 1381 SAAADATEAKNAKHAHEAERIAASAVQKNATSTKAEAEARTFAEVTDLNNEVNNMLKQLEAEK 1440
Qy 1474 ELKRKQDDADQDMVMAGMASQAAQAEAEINARKAKNSVTSLLSIINDLLEQLGLDITVDLN 1533
Db 1441 ELKRKQDDADQDMVMAGMASQAAQAEAEINARKAKNSVTSLLSIINDLLEQLGLDITVDLN 1500
Qy 1534 KLNEIEGTLNKADEMKSVDLDRKVSVDLENAKKQEAAMDVNREIEEIMKDIRNLEDIR 1593
Db 1501 KLNEIEGTLNKADEMKSVDLDRKVSVDLENAKKQEAAMDVNREIEEIMKDIRNLEDIR 1560
Qy 1594 KTLPSGCFNTPSIEKP 1609
Db 1561 KTLPSGCFNTPSIEKP 1576

RESULT 6

US-09-562-702A-28
; Sequence 28, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 1584
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-28

Query Match 98.1%; Score 8544; DB 4; Length 1584;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 34 QAAMDECTDEGGRPQRCMPPEFVNAAFNVTVATNTCGTPPEEYCVQTVGTGVTKSCHLCD 93
Db 1 QAAMDECTDEGGRPQRCMPPEFVNAAFNVTVATNTCGTPPEEYCVQTVGTGVTKSCHLCD 60
Qy 94 AGOPHLQHGAFLTDYNNQADTTWQSQTMLAGVQYPPSSINLTLHLGKAFDITYVRLKFX 153
Db 61 AGOPHLQHGAFLTDYNNQADTTWQSQTMLAGVQYPPSSINLTLHLGKAFDITYVRLKFX 120
Qy 154 TSRPESFAIYKRTREDGPWIPYQYYSGSCENTYSKANRGFIRTTGGDEQQAALCTDEFSDIS 213
Db 121 TSRPESFAIYKRTREDGPWIPYQYYSGSCENTYSKANRGFIRTTGGDEQQAALCTDEFSDIS 180
Qy 214 PLTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSY 273
Db 181 PLTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSY 240
Qy 274 YYAISDFAVGGRCKCNHGHASECMKNEFDKLVCKNCKHNTYGVDCCKCLPFFNDRPWRATA 333
Db 241 YYAISDFAVGGRCKCNHGHASECMKNEFDKLVCKNCKHNTYGVDCCKCLPFFNDRPWRATA 300
Qy 334 ESASECLPCDCNCRSQBCYFDPPELYRSTGHGCHCTNCQDNTDGAHCRCRENFRLGNNE 393
Db 301 ESASECLPCDCNCRSQBCYFDPPELYRSTGHGCHCTNCQDNTDGAHCRCRENFRLGNNE 360
Qy 394 ACSSCHCSPVGSLSLSTQDSYGRCSCKPGVMGDKDCRCQPGFHSLTEAGCRPCSCDPSGSI 453
Db 361 ACSSCHCSPVGSLSLSTQDSYGRCSCKPGVMGDKDCRCQPGFHSLTEAGCRPCSCDPSGSI 420
Qy 454 DECNVETGRCVCKDNVEGFNCERCCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGSYVY 513
Db 421 DECNVETGRCVCKDNVEGFNCERCCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGSYVY 480
Qy 514 SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPRIYFIAPAKFLGKQVLSY 573
Db 481 SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPRIYFIAPAKFLGKQVLSY 540
Qy 574 GQNLFSFRVDRDRTRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYVFRLEHATDY 633
Db 541 GQNLFSFRVDRDRTRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYVFRLEHATDY 600
Qy 634 PWRPALTPFEFQKLLNLTSLIKIRGTYSERSAGYLDVTLASARPGGVPATWVESCTCP 693
Db 601 PWRPALTPFEFQKLLNLTSLIKIRGTYSERSAGYLDVTLASARPGGVPATWVESCTCP 660
Qy 694 VGYGGQFCEMCLSGYRRETPNLGYPSPCVLCAACNGHSETCDPETGVCNCRDNTAGPHCEK 753
Db 661 VGYGGQFCEMCLSGYRRETPNLGYPSPCVLCAACNGHSETCDPETGVCNCRDNTAGPHCEK 720
Qy 754 CSDGYGDSYTAGTSSDCQPCPCPGSSCAVVPKTKVWCTNCPGTGTGKRCCELDDGYFG 813
Db 721 CSDGYGDSYTAGTSSDCQPCPCPGSSCAVVPKTKVWCTNCPGTGTGKRCCELDDGYFG 780
Qy 814 DPLGRNGPVRRLCRLCQSDNIDPNAVGNCRNLTGECCLKIYNTAGFYCDRCKDGFNPL 873
Db 781 DPLGRNGPVRRLCRLCQSDNIDPNAVGNCRNLTGECCLKIYNTAGFYCDRCKDGFNPL 840
Qy 874 APNPADKCKACNCNPFYGTMTKQSSCNPNVTGQCECLPHVTGQDCGACDPGFYNLQSGQGE 933
Db 841 APNPADKCKACNCNPFYGTMTKQSSCNPNVTGQCECLPHVTGQDCGACDPGFYNLQSGQGE 900
Qy 934 RCDCHALGSTNGQCDIRGTGQCECQPGITGQHCHCERCEVNHFGFEGCKPCDCHPEGSLSL 993
Db 901 RCDCHALGSTNGQCDIRGTGQCECQPGITGQHCHCERCEVNHFGFEGCKPCDCHPEGSLSL 960
Qy 994 QCKDDGRCECREGFGVGNRCDCQCEENFYNRSWPGCQCEPACVRLVKDKVADHRVKLQELE 1053
Db 961 QCKDDGRCECREGFGVGNRCDCQCEENFYNRSWPGCQCEPACVRLVKDKVADHRVKLQELE 1020
Qy 1054 SLIANLGTGDEMVTDAQAFEDRLKEAEREVMDLLREAQDVVDQNLMDRLQRVNNTLSSQ 1113

Db 1021 SLIANLGTGDEMVTDOAFEDRLKEAREVMDLLREAOQVDVQNLMDRLQRVNNLTSSQ 1080
Qy 1114 ISRLQIRNTIETGNLAEOARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1173
Db 1081 ISRLQIRNTIETGNLAEOARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1140
Qy 1174 NNMTLLAEEARKLAERHKEADDDIVRAKTANDTSTEAYNLLRTLAGENQTAFAIEELN 1233
Db 1141 NNMTLLAEEARKLAERHKEADDDIVRAKTANDTSTEAYNLLRTLAGENQTAFAIEELN 1200
Qy 1234 RKYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDSETLENEANNIKNEA 1293
Db 1201 RKYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDSETLENEANNIKNEA 1260
Qy 1294 ENLEQLIDQKLKDYEDLREDMRGKELEVKNLLEKKGTEQQTADQLLARADAAKALAEZAA 1353
Db 1261 ENLEQLIDQKLKDYEDLREDMRGKELEVKNLLEKKGTEQQTADQLLARADAAKALAEZAA 1320
Qy 1354 KKGRTDLEANDILNNLKDFDRRVNDNKTAEEALRKIPAINQITTEANEKTRAAQQAALG 1413
Db 1321 KKGRTDLEANDILNNLKDFDRRVNDNKTAEEALRKIPAINQITTEANEKTRAAQQAALG 1380
Qy 1414 SAAADATEAKNKAHEAERIAASAVQKNATSTKAEARTFAEVTDLNEVNNMLKQLQEAEK 1473
Db 1381 SAAADATEAKNKAHEAERIAASAVQKNATSTKAEARTFAEVTDLNEVNNMLKQLQEAEK 1440
Qy 1474 ELKRKQDDADQDMMAGMASQAQAEAINARKAKNSVTSLLSIINDLLEQLGQDLDVNLN 1533
Db 1441 ELKRKQDDADQDMMAGMASQAQAEAINARKAKNSVTSLLSIINDLLEQLGQDLDVNLN 1500
Qy 1534 KLINEIEGTLNKADEMKSVDLDRKVSQDLENEAKKQEAAIMDYNRDIEEIMKDIRNLEDIR 1593
Db 1501 KLINEIEGTLNKADEMKSVDLDRKVSQDLENEAKKQEAAIMDYNRDIEEIMKDIRNLEDIR 1560
Qy 1594 KTLPSGCFNTPTSEKP 1609
Db 1561 KTLPSGCFNTPTSEKP 1576

RESULT 7
US-09-562-702A-30
; Sequence 30, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 1605
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-562-702A-30

Query Match 93.5%; Score 8148; DB 4; Length 1605;
Best Local Similarity 92.8%; Pred. No. 0;
Matches 1493; Conservative 59; Mismatches 53; Indels 4; Gaps 3;
Qy 1 MRGSHRAAPALPRGRLLWPLVLAIAAAAGCAQAAMDECTDEGGPQRCMPFVNAAFN 60
Db 1 MTGGGRAALALQPRGRLLWPLLAVL--AAVAGCVRAAMDECADEGGPQRCMPFVNAAFN 58

Qy 61 VTVVATNTCGTTPPEEYCVQTVGTGVTKSCHLCDAGQPHLQHGAAFLTDYNNQADTTWQS 120
Db 59 VTVVATNTCGTTPPEEYCVQTVGTGVTKSCHLCDAGQQHLQHGAAFLTDYNNQADTTWQS 118
Qy 121 QTMLAGVQYPPSSINLTHLGKAFDITYVRLKFHTSRPESFAIYKHTREDGPWIPYQYYSG 180
Db 119 QTMLAGVQYPPSSINLTHLGKAFDITYVRLKFHTSRPESFAIYKHTREDGPWIPYQYYSG 178
Qy 181 SCENTYSKANRGEFIRTTGGDEQOALCTDEFSDISPLTGGNVAFSTILEGRPSAYNFDNSPVL 240
Db 179 SCENTYSKANRGEFIRTTGGDEQOALCTDEFSDISPLTGGNVAFSTILEGRPSAYNFDNSPVL 238
Qy 241 QEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSYYYAISDFAVGGRCKCNGHASECMKNEF 300
Db 239 QEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSYYYAISDFAVGGRCKCNGHASECMKNEF 298
Qy 301 DKLVCNCKHNTYGVDCCEKCLPFFNDRPWRRTAESAECPLPCDCNCRSQECYFDPPELYRS 360
Db 299 DKLVCNCKHNTYGVDCCEKCLPFFNDRPWRRTAESAECPLPCDCNCRSQECYFDPPELYRS 358
Qy 361 TGHGGHCTNCQDNTDGAHCERCRENFFRLGNNEACSSCHSPVGSLSLSTQCDSDYGRCSCKP 420
Db 359 TGHGGHCTNCQDNTDGAHCERCRENFFRLGNNEACSSCHSPVGSLSLSTQCDSDYGRCSCKP 418
Qy 421 GVMGDKCDRCQPGFHSLSLTAAGCRPCSCDPSGSDIENETGRCVCKDNVEGFNCERCCKPG 480
Db 419 GVMGDKCDRCQPGFHSLSLTAAGCRPCSCDPSGSDIENETGRCVCKDNVEGFNCERCCKPG 478
Qy 481 FFNLESSNPRGCTPCFCFGHSSVCTNAVGSYVYSSISSTFQIDEDGWRAEQRDGSEASLEW 540
Db 479 FFNLESSNPKGCTPCFCFGHSSVCTNAVGSYVYSSISSTFQIDEDGWRAEQRDGSEASLEW 538
Qy 541 SSERQDIAVISDSYFPFRIYFIAPAKFLGKQVLSYQNLSPSFRVDRDRDTRLSAEDLVLEGA 600
Db 539 SSERQDIAVISDSYFPFRIYFIAPAKFLGKQVLSYQNLSPSFRVDRDRDTRLSAEDLVLEGA 598
Qy 601 GLRVSVPLIAQGNSTPSETTVKYVFRLEHATDYPWRPALTPFEFQKLLNNLTSLIKIRGTY 660
Db 599 GLRVSVPLIAQGNSTPSETTVKYVFRLEHATDYPWRPALTPFEFQKLLNNLTSLIKIRGTY 658
Qy 661 SERSAGYLDVTLASARPGVPATWVESCTCPVGYGGQFCMCLSGYRRRETPLNGPYSP 720
Db 659 SERSAGYLDVTLASARPGVPATWVESCTCPVGYGGQFCMCLSGYRRRETPLNGPYSP 718
Qy 721 CVLCACNGHSETCDPBTGVCNCRDNTAGPHCEKCSDDGYGDSYTAGTSSDCQPCPCPGSS 780
Db 719 CVLCACNGHSETCDPBTGVCNCRDNTAGPHCEKCSDDGYGDSYTAGTSSDCQPCPCPGSS 778
Qy 781 CAIVPKTKEVVCNCTGTTGKRCCELDDGYFGDPLGRNGPVRLCLQCSDNIDPNAVG 840
Db 779 CAIVPKTKEVVCNCTGTTGKRCCELDDGYFGDPLGRNGPVRLCLQCSDNIDPNAVG 838
Qy 841 NCNRLTGECLKCIYNTAGFYCDRCXGDFGNGPLAPNPADKCKACNPNPYGTMKQSSCNP 900
Db 839 NCNRLTGECLKCIYNTAGFYCDRCXGDFGNGPLAPNPADKCKACNPNPYGTMKQSSCNP 897
Qy 901 VTGQCECLPHVTGQPCGACDPGFYVNLQSGGGERCDCHALGSTNGQCDIRTGQCECQPGI 960
Db 898 VTGQCECLPHVTGQPCGACDPGFYVNLQSGGGERCDCHALGSTNGQCDIRTGQCECQPGI 957
Qy 961 TGOHCERCEVNHFGFEGEGCKPCDCHPEGSLSLQCKDDGRCECREGFGVNRCDQCEENYF 1020
Db 958 TGOHCERCEVNHFGFEGEGCKPCDCHPEGSLSLQCKDDGRCECREGFGVNRCDQCEENYF 1017
Qy 1021 YNRSWPGCQECPCYRLVKDKVADHRVKLQELLESILIANLGTGDEMVTDOAFEDRLKEAER 1080
Db 1018 YNRSWPGCQECPCYRLVKDKVADHRVKLQELLESILIANLGTGDEMVTDOAFEDRLKEAER 1077
Qy 1081 EVMDDLLEAQVDVQNLMDRLQRVNNLTSSQISRLQIRNTIETGNLAEOARAHVEN 1140
Db 1078 EVMDDLLEAQVDVQNLMDRLQRVNNLTSSQISRLQIRNTIETGNLAEOARAHVEN 1137

Qy 1141 TERLIEIASRELEKAKVAAANVSVTQPESTGDPNNMTLLAEARKLAERHKQEAADDIVRV 1200
Db 1138 TEOLIEIASRELEKAKM-AANVSITQPESTGEPPNNMTLLAEARRLAERHKQEAADDIVRV 1196
Qy 1201 AKTANDTSTEAYNLLRLTLTLAGENQTAFAIEELNRKYEQAKNISQDLEKQAAARVHEEAKRA 1260
Db 1197 AKTANETSABAYNLLRLTLTLAGENQTALEIEELNRKYEQAKNISQDLEKQAAARVHEEAKRA 1256
Qy 1261 GDKAVEIYASVAQLSPDLSETLENEANNIKMEAEENLEQLIDQKLKDYEDLREDMRGKELE 1320
Db 1257 GDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLRLIDQKLKDYEDLREDMRGKEHE 1316
Qy 1321 VKNLLLEKGTQEQQTADQOLLARADAALAEAAKKGRTTLQEAANDILNLLKDFDRRVNDN 1380
Db 1317 VKNLLLEKGAEQQTADQOLLARADAALAEAAKKGRTTLQEAANDILNLLKDFDRRVNDN 1376
Qy 1381 KTAEEALRKIPAINQITTEANEKTRAQQAALGSAADATEAKNKAHEAERIAASAVQKNA 1440
Db 1377 KTAEEALRRIPAINRTIAANEKTRAQALALGNAADATEAKNKAHEAERIAASAAQKNA 1436
Qy 1441 TSTKAEARTFAEVTDLNEVNNMLKQIQAELKQKQDDADQDMMAGMASQAQAEAB 1500
Db 1437 TSTKADAERTFGEVTDLDNEVNGMLRQLEEAENELKQKQDDADQDMMAGMASQAQAEAB 1496
Qy 1501 INARKAKNSVTSLSIIINDLLEQLQGLDPTVDLNLKLEIEGTLNKADEMKSVDLDRKVS 1560
Db 1497 LNARKAKNSVSSLSQLNLLDQLGLDPTVDLNLKLEIEGSLNKADEMKSVDLDRKVS 1556
Qy 1561 LENEAKKQEAALMDYNRDIEEIMKDIRNLEDIRKTLPSGCFNTPSIEKP 1609
Db 1557 LESEARKQEAALMDYNRDIAEIIKDIHNELEIKKTLPTGCFNTPSIEKP 1605

RESULT 8

US-09-561-818A-26
; Sequence 26, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortessmaa, Jarkko
; APPLICANT: Tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 1605
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-561-818A-26

Query Match 93.5%; Score 8148; DB 4; Length 1605;
Best Local Similarity 92.8%; Pred. No. 0;
Matches 1493; Conservative 59; Mismatches 53; Indels 4; Gaps 3;

Qy 1 MRGSHRAAPALRPRGRLLWPLVAVLAAAAAGCAQAAMDECTDEGGRPQRCMPPEFVNAAFN 60
Db 1 NTGGGRAALALQPRGRLLWPLVAVL--AAVAGCVRAAMDECADEGGRPQRCMPPEFVNAAFN 58
Qy 61 VTVVATNTCGTPPEEYCVQTGVTGVTKSCHLCDAGQPHLOHGAFLTDYNNQADTTWQOS 120
Db 59 VTVVATNTCGTPPEEYCVQTGVTGVTKSCHLCDAGQPHLOHGAFLTDYNNQADTTWQOS 118
Qy 121 QTMLAGVQYPSSINLTLLHKGAFDITYVRLKFTSRPESFAIYKRTREDGWPWIPYQYISG 180
Db 119 QTMLAGVQYPNSINLTLLHKGAFDITYVRLKFTSRPESFAIYKRTREDGWPWIPYQYISG 178
Qy 181 SCENTYSKANRGFIRTGDEQQALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFDNSPVL 240
Db 179 SCENTYSKANRGFIRTGDEQQALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFDNSPVL 238
Qy 241 QEWVTATDIRVTNLNLTFGDEVFNDPKVLKSYYYAISDAVGGRCCKNGHASECMKNEF 300

Db 239 QEWVTATDIRVTNLNLTFGDEVFNDPKVLKSYYYAISDAVGGRCCKNGHASECMKNEF 298
Qy 301 DXLVNCNKHNTYGVDCCKLPFFNDRPWRRATAESASECLPCDCNGRSQECYFDPPELYRS 360
Db 299 DXLMCNCKHNTYGVDCCKLPFFNDRPWRRATAESASECLPCDCNGRSQECYFDPPELYRS 358
Qy 361 TGHGGHCTNCQDNTDGAHCERCERENFFRLGNNEACSSCHCSPVGSLSLTCDSYGRCSCKP 420
Db 359 TGHGGHCTNCRDNTDGAHCERCERENFFRLGNTEACSPCHCSPVGSLSLTCDSYGRCSCKP 418
Qy 421 GVMGDKCDRCQPGPHSLTEAGCRPCSCDPSGSDIECNVETGRVCVKDNVEGFNCERCCKPG 480
Db 419 GVMGDKCDRCQPGPHSLTEAGCRPCSCDPSGSDIECNVETGRVCVKDNVEGFNCERCCKPG 478
Qy 481 FFNLESSNPRGCTPCFCFGHSSVCTNAVGYSVYSISSTFQIDEDGWRABEQDSEASLEW 540
Db 479 FFNLESSNPKGCTPCFCFGHSSVCTNAVGYSVYDISSTFQIDEDGWRABEQDSEASLEW 538
Qy 541 SSERQDIAVISDSYFPRYFIAPAKFLGKQVLSYGQNLSPSFRVDRDRDTRLAEDLVLEGA 600
Db 539 SSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYGQNLSPSFRVDRDRDTRLAEDLVLEGA 598
Qy 601 GLRVSVPLIAQNSYPSSETTVKYVFRLHEATDYPWRPALTPFEFQKLLNNLTSIKIRGT 660
Db 599 GLRVSVPLIAQNSYPSSETTVKYIFRLHEATDYPWRPALSPFEFQKLLNNLTSIKIRGT 658
Qy 661 SERSAGYLDVTLASARPGVPATWVESCTCPVYGGQFCMCLSGYRRRETNPGLPYSP 720
Db 659 SERSAGYLDVTLQ SARPGVPATWVESCTCPVYGGQFCETCLPGYRRRETNPGLPYSP 718
Qy 721 CVLCAACNGHSETCDPETGVNCRDNTAGPHCEKCSGYYGDSGTAGTSSDCQPCPCGGSS 780
Db 719 CVLCTCNGHSETCDPETGVCDNRDNTAGPHCEKCSGYYGDSGTAGTSSDCQPCPCGGSS 778
Qy 781 CAVPKTKEVVCTNCPTGTTGKRCCLCDDGYFGDPLGRNGPVLRLCQCSDNIDPNAV 840
Db 779 CAIVPKTKEVVCTHCPTGTAGKRCCLCDDGYFGDPLGNSGPNVRLCRPCQCNIDPNAV 838
Qy 841 NCNRLTGECLKIYNTAGFYCDRCCKGFFGNPLAPNPADKCKACNPNPYGTMKQSSCNP 900
Db 839 NCNRLTGECLKIYNTAGFYCDRCCKGFFGNPLAPNPADKCKACNPNPYGTMKQSSCNP 897
Qy 901 VTGQCECLPHVTGDCGACDPGFYNLQSGGQCCERCDCHALGSTNGQDIRTGQCECQPGI 960
Db 898 VTGQCQCLPHVSGRDCGTCDPGYNNLQSGGQCCERCDCHALGSTNGQDIRTGQCECQPGI 957
Qy 961 TGOHCERCEVNHFGPEGCKPCDCHPEGSLQCKDDGRCEGFGVGNRCDCQCEENYF 1020
Db 958 TGOHCERCETNHFEGPEGCKPCDCHHEGSLQCKDDGRCEGFGVGNRCDCQCEENYF 1017
Qy 1021 YNRSWPGCQCECPACVRLVKDKVADHRVKLOELESIANLGTGDEMVTDAQAFEDRLKEAER 1080
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Qy 1081 EVMDDLREAOQVXDQNLMDRLQRVNNTLSSQISRLQNRNIRNTIETGNLAEQARAHVEN 1140
Db 1078 EVTDLREAOQVXDQNLMDRLQRVNNTLSSQISRLQNRNIRNTIETGILAEARARSVES 1137
Qy 1141 TERLIEIASRELEKAKVAAANVSVTQPESTGDPNNMTLLAEARKLAERHKQEAADDIVRV 1200
Db 1138 TEOLIEIASRELEKAKM-AANVSITQPESTGEPPNNMTLLAEARRLAERHKQEAADDIVRV 1196
Qy 1201 AKTANDTSTEAYNLLRLTLTLAGENQTAFAIEELNRKYEQAKNISQDLEKQAAARVHEEAKRA 1260
Db 1197 AKTANETSABAYNLLRLTLTLAGENQTALEIEELNRKYEQAKNISQDLEKQAAARVHEEAKRA 1256
Qy 1261 GDKAVEIYASVAQLSPDLSETLENEANNIKMEAEENLEQLIDQKLKDYEDLREDMRGKELE 1320
Db 1257 GDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLRLIDQKLKDYEDLREDMRGKEHE 1316
Qy 1321 VKNLLLEKGTQEQQTADQOLLARADAALAEAAKKGRTTLQEAANDILNLLKDFDRRVNDN 1380

Db 1317 VKNLLEKGAEQQTADQLLARADAAKALAEAAKGRSTLQEAANDILNKLKDFDRRVNDN 1376
Qy 1381 KTAABEALRKIPAINQITTEANEKTRTAAQALGSAADATEAKNKAHEABERIASAVQKNA 1440
Db 1377 KTAABEALRRIPAINRTIAEANEKTRTAAQALGSAADATEAKNKAHEABERIASAAQKNA 1436
Qy 1441 TSTKABAEARTFAEVTDLNEVNNMLKQLOBAEKELKRQDDADQDMMAGWASQAAQAE 1500
Db 1437 TSTKABAEARTFGEVTDLDNEVNGMLRQLEEAENELKRQDDADQDMMAGWASQAAQAE 1496
Qy 1501 INARKAKNSVTSLLSIINDLLEQLGQDQDQDQDQDQDQDQDQDQDQDQDQDQDQDQDQD 1560
Db 1497 INARKAKNSVSSLLSQQNLNLDQDQDQDQDQDQDQDQDQDQDQDQDQDQDQDQDQD 1556
Qy 1561 LENEAKKQEAAMINDYNDRIEIMKDINLEDIRKTLPSGCFNTPSIEKP 1609
Db 1557 LESEARKQEAAMINDYNDRIEIMKDINLEDIRKTLPSGCFNTPSIEKP 1605

RESULT 9
US-09-562-702A-32
; Sequence 32, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 1572
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-562-702A-32

Query Match 92.3%; Score 8038; DB 4; Length 1572;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;

Qy 36 AMDECTDEGGRPQRCMPEFVNAAFNVTVATNTCGTPPEEYCVQGTGVTGTSCHLCDAG 95
Db 1 AMDECADEGGRPQRCMPEFVNAAFNVTVATNTCGTPPEEYCVQGTGVTGTSCHLCDAG 60
Qy 96 QPHLQGAFLTDYNNQADTTWQSQTMLAGVQYPPSSINLTLHLGKAFDITYVRLKFHTS 155
Db 61 QHLQGAFLTDYNNQADTTWQSQTMLAGVQYPPSSINLTLHLGKAFDITYVRLKFHTS 120
Qy 156 RPESAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQALCTDFSDISPL 215
Db 121 RPESAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQALCTDFSDISPL 180
Qy 216 TGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVNDPKVLKSYYY 275
Db 181 TGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVNDPKVLKSYYY 240
Qy 276 AISDFAVGGRCKCNGHASECMKNEFDKLVCKNCKHNTYGVDCCKLPPFNDRPWRATAES 335
Db 241 AISDFAVGGRCKCNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPPFNDRPWRATAES 300
Qy 336 ASECLPCDCNGRSQECYFDPPELYRSTGHGGHCTNCQDNTDGAHCERCRCRENFELGNNEAC 395
Db 301 ASECLPCDCNGRSQECYFDPPELYRSTGHGGHCTNCRDNTDGAHCERCRCRENFELGNTEAC 360

Qy 396 SSCHCSPVGLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLSLTAAGRPCSCDPSGSGSIDE 455
Db 361 SPCHCSPVGLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLSLTAAGRPCSCDPSGSGTDE 420
Qy 456 CNVETGRCVCKDNVEGNCERCKPGFFNFLESSNPRGCTPCFCFSGHSSVCTNAVGSVYSI 515
Db 421 CNVETGRCVCKDNVEGNCERCKPGFFNFLESSNPRGCTPCFCFSGHSSVCTNAVGSVYDI 480
Qy 516 SSTFQIDEDGWAEQRDSEASLEWSSERQDIAVTSDSYFPRYFIAPAKFLGKQVLSYQ 575
Db 481 SSTFQIDEDGWRVEQRDSEASLEWSSDRQYIAVTSDSYFPRYFIAPVKFLGNQVLSYQ 540
Qy 576 NLSFSFRVDRRDLRLSAEDLVLEGAGLRVSPLIAQNSYSPSETTVKYVFRLEHATDYPW 635
Db 541 NLSFSFRVDRRDLRLSAEDLVLEGAGLRVSPLIAQNSYSPSETTVKYVFRLEHATDYPW 600
Qy 636 RPALTPEFQKLLNLTSLKIRGTYSERSAGYLDVTLASARPGVGPATWVESCTCPVG 695
Db 601 RPALSPFEFQKLLNLTSLKIRGTYSERSAGYLDVTLQASRPGVGPATWVESCTCPVG 660
Qy 696 YGQFCMCLSGYRRTPNLGPSPCVLCAENGHSETCDPETGVNCNRDNTAGPHECKCS 755
Db 661 YGQFCETCLPGYRRTPSLGPSPCVLCTCNGHSETCDPETGVCDNRDNTAGPHECKCS 720
Qy 756 DGYGDSSTAGTSSDQPCPCPGSSCAVVPKTKVCTNCPTGTTGKRCELDDGYFGDP 815
Db 721 DGYGDSSTAGTSSDQPCPCPGSSCAVVPKTKVCTNCPTGTTGKRCELDDGYFGDP 780
Qy 816 LGRNGPVRLLCRLCQCSNDIDPNAVGNLRTGECLKCIYNTAGFYCDCKDGFENPLAP 875
Db 781 LGSNGPVRLLCRLCQCSNDIDPNAVGNLRTGECLKCIYNTAGFYCDCKDGFENPLAP 840
Qy 876 NPADKCKACNPNPYGTMKQSSCNPNVTGQCECLPHVTGQDCGACDPGFYNLQSGQCERC 935
Db 841 NPADKCKACACN- YGTVQOQSSCNPNVTGQCCPLPHVSRDCTGCDPGYYNLQSGQCERC 899
Qy 936 DCHALGSTNGQCDIRTGQCEQPGITGQHCHERCENHFGFEGCKPCDCHPEGSLSLQC 995
Db 900 DCHALGSTNGQCDIRTGQCEQPGITGQHCHERCENHFGFEGCKPCDCHPEGSLSLQC 959
Qy 996 KDDGRCEGREGFVGNRCDCQCBENYFYNRSWPGCQCPACRYLVKDKVADHRVKLQLESL 1055
Db 960 KDDGRCEGREGFVGNRCDCQCBENYFYNRSWPGCQCPACRYLVKDKAAEHRVKLQLESL 1019
Qy 1056 IANLGTGDEMVTDAQFEDRLKEAEREVMDLLREAQDVKDQVQDQNLMDRLQRVNNTLSSQIS 1115
Db 1020 IANLGTGDDMVTDAQFEDRLKEAEREVTDLLREAQDVKDQVQDQNLMDRLQRVNNTLSSQIS 1079
Qy 1116 RLQNTIRNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDPNN 1175
Db 1080 RLQNTIRNTIETGILAEARARSRVESTEQLIEIASRELEKAKM-AANVSITQPESTGEPNN 1138
Qy 1176 MTLAAEEARKLAERHKQEAADDIVRVAKTANDTSTEAYNLLRLTLAGENQTAFEIEELNRK 1235
Db 1139 MTLAAEEARRLAERHKQEAADDIVRVAKTANETSABEAYNLLRLTLAGENQTALEIEELNRK 1198
Qy 1236 YEOAKNISQDLEKQAAARVHEBAKAGDKAVEIYASVAQLSPDSETLEANEANNIKMEAE 1295
Db 1199 YEOAKNISQDLEKQAAARVHEBAKAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAAD 1258
Qy 1296 LEQLIDQKLKDYEDLREDMRGKELEVKNLLEKKGTEQQTADOLLARADAAKALAEBAK 1355
Db 1259 LDRLIDQKLKDYEDLREDMRGKEHEVKNLLEKKGAEQQTADOLLARADAAKALAEBAK 1318
Qy 1356 GRDTLQEAANDILNKLKDFDRRVNDNKTAAEBALRKIPAINQITTEANEKTRTAAQALGSA 1415
Db 1319 GRSTLQEAANDILNKLKDFDRRVNDNKTAAEBALRRIPAINRTIAEANEKTRTAAQALGNA 1378
Qy 1416 AADATEAKNKAHEAERIAASVQKNATSTKAAEAERTFAEVTDLNEVNNMLKQLOBAEKEL 1475
Db 1379 AADATEAKNKAHEAERIAASVQKNATSTKAAEAERTFAEVTDLNEVNGMLRQLEEAENEL 1438
Qy 1476 KRQDDADQDMMAGMASQAAQEAENARKAKNSVTSLLSIINDLLEQLGQDQDQDQDQDQD 1535

Db 1439 KRKQDDADQDMMAGMASQAQAELNARKAKNSVSSLLSQNNLLDQLGQDLDVLDNKL 1498
Qy 1536 NEIEGTLNKADEMKSVDLDRKVSLENEAKKQEAAMNDYNRDIEEIMKDIRNLEDIRKT 1595
Db 1499 NEIEGSLNKADEMKSVDLDRKVSLENEAKKQEAAMNDYNRDIAEIIKDIHNELEDIRKT 1558
Qy 1596 LPSGCFNTPSIEKP 1609
Db 1559 LPTGCFNTPSIEKP 1572

RESULT 10

US-09-561-818A-28
; Sequence 28, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortessmaa, Jarrko
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 28
; LENGTH: 1572
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-561-818A-28

Query Match 92.3%; Score 8038; DB 4; Length 1572;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;

Qy 36 AMDECTDEGRPQRCMPEFVNAFNVVATNTCGTPPEEYCVQGTGVTGKSKCHLCLDAG 95
Db 1 AMDECADEGRPQRCMPEFVNAFNVVATNTCGTPPEEYCVQGTGVTGKSKCHLCLDAG 60
Qy 96 QPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYPSINLTLLHKGAFDITYVRLKFHTS 155
Db 61 QHQLHGAAFLTDYNNQADTTWQSQTMLAGVQYPSINLTLLHKGAFDITYVRLKFHTS 120
Qy 156 RPESFALYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDISPL 215
Db 121 RPESFALYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDISPL 180
Qy 216 TGGNVAFSTLEGRPSAYNFEDNSPVLQEWVATDIRVTNLRNTFGDEVNDPKVLKSYVY 275
Db 181 TGGNVAFSTLEGRPSAYNFEDNSPVLQEWVATDIRVTNLRNTFGDEVNDPKVLKSYVY 240
Qy 276 AISDFAVGRCKCNGHASECMKVEFDFKLVNCNKHNTYGVDCCKLPFFNDRPWRRTAES 335
Db 241 AISDFAVGRCKCNGHASECMKVEFDFKLVNCNKHNTYGVDCCKLPFFNDRPWRRTAES 300
Qy 336 ASECLPCDCNGRSQECYFDPPELYRSTGHGGHCTNCDNTDGAHCRCRCRENFFRLGNNEAC 395
Db 301 ASECLPCDCNGRSQECYFDPPELYRSTGHGGHCTNCDNTDGAHCRCRCRENFFRLGNTEAC 360
Qy 396 SSCHCSPVGLSTQCDYSGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSIDE 455
Db 361 SPCHCSPVGLSTQCDYSGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSTDE 420
Qy 456 CNVETGRVCVKDNVEGFNCRCCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGSYVSI 515
Db 421 CNVETGRVCVKDNVEGFNCRCCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGSYVSI 480
Qy 516 SSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVSDSYFFPRYFIAPAKFLGKQVLSYGQ 575
Db 481 SSTFQIDEDGWRAEQRDGSEASLEWSSDRQYIAVSDSYFFPRYFIAPVKFLGNQVLSYGQ 540
Qy 576 NLSFSFRVDRDRLSAEDLVLEGAGLRVSVPLIAQNSYPSSETTVKYIFRLHEATDYPW 635

Db 541 NLSFSFRVDRDRLSAEDLVLEGAGLRVSVPLIAQNSYPSSETTVKYIFRLHEATDYPW 600
Qy 636 RPALTPFEFQKLLNNLTISKIRGTYSERSAGYDDVTLASARPGPGVPATWVESCTCPVG 695
Db 601 RPALSPFEFQKLLNNLTISKIRGTYSERSAGYDDVTLQASRPGPGVPATWVESCTCPVG 660
Qy 696 YGGQFCMCLSGYRRETPNLGPYSPCVLCACNGHSETCDPETGVNCRDNTAGPHCEKCS 755
Db 661 YGGQFCETCLPGYRRETPSLGPYSPCVLCTCNGHSETCDPETGVNCRDNTAGPHCEKCS 720
Qy 756 DGYYGDSSTAGTSDCQPCPCPGSSCAVVPKTKVCTNCTPTGTTGKRCCELDDGYFGDP 815
Db 721 DGYYGDSSTAGTSDCQPCPCPGSSCAVVPKTKVCTNCTPTGTTGKRCCELDDGYFGDP 780
Qy 816 LGRNGPVRLLCRLCQSDNIDPNAVGNCRNLTGECLKCIYNTAGFYCDRCCKGFFGNPLAP 875
Db 781 LGSNGPVRLLCRLCQSDNIDPNAVGNCRNLTGECLKCIYNTAGFYCDRCCKGFFGNPLAP 840
Qy 876 NPADKCKACNCPYGTMKQSSCNPVTCQCECLPHVTGQDCGACDPPGFYNLQSGQGCRERC 935
Db 841 NPADKCKACACN-YGTVQQSSCNPVTCQCCQLPHVSGRDCGTCDPGYNNLQSGQGCRERC 899
Qy 936 DCHALGSTNGQCDIRTGQCECQPGITGQHCHERCENHFGFEGCKPCDCHPEGSLSLQC 995
Db 900 DCHALGSTNGQCDIRTGQCECQPGITGQHCHERCENHFGFEGCKPCDCHPEGSLSLQC 959
Qy 996 KDDGRCECREGFGVGNRCDCQCEENYFYNRSMWPGCQCPACVRLVKDKVADHRVKLOELES 1055
Db 960 KDDGRCECREGFGVGNRCDCQCEENYFYNRSMWPGCQCPACVRLVKDKVADHRVKLOELES 1019
Qy 1056 IANLGTGDEMVTQAPEDRLKEAREVMDLLREAAQVDKVDQNLMDRLQRVNNTLSQSIS 1115
Db 1020 IANLGTGDEMVTQAPEDRLKEAREVMDLLREAAQVDKVDQNLMDRLQRVNNTLSQSIS 1079
Qy 1116 RLQNRNTIETGNLAEOQARAHVENTERLIEIASRELEKAKAAANVSITQPESTGDPNN 1175
Db 1080 RLQNRNTIETGILAEARARSVESTEOLEIEIASRELEKAKAAANVSITQPESTGEPNN 1138
Qy 1176 MTLLEAEARKLAERHKEADDIVRVAKTANDTSTEAVNLLRLTLAGEQTAFIEELNRK 1235
Db 1139 MTLLEAEARKLAERHKEADDIVRVAKTANETSAAEAVNLLRLTLAGEQTAFIEELNRK 1198
Qy 1236 YEQAKNISQDLEKQAAARVHEEAKAGDKAVEIYASVAQLSPLDSETLENEANNIKHAEAN 1295
Db 1199 YEQAKNISQDLEKQAAARVHEEAKAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAAD 1258
Qy 1296 LEQLIDQKLDYEDLREDMRGKELEVNKLEKGTQEQADQALLARADAALAEBAK 1355
Db 1259 LDRLIDQKLDYEDLREDMRGKELEVNKLEKGTQEQADQALLARADAALAEBAK 1318
Qy 1356 GRDTLOEANDILNNLKDFDRRVNDNKTAAEALRKIPAINQITTEANEKTRAEQAALGSA 1415
Db 1319 GRSTLOEANDILNNLKDFDRRVNDNKTAAEALRRIPAINRTIAEANEKTRAEQAALGNA 1378
Qy 1416 AADATEAKNKAHEAERIAASAVQKNATSTKAEAEARTFAEVTDLNNEVNNMLKQLEABKEL 1475
Db 1379 AADATEAKNKAHEAERIAASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAENEL 1438
Qy 1476 KRKQDDADQDMMAGMASQAQAEBAINARKAKNSVTSLSIINDLLEQLGQDLDVLDNKL 1535
Db 1439 KRKQDDADQDMMAGMASQAQAEBAINARKAKNSVTSLSIINDLLEQLGQDLDVLDNKL 1498
Qy 1536 NEIEGTLNKADEMKSVDLDRKVSLENEAKKQEAAMNDYNRDIEEIMKDIRNLEDIRKT 1595
Db 1499 NEIEGSLNKADEMKSVDLDRKVSLENEAKKQEAAMNDYNRDIAEIIKDIHNELEDIRKT 1558
Qy 1596 LPSGCFNTPSIEKP 1609
Db 1559 LPTGCFNTPSIEKP 1572

RESULT 11
US-09-845-583A-10

; Sequence 10, Application US/09845583A
; Patent No. 6635616
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Brunken, William Joseph
; APPLICANT: Champliand, Marie-France
; APPLICANT: Hunter, Dale
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
; FILE REFERENCE: 10287-056001
; CURRENT APPLICATION NUMBER: US/09/845,583A
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/200,863
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1587
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-845-583A-10

Query Match 41.4%; Score 3611; DB 4; Length 1587;
Best Local Similarity 43.5%; Pred. No. 6.7e-202;
Matches 701; Conservative 264; Mismatches 578; Indels 68; Gaps 21;

QY 21 LAVIAAAGCAQAAMDECTDEGRPQRCMPEFVNAFNVTVATNTCTPPEEYCVQT 80
DB 10 LALLAPRAAG---AGMGACYDGAGRPQRCLEPVFENAAFGRLAQASHTCGSPPEDFCPHV 65
QY 81 GVTGYTKSCHLDAQPHLOHGAFLTDYNNQADTTWQSQTMLAGVQYPSINLTLHLG 140
DB 66 GAAGAGAHQRCDAADPQRHNASYLTDFHSQSDSTWQSPSMAFGVQYPTSVNITLRLG 125
QY 141 KAFDITYVRLKFHTSRPESFAYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDE 200
DB 126 KAVEITYVRLKFHTSRPESFAYKRSRADGPWEPIQYFASQKTYGRPEGQYLRPGEDE 185
QY 201 QOALCTDEFSDISPLTGGNVAFSTLEGPSAYNFDSNPSVLQEWVTATDIRVTLNRLNTFG 260
DB 186 RVAFCTSEFSDISPLSGGNVAFSTLEGPSAYNFESGPGLEWVTSTELLISLDRNLNFG 245
QY 261 DEVNDPKVLKSYYYAISDFAVGGRCKNGHASECMKNEFDKLVNCNKHNTYGVDCCKCL 320
DB 246 DDIFDKPKVLQSYYYAVSDFSVGGRCKNGHASECGPDVAGQLACRCQHNNTGTDCCERCL 305
QY 321 PFFNDPWRRTAESAECPLDCDNGRSQECYFDPPELYRSTGHGHCNTCQNDTDGAHCE 380
DB 306 PFFQDRPWARGTAAEAHECLPCNCSGRSECTFDRLEFRSTGHGGRCHCRDHTAGPHCE 365
QY 381 RCRENFRLLGNNEACSSCHCSFVGSLSLTCQDSYGRCSCKPGVMGDKCDRCQPGFSLTEA 440
DB 366 RCQENFYHWDPRMPCQPCDCQASAGSLHLQCDTGTCTACKPTVTGWKCDRCCLPFGFSLSEG 425
QY 441 GCRPCSDPSGSDIECNVETGRVCVKDNVEGFNCERCKPGFFNLESNNPRGCTPCFCFGH 500
DB 426 GCRPCTCNPAGSLDTC DPRSGRCPCKENVEGNLCDCRCPGTENLQPHNPAGCSCFCYGH 485
QY 501 SSVCTNAVGSYVYSISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDFPRYFI 560
DB 486 SKVCASTAQFQVHHILSDFHQAGCGWARSVGGSEHSPQWSPN---GVLLSPDEDEEELT 541
QY 561 APAKFLGKQVLSYQNLFSFRVDRDRTRLSEAEDLVLEGAGLRVSVPLIAQGNSTPSETT 620
DB 542 APGKFLGQRFQSYGQPLILTRFVPPGDSPLPVQ-LRLEGTGLALS--LRHSSLSGPDAR 598
QY 621 VKYVFRLLH---EATDYPWRPALTPPEFQKLLNLTSTIKIRGTYSERSAG--YLLDDVTLAS 675
DB 599 ASQGRAGVPLQETSEDVAPPLPPHFQRLANLTSLRVSFPGSPAGPVFLTEVRLTS 658
QY 676 ARPGPGVATWVESCTCPVYGQFCMCLSGYRRTPNLGPPSPCVLCAACNGHSETCDP 735
DB 659 ARPGLSPASWVEICSCPTGYTGQFCESCAPGYKREMPQGPYASCVPCTCNQEG-TCDP 717

QY 736 ETGVCNCRDNTAGHCEKCSGDYGYGDSHTAGTSSDCQPCPCPGSSCAVVPKTKEVVCTNC 795
DB 718 NTGICVCSHHTEGPSCERCLPGFYGNPFAGADDDCQPCPCPGQSACTTIPESGEVCTHC 777
QY 796 PTGTTGRCCELDDGYFGDPLGRNGFVRLCRLCOCSDNIDPNVAGNCNRLTGECLKCIYN 855
DB 778 PPGQRRRCCEVDDGDFGDFLGLFGHPQPCQCOCSGNVDPNAVGNCDPLSGHCLRLCHN 837
QY 856 TAGFYCDRCCKDGFPGNPLAPNADCKKACNCNPNYGTMTKQSSCNPNVTGQCECLPHVTGQD 915
DB 838 TTGDHCEHCQEGFYGSALAPRPADKCMPCSCHPQGSVSEOMPDPVTGQCSCLPHVTARD 897
QY 916 CGACDPGFYNLQSGQGCERCDCHALGSTNGQCDIQTGCECQPGITGQHCEVNVHFGF 975
DB 898 CSRCYFGFDFLQPGRCRSCKCHPLGSOEDQCHPKTQCTCRPGVTGQACDRCOLGFFGS 957
QY 976 GPEGCKPCDCHPEGSLQCKDDGRCECREGFGVGNRCDOCEENFYNRSWPQCECPACY 1035
DB 958 SIKGRACRCSPLGAASAQCHYNGTVCVRPGFEGYKCDRCHYNFFLTADGTHCQCPSCY 1017
QY 1036 RLVKDKVADHRVKLQELSLIANLGTGDEMVTDOAFEDRLKEAEREVMDDLREAAQDVKD 1095
DB 1018 ALVKEETAKLKARLTTEGLQSGDCGSPW---GPLDILLGEAPRG--DVYQGHLLPGA 1072
QY 1096 DONLMDRLQRVNNTLSSQISRLQNRNTIETETGNLAQARAHVENTERLIEIASRELEKA 1155
DB 1073 REAFLEQMMGLEGA VKAAREQLQRLNKGARCAQAGSQKTCTQLADLEAVLESSEEEILHA 1132
QY 1156 KVAANVSVTQPESTGDPNNNTLLAEERKLAERHKEADDIRVAKTANDTSTEAYNLL 1215
DB 1133 AAILASLEIPQ-EGPSQPTKWSHLAEARALARSHRDRTATKIAATAWRALLASNTSYALL 1191
QY 1216 LRTLAGENQTAFEIE-ELNRYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIVASVAQL 1274
DB 1192 WNLL--EGRVALETORDLEDYQEVQAAQKALRTVAEVLPEAE-----SVLATVQQV 1242
QY 1275 SPLDSETL-----ENEANNIKMEAEENLEQLIDQKLQDYEDLREDMRGKELEVKN 1323
DB 1243 GADTAPYLALLASPGALPKSRAEDLGLKAKALEXTV---ASWQHMAATE-AARTLQTAA 1297
QY 1324 LLEKGTQEQT-----ADQLLARADAALAEBAKGRDITLQEAANDILNLLKDF 1373
DB 1298 QATLRQTEPLTMARSRLTATFASQLHQGARAALTOASSSVQAATVTVMGARTLLADLEG 1357
QY 1374 DRRVNDNKTAABEALRKIPAINQITTEANEKTRQAQALGSAADATEAKNKAHEAERIA 1433
DB 1358 KLQFPKPQDAALQKADSVSDRLADTRKTKQAERMLGNAAPLSSAKKKGREAEVLA 1417
QY 1434 SAVQKNATSTKAEARTFAEVTDLNEVNNMLQL-QBAEKELKRKQDDADQDMMAGMA 1492
DB 1418 KDSAKLAKALLRERKQARRASRLTSQTATLQASQOVLAASEARRQEELEAEVAGLS 1477
QY 1493 SQAQAEABINARKAKNSVTLSIINDLLEQLQGLDT--VDLNKLEIEGTLNKAKDEM- 1549
DB 1478 -----EMEQIRESRISLEKDIETLSSELLARLGSLDTHQAPALNETQWALERLRLQ 1532
QY 1550 KVSLLDRKVSDDLENAKKQEAAMINDYNRDIEEIMKDIRNLEDIRKTLPSGC 1600
DB 1533 SPGSLQFKLSLLEQESQQEQLEIQGFESDLAEIRADKQNLKQNLKAILHSLPENC 1583

RESULT 12
US-09-561-709B-3
; Sequence 3, Application US/09561709B
; Patent No. 6682911
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Champliand, Marie-France
; APPLICANT: Olson, Pamela
; APPLICANT: Koch, Manuel
; APPLICANT: Brunken, William
; TITLE OF INVENTION: LAMININS AND USES THEREOF
; FILE REFERENCE: 10287-060001

QY	856	TAGFYCDRC	KDGF	GNPLAPN	PADKCKAC	NCNPFY	GTMKQSS	CNPVTG	QCCE	CLPH	VTGQD	915							
DB	838	TTGDHCE	HCEQ	GFYGS	ALAPR	PADKCM	PCSC	HPQGS	VEQMP	CDPVTG	QCSC	CLPH	VTARD	897					
QY	916	CGACDP	GFYNL	QSGG	CERC	CDCH	ALGST	NGQCD	IR	TGQCE	CPG	IGTGH	CERCE	VNHF	GF	975			
DB	898	CSRCY	PGFFD	LQPR	GRCS	CKCH	PLGS	QEDQ	CH	PKT	GQCT	CRPG	VTGQ	ACDR	COLG	FFGS	957		
QY	976	GPEGK	PCDCH	PEGS	LSLQ	KDDG	RCCE	REGF	VGNR	CDQCE	ENFY	FNRS	WP	GCQCE	PAC	Y	1035		
DB	958	SIXGR	ACRCS	PLGA	ASQA	CHYNG	TCVCR	PGFEGY	KCDR	CHYN	FFLT	ADG	THCQ	QC	PC	SCY	1017		
QY	1036	RLVKD	KVAD	HRVK	LQEL	ESLI	ANLGT	GDEM	VTDQ	AFED	RLKE	ABRE	VNDL	LLRE	AO	DVKD	V	1095	
DB	1018	ALVKE	ETAKL	KARL	TLT	EGW	LQSD	CGSP	W---	GPLD	ILLGE	APRG-	DVY	QGH	LL	PGA	1072		
QY	1096	DQNLMD	RLQR	VNNT	LTSS	QISRL	QNRNT	IEET	GNLAE	QARAH	VENTER	LIEI	AS	RE	LEKA	1155			
DB	1073	REAFLE	QM	GLEGA	VKAARE	Q	LRLN	KGAR	CAQAG	SQKTC	TQLAD	LEAV	LESSE	EE	ILHA	1132			
QY	1156	KVAAN	VS	VTQPE	STGDP	NNMT	LLABE	ARKLA	ERHK	QEA	DDI	VR	VAK	TAND	TSTEA	YNLL	1215		
DB	1133	AAILAS	LEIPQ	-EGP	SQPT	TKW	SLAIE	ARAL	ARSH	RD	TATK	IAATA	WR	ALLAS	NTS	YALL	1191		
QY	1216	LRTL	AGEN	QTAF	EIE-ELN	KY	EQAK	NISQ	DLEK	QAA	RVHEE	EAKR	AGD	KAVE	IYAS	VAQL	1274		
DB	1192	WNLL--	EGR	VALETQ	RDL	EDRY	QEVQ	AAQK	ALRTA	VAEVL	PEAE	-----	SVL	ATV	QOV	1242			
QY	1275	SPLD	SETL	-----	ENE	ANNI	KME	AE	NLEQL	IDQ	LKDY	ED	RED	MRG	KE	LEVKN	1323		
DB	1243	GADT	APYL	ALLAS	PGAL	PQKS	RAED	GLK	KAKA	LEKTV	---ASW	QH	MATE	-AART	LQ	TAA	1297		
QY	1324	LLEK	GKTE	QQT	-----	ADQ	LLAR	ADA	AKALAE	AAKKG	RDTL	QEA	NDI	LNN	LKDF	1373			
DB	1298	QATLR	QTEPL	TMA	RSRL	TATF	ASQL	HQ	ARAAL	TQASS	SVQA	ATVT	VMG	ART	LLAD	LEGM	1357		
QY	1374	DRRVND	NKTA	AAEAL	RKIP	A	INQ	TTEAN	EKTRE	AQAL	GSAA	ADATE	AKN	KA	HEA	ERIA	1433		
DB	1358	KLQF	PRPKD	QAAL	QKAD	SVSD	RL	LADTR	KKTK	QAE	RM	LGNAAP	LUSS	SAK	KKG	REAE	VL	1417	
QY	1434	SAVQ	KNAT	STKAE	ARTFAE	VTDL	DNE	VNNML	KQL-QE	AEKEL	KRQ	DDAD	QDMM	MAGMA	1492				
DB	1418	KDSAK	LAKAL	LLRER	QOAH	RRAS	RLTSQ	TATL	QOAS	QOV	LASE	ARRQ	EE	EA	RV	GAGLS	1477		
QY	1493	SQAQ	EA	EBIN	ARKAK	NSVT	LLSI	I	NDL	LEQL	GQ	LDT--	VDL	NKL	NEI	EGL	NKAK	DEM-	1549
DB	1478	-----	ENE	QOIR	ES	ISLE	KDIE	TL	SELL	ARL	GLSD	THQAP	QAQAL	NETQ	WALER	LR	LQLG	1532	
QY	1550	KVSD	LR	KVSD	LE	NEAK	KQEA	A	IMD	YNRD	IEB	IMK	DIR	NLED	IR	K	TLP	SGC	1600
DB	1533	SPGS	LQR	KL	SLLE	QESQ	QQLQ	IO	QFES	D	LA	EBIR	ADK	QN	LEA	ILH	S	PENC	1583

QY	561	APAKFLGKQVLSYGONLSFSFRVDRDTRLAEDLVLEGAGLRVSVPPLIAQGSYPSETT	620
Dd	542	APCKFLGDQRFSYGQPLILTFRVPDGDSPLPVQ-LRLEGTGLALS--LRHSSLSGPQDAR	598
QY	621	VKYVFERLH--EATDYFWRPALTPPEEFQKLNLNLTISIIRGYTSERSAG--YLDDVTLAS	675
Dd	599	ASQGGAQVPLQETSEDVAPLPFFHFQRLLANLTSLRLRVSPGSPAGPVLTEVR LTS	658
QY	676	ARPGGVPA TWVESCTCPVGYGGQFCMCLSGYRRRETNLGPYPCVLCA CNGHSETCDP	735
Dd	659	ARPGLSPPASWVEICSCPTGYTGQFCESCAPGYKREMPQGGPYASCVPCTCNQHG-TCDP	717
QY	736	ETGVGNCRDNTAGPHCEKCSGDYYG DSTAGTSSDCQPCPCPGGSSCA VPKTKEVVCTNC	795
Dd	718	NTGICVCSHTTEGPS CERCLPGFYGNFPAGQADDCCPCPCPGQSACTIPESGEWCTHC	777
QY	796	PTGTTGXCELCD DGYFGDPLGRNGPVRLCRLCQCSDNIDPN AVGNCNRLTGETCLKCIYN	855
Dd	728	PBCCBCTBCTVCNDGEGDVGIFGHBQBCHOCOC SGNVDPNAVGNCP LSGHCLRLCLHN	837

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,450B
FILING DATE: 04-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Chao, Mark
REGISTRATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 94,778
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1193 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-317-450B-13

Query Match 30.3%; Score 2637; DB 1; Length 1193;
Best Local Similarity 39.4%; Pred. No. 2.4e-145;
Matches 515; Conservative 235; Mismatches 418; Indels 138; Gaps 12;

QY 319 CLPFFNDRPWRRAATASASECLPCDNGRSQECYFDPPELYRSTGHGCHCTNCQDNTDGAH 378
D 9 CLCFSLLLPAARATSRRE----VCDNGKSRQCFIDRELHRTGTNGFRCLNCNDNTDGIH 64
QY 379 CERCFNFRRLGNNEACSSCHSPVGSLSQDSDYGRCSCKPGVMGDKCDRCQPGFHSLT 438
D 65 CEKCKNGFYHRERDRCLPCNCNSKGSLSARCDNSGRCSCKPGVTGARCDRLPLGFHMLT 124
QY 439 EAGC-----RPCSDPSSGSDIECNVETGRVCYKDNVEGFNCERCKPGFFNLESSNPR 490
D 125 DAGCTQDQRLLDKCDPAGIAGPC--DAGRCVCKPAVTGERCDRCRSGYNNLDGGNPE 182
QY 491 GCTPCFCFGHSSVCTNAVGSYVSISSSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVI 550
D 183 GCTQCFCYGHSSASCRSAEYSVHKITSTFHQVDVGWKAQVQNGSPAKLQMSQRHQDVFS 242
QY 551 SDSYFPFYFIAPAKFLGKQVLSYQNLSSFSFRVDRDRRLSAEDLVLEGAGLRVSVPLIA 610
D 243 AQRDLPVYFVAPAKFLGNQVQVSYGQSLSFYRVDGRGHRPSAHDVILEGAGLRITAPLMP 302
QY 611 QGNSYPSSETTVKYVFRHEATDYPWRPALTPFFBQKLLNNLTSIKIRGYSEASAGYLD 670
D 303 LGKTLPCGLTKTYTFRLENEHPSNNWSPQLSYFEYRLLRLNLTLRIRATYGEYSTGYIDN 362
QY 671 VTLASARPGVPATVVBESCTCPVGYGGQFCMCLSGYRRETPLNLPYSPCVLCACNGHS 730
D 363 VTLISARPVSGAPAPWVEQICPVGYKGQFCQDCASGYKRD SARLGPFGTCIPCNCOG-G 421
QY 731 ETCDPETGVCNCRDNTAGPHCEKCSGSDGYGDSCTAGTSSDCQPCPCPGSSCAVVPKTEV 790
D 422 GACDPDTGDCYSGDENPDIECADCPIGFYNDPHPRS--CKPCCHNGFSCSVIPETEEV 479
QY 791 VCTNCPGTGKRCCLCDDGYFGDPLGRNGPVRCLRCQCSDNIDPNAVGNCRNLTGEC 850
D 480 VCNNPCPGVTGARCELADGYFGDPFGEHGPVPCQPCQCNNSVDPSPASGNCRLTGRCL 539
QY 851 KCIYNTAGFYCDRCCKDGFEGNPLAPNPADKCKACNCPYGTMTKQQSSCNVPTGQCECLPH 910
D 540 KCIHNTAGIYCDQCKAGYFGDPLAPNPADKCRACNCPMGS----- 580
QY 911 VTGQDCGACDPGFYNLQSGQGCERCDCALGSTNGQCDIRTGQCECQPGITGHCERCEV 970
D 581 ----- 580
QY 971 NHFGFEGCKPCDCHPEGSLSLQCKDDGRCEBGFVGNRCQCEENTFYNRSWPGCQE 1030

581 -----EPVG-----CRSDGTCVCKPGFGGPNCEH-----GAFS 608
QY 1031 CPACYRLVKDVADHRVKLQLESLIANLGTGDEMVTDAQAFEDRLKEAREVMDLLREAQ 1090
D 609 CPACYNQVKIQMDQFMQQLQRMALISKAQGGDGVVPDTELEGRMQAEQALQDILRDAQ 668
QY 1091 DVKDQVQNLMDRLQRVNNTLSSQISRLQINRNTIETGNLAEQARAVENTERLIEIASR 1150
D 669 ISEGASRSLGLQAKVRSQENSYSQSLRDLDKMTVERVRALGSQYQNRVDRDTHRLITQML 728
QY 1151 ELEKAKVAAANVSVTQPESTGDPNNMTLLAEARKLAERHKQEAADDIVRVAKTANDTSTE 1210
D 729 SLAESEASLGNTPASDHVVGPNFGFKSLAQEATRLAESHVESASNMELQTRATEDYSKQ 788
QY 1211 AYNLLRLTL-----AGENQTAFEIEELNRKYEQAQKNISQDLEKQAARVHEEAKRAGDK 1263
D 789 ALSLVKALHEGVSGSGSPDGAV-VQGLVEKLEKTKSLAQQLTREATQAEIEADRSYQH 847
QY 1264 AVEIYASVAQSLDSETLE-NEANNIKMEAEENLEQLIDQKLKDYEDLREDMRGKELEVK 1322
D 848 SRLLLDSVSPLOGVSDQSFOVEEAKRIKQKADSLSSLVTRHMDPEFKTKQNLGNWKEEAQ 907
QY 1323 NLEKKGTEQQTADQLLARADAAKALAEAAKKGRTDLOEANDILNKLKDFDRRVNDNKT 1382
D 908 QLLQNGKSGREKSDQLLSRANLAKSRAQEAALSMGNATFYEVESILKNLREFDLQVDNRKA 967
QY 1383 AAEALRKIPAINQITTEANEKTRAQOALGSAADAAATEAKNKAHEAERIASAVQKNATS 1442
D 968 EAEAMKRLSYISQKVSADSKTQQAERALGSAADAAQRAKNGAGAEALISSEIEQEIGS 1027
QY 1443 TKAEAEARTFAEVTDLNEVNNMLKQLOEAEKELKRQDDADQDMMAGMASQAQAEAIN 1502
D 1028 LNLEANVTADGALAMEKGLASLKSEMEVEGELERKELEFDTNMDAVQMVITEAQKVDTR 1087
QY 1503 ARKAKNSVTLSIIINDLLEQLGQDVTVDLKNLNEIEGTLNKADEMKVSDLDLDRKVSdle 1562
D 1088 AKNAGVTIQDTLNTLDGLLHMDQPLSVDEGLVLEQLKSLRAKTQIN-SQLRPMSELE 1146
QY 1563 NEAKKQEAAIMDYNRDIIEIMKDINLEDIRKTLPSGCFNTPSIEK 1608
D 1147 BRARQQRGHLHLETSIDGILADVKNLENIRDNLPFGCYNTOALEQ 1192

RESULT 14

US-08-800-593-13
; Sequence 13, Application US/08800593
; Patent No. 6143505
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Kallunki, Pekka
; APPLICANT: Pyke, Charles
; TITLE OF INVENTION: Laminin Chains: Diagnostic and
; TITLE OF INVENTION: Therapeutic Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boenhen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800,593
; FILING DATE: 18-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/317,450
; FILING DATE: 04-OCT-1994

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Chao, Mark
REGISTRATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 94,778-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1193 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-800-593-13
Query Match 30.3%; Score 2637; DB 3; Length 1193;
Best Local Similarity 39.4%; Pred. No. 2.4e-145;
Matches 515; Conservative 235; Mismatches 418; Indels 138; Gaps 12;
QY 319 CLPFFNDRPWRRTAESAECPLDCNCRSQECYFDPFLYRSTGHGCHTCNCDNTDGAH 378
Db 9 CLCFSLLPAAARATSRRE---VDCNKGSRQCIFDRELHRTQNGFRCLNCNDNTDGIH 64
QY 379 CERCRENFFRLGNNEACSSCHSPVGSLSLSTQDSYGRCSCKPGVMGDKCDRCQPGFHSLT 438
Db 65 CEKCKNGFYHRERDRCLPCNCSKGSLSARCDNSGRCSCKPGVTGARCDRCCLPGFHWLT 124
QY 439 EAGC-----RPCSDPSSIDEENVTGRCVKONVEGNCERCKPGFFNLESSNPR 490
Db 125 DAGCTQDRLDLSKDCDPAIAGPC--DAGRCVCKPAVTGERCDRCRSYVNLDCGNPE 182
QY 491 GCTPCFCFGHSSVCTNAVGSYVSYSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVI 550
Db 183 GCTQCFCYGHSGASCRSSAEYSVHKITSTFHFQDVGWKAQVRNGSPAKLQWSQRHQDVFS 242
QY 551 SDSYFPRFYFLAPAKFLGKQVLSYQNLSPFSFRVDRDRRLSABDLVLEGALRVSVELIA 610
Db 243 AQLDLPVYFVAPAKFLGNQVSYQSLSFDYRVDGRGHRPSAHDVILEGALRITAPLMP 302
QY 611 QGNSYSETTVKYVFLRHEATDYPWRPALTPFEFQKLLNLTSLIKIRGTYSERSAGYLD 670
Db 303 LGKTLPCGLTKTYTFRLEHPSNWSQVSYFEYRLLRLNLTLALRATIRATYGEYSTGYDN 362
QY 671 VTLASARPGVPATWVESCTCPVGYGSCFCEMCLSGYRRETNLPGYSPCVLCAACNGHS 730
Db 363 VTLISARPVSGAPAPWVEQICPVGYKGFQDCASGYKRDARSALPGFTGTCPCNCG-G 421
QY 731 ETCDPETGVNCRDNTAGPHCEKCSGDYGYDSTAGTSSDCQPCPCPGSSCAVVPKTEV 790
Db 422 GACDPTDGCYSGDENPDIEACDPCIGFYNDPHDPRS--CKPCCHNGFSCSVIPETEEV 479
QY 791 VCTNCPTGTTKRCCLCDDGYFGDPLGRNGPVRRLCRLCQCSNDIDPNAVGNCRNLGTGCL 850
Db 480 VCNNCPGVGTGARCCLCAGYFGDPFGEHGPVRPCQPCQNSNVDPFASGNCRLTGRCL 539
QY 851 KCIYNTAGFYCDRCCKDGGFFGNPLAPNPADKCKACNCNPGYGTMKQQSSCNVPTGQCECLPH 910
Db 540 KCIHNTAGIYCDQCKAGYFGDPLAPNPADKCRACNCNPMGS----- 580
QY 911 VTGQDCGACDPGFYNLQSGQGCERCDCDHALGSTNGQCDIRTGQCECQPGITGQHCEV 970
Db 581 ----- 580
QY 971 NHFGFGECKPCDCHPEGSLSLQCKDDGRCECREGVGNRCDCQCEENFYNRSWPGCQE 1030
Db 581 -----EPVG-----CRSDGTVCCKPGFGGPNCEH-----GAFS 608
QY 1031 CPACYRLVKQKADHRVKLQLESILIANLTGDEMVTQDAFEDRLKABREVMDDLREAQ 1090
Db 609 CPACYNQVKIQMDQFMQOLQRMELISKAQGGDGVVDPDTELEGRMQQAEQALQDILRDAQ 668
QY 1091 DVKDVQDQNLMDRLQVRVNTLSQISRLQNTIRNTIETGNLAEQARAHVENTERLIEIASR 1150

Db 669 ISEGASRSLGLQAKVRSQENSYSQSRLLDDLMKMTVERVRLGSGYQNRVDRDTHRLITQML 728
QY 1151 ELEKAKVAAANVSVTQPESTGDDNNMTLLAEEARKLAERHKEADDDIVRVAKTANDTSTE 1210
Db 729 SLAESEASLGNTNIPASDHYVVGNGFKSLAQEAATRLAESHVESASNMEOLTRATEDYSKQ 788
QY 1211 AYNLLRLTL-----AGENQTAPEIEELNRKYEQAKNYSQDLEKQAAARVHEEAKRAGDK 1263
Db 789 ALSLVKALHEGVGSGSGSPDGA-VQGLVEKLEKTKSLAQOLTREATQAEIEADRSYQH 847
QY 1264 AVEIYASVAQLSPDLSETLE-NEANNIKMEAEENLEQLIDQKLKDYEDLREDMRGKELEVK 1322
Db 848 SLRLDLSVSPLOQGVSDQSFQVEEAKRIKQKADSLSSLVTRHNDKFKRTQKNLGNWKEEAQ 907
QY 1323 NLLEKGTETQQTADQLLARADAKALAEAAKGRDTLQEAANDILNNLKDFFRRVNDNKT 1382
Db 908 QLLQNGKSGREKSDQLLSRANLAKSRAQEAALSMGNATFYEVESILKNLREFDLQVDNRKA 967
QY 1383 AAEALRKIPAINQITITEANEKTRBAQQAALGSAADAAATEAKNKAHEAERIASAVQKNATS 1442
Db 968 EAEEMKRLSYISKVSDASDKTQQAERALGSAADAAQRAKNGAGEALEISSEIEQEIGS 1027
QY 1443 TKAEARTFAEVTDLNENNNMLQQLQEAELKRRKQDDADQDMMAGMASQAAQAEAEIN 1502
Db 1028 LNLEANTADGALAMEKGLASLSEMEVEGELEKLEFDTNMDAVQMVITEAQKVDTR 1087
QY 1503 ARKAKNSVTSLSIINDLLEQLGQDVTDLNKLNEIEGTLLNKADEMVKVSDLDKRVSDLE 1562
Db 1088 AKNAGVTIQTDLTLNLTDLGLHLMQDPLSVDEGLVLLEQLKSLRAKTQIN-SQLRPMSELE 1146
QY 1563 NEAKQEAATMDYNRDIEEIMKDINLEDIRKTLPSGCFNTPSIEK 1608
Db 1147 ERARQQRGHLLHLETSIDGILADVKNLENIRDNLPFGCYNTQALEQ 1192
RESULT 15
US-08-317-450B-15
Sequence 15, Application US/08317450B
Patent No. 5660982
GENERAL INFORMATION:
APPLICANT: Tryggvason, Karl
APPLICANT: Kallunki, Pekka
APPLICANT: Pyke, Charles
TITLE OF INVENTION: Laminin Chains: Diagnostic and
TITLE OF INVENTION: Therapeutic Use
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER & ALLEGRETTI, LTD.
STREET: Ten South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,450B
FILING DATE: 04-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Chao, Mark
REGISTRATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 94,778
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1111 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-317-450B-15

Query Match 28.9%; Score 2516.5; DB 1; Length 1111;
Best Local Similarity 39.7%; Pred. No. 2.2e-138;
Matches 486; Conservative 215; Mismatches 385; Indels 137; Gaps 11;

QY	319	CLPFFNDRPWRRTAESASECLPCDCNGRSQECYFDPPELYRSTGHGHCTNCQDNTDGAH	378
Db	9	CLCFSLLLPAARATSRRE----VDCNGKSRQCIFDRELHRQTGNGFRCLNCNDNTDGIH	64
QY	379	CERCRENFFRLGNNEACSSCHCSPVGSLSQCDSYGRCSCKPGVMGDKCDRCQPGFHSLT	438
Db	65	CEKCKNGFYHRERDRCLPCNCNSKGSLSARCDNSGRCSCKPGVTGARCDCLPGFHMLT	124
QY	439	BAGC-----RPCSCDPGSGIDECNVETGRCVCCKDNVEGFCERCCKPGFENLESSNPR	490
Db	125	DAGCTQDQRLLDKCDKCDPAGIAGPC--DAGRCVCCKPAVTGERCDRCRSGYNNLDGGNPE	182
QY	491	GCTPCFCFGHSSVCTNAVGYSVYSISSTFQIDEDGWRAEQRDGSEASLENSSERQDIAVI	550
Db	183	GCTQCFCYGHASACRSSAEYSVHKITSTFHQDVGWKAQVRNGSPAKLQWQRHQDVFS	242
QY	551	SDSYFPRYFIAPAKFLGKQVLSYGQNLSPFRVDRDRTRLAEDLVLEGAGLRVSVPLIA	610
Db	243	AQRLDPVYFVAPAKFLGNQOQVSYGQSLSFDRVDRGRGHPSAHDVILEGAGLRITAPLMP	302
QY	611	QGNSYPSETTVKIVFRLHEATDYPWRPALTPFEFQKLLNNLTSIKIRGTYSERSAGYLDD	670
Db	303	LGKTLPCGLTKTYTFRLNEHPSNNWSPQLSYFEYRLLRLNLALTALRIRATYGEYSTGYIDN	362
QY	671	VTLASARPGVPATWVESCTCPVGYGGQFCMCLSGYRRETNPNLGPYSPCVLCACNGHS	730
Db	363	VTLISARPVSGAPAPWVEQCICPVYKGQFCQDCASGYKRD SARLPGFTGTCIPCNCOG-G	421
QY	731	ETCDPETGVNCRDNTAGPHCEKCSGDGYYGDSSTAGTSSDCQPCPCPGSSCAVVPKTEV	790
Db	422	GACDDTGDYSGDENPDIECADCPIGFYNDPHDPRS--CKPCCHNGFSCSVIPETEEV	479
QY	791	VCTNCPGTGTTKRCELDDGYFGDPLGRNGPVRRLCLQCSDNIDPNVAGNCNRLTGECL	850
Db	480	VCNNCPPGVTGARCELCADGYFGDPFGEHGPVRPCPCQCNSNVDPSPASGNCDRLTGRCL	539
QY	851	KCIYNTAGFYCDRCCKDGFEGNPLAPNPADKCKACNCNPYGTMKQQSSCNVPTGQCECLPH	910
Db	540	KCIHNTAGIYCDQCKAGYFGDPLAPNPADKCRACNCNPMGS-----	580
QY	911	VTGQDCGACDPGFYNLQSGQGCERCDCHALGSTNGQCIRTGQCECQPGITGOHCERCEV	970
Db	581	-----	580
QY	971	NHFGFGECKPCDCHPEGSLSLQCKDDGRCECREGFVGNRCDDQCEENFYFNRSWPGCQE	1030
Db	581	-----EPVG-----CRSDGTCVCKPGFGGPNCEH-----GAFS	608
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Db	609	CPACYNQVKIQMDQFMQQLQRMALISKAAQGGDGVVPDTELEGRMQQAEQALQDILRDAQ	668
QY	1091	DVKDVDONLMDRLQVRNNTLSQISRLQNIIRNTIEETGNLAEQARAHVENTERLIEIASR	1150
Db	669	ISEGASRSLGLQAKVRSQENSYSRLDDLKMTVERVREALGSYQNRVRDTHRLITOMQL	728
QY	1151	ELEKAKVAAANVSVTQPESTGDPNNMTLLAEAEARKLAERHKQEADDIVRVAKTANDTSTE	1210
Db	729	SLAESBASLGNTNIPASDHYVGPNGFKSLAQEAATRLAESHVESASNMEQLTRETEDYSKQ	788
QY	1211	AYNLILRLTL-----AGENCYAFETIEELNRKYEQAKNISQDLEKQAARVHEEAKRAGDK	1263
Db	789	ALSLVRKALHEGVGSGSGSPDGAV-VQGLVEKLEKTKSLAQQLTREATQAEIADRSYQH	847

QY	1264	AVEIYASVAQLSPLDSETLE-NEANNIKMEAEENLEQLIDQKLKQYEDLREDMRGKELEVK	1322
Db	848	SLRLDSDVSPLOQVSDQSFQVEEAKRIKQKADSLSSLVTRHMDEFKRTQKNLGNWKEEAQ	907
QY	1323	NLLEKKGKTEQQTADQLLARADAAKALAEAAKKGKGRDTLQEAANDILNNLKDFDRRVNDNKT	1382
Db	908	QLLQNGKSGREKSDQLLSRANLAKSRAQEAQALSGMGNATFYEVESILKNLREFDLQVDNRKA	967
QY	1383	AAEBALRKIPAINQITTEANEKTRAQQAALGSAADAAATEAKNKAHEAERIAASAVQKNATS	1442
Db	968	EAEEAMKRLSYISQKVSADSKTQQAERALGSAADAAQRAKNAGAGEALEISSIEIEQSIG	1027
QY	1443	TKAEABERTFAEVTDLNEVNNMLKQLQEAEEKELKRKQDDADQDDMMAGMASQAQAEAEIN	1502
Db	1028	LNLEAVNTADGALAMEKGLASLKSEMREVEGELEKELEFDTNMDAVQMVITEAQKVDTR	1087
QY	1503	ARKAKNSVTSLLSIINDLLEQLG	1525
Db	1088	AKNAGVTIQDTLNTLDGLLHLMG	1110

Search completed: May 18, 2004, 15:02:26
Job time : 19.1718 secs

Db 121 QTMLAGVQYPSINLTLHLGKAFDITYVRLKFHTSRPESFAIYKRTREDGPWIPYQYYS 180

QY 181 SCENTYSKANRGFIIRTGDEQQALCTDEFSDISPLTGNVAFSTLEGRPSAYNFDSN 240

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Db 241 QEWVTATDIRVTNLNRLNTFGDEVNDPKVLKSYYYAISDAVAGGRCKNCNGHASECMKNEF 300

QY 301 DKLVNCNKHTYGVDCCKLPPFFNDRPWRRATAESASECLPCDCNGRSQECYFDPBELYRS 360

Db 301 DKLVNCNKHTYGVDCCKLPPFFNDRPWRRATAESASECLPCDCNGRSQECYFDPBELYRS 360

QY 361 TGHGGHCTNCQDNTDGAHCERCENEFRLGNNEACSSCHSPVGSLSLTCQDSYGRCSCKP 420

Db 361 TGHGGHCTNCQDNTDGAHCERCENEFRLGNNEACSSCHSPVGSLSLTCQDSYGRCSCKP 420

QY 421 GVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSDIECNVETGRVCCKDNVEGFNCERCKPG 480

Db 421 GVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSDIECNVETGRVCCKDNVEGFNCERCKPG 480

QY 481 FFNLESSNPRGTCPCFCFHSSVCTNAVGSVYSISSTFQIDEDGWRAEQRDGSEASLEW 540

Db 481 FFNLESSNPRGTCPCFCFHSSVCTNAVGSVYSISSTFQIDEDGWRAEQRDGSEASLEW 540

QY 541 SSERQDIAVISDSYFPRYFIAPAKFLGKQVLSYGONLSFSFRVDRDRTRLSAEDLVLEGA 600

Db 541 SSERQDIAVISDSYFPRYFIAPAKFLGKQVLSYGONLSFSFRVDRDRTRLSAEDLVLEGA 600

QY 601 GLRVSVPLIAQNSYPSETTVKYVFRHLHEATDYPWRPALTPPFQKLLNLTLSIKIRGTY 660

Db 601 GLRVSVPLIAQNSYPSETTVKYVFRHLHEATDYPWRPALTPPFQKLLNLTLSIKIRGTY 660

QY 661 SERSAGYLDVTLASARPGVPATWVESTCPVGYGGQFCMCLSGYRRETNLGPYSP 720

Db 661 SERSAGYLDVTLASARPGVPATWVESTCPVGYGGQFCMCLSGYRRETNLGPYSP 720

QY 721 CVLCAACNGHSETCDPETGVCNCRDNTAGPHCEKCSDDGYGSDTAGTSSDCQPCPCPGSS 780

Db 721 CVLCAACNGHSETCDPETGVCNCRDNTAGPHCEKCSDDGYGSDTAGTSSDCQPCPCPGSS 780

QY 781 CAVVPKTKVVCTNCPTGTTGKRCELCDGDFGDPPLGRNGPVRCLRCQCSNDIDPNAVG 840

Db 781 CAVVPKTKVVCTNCPTGTTGKRCELCDGDFGDPPLGRNGPVRCLRCQCSNDIDPNAVG 840

QY 841 NCNRLTGECLKCIYNTAGFYCDRCCKDGGFFGNPLAPNPADKCKACNCPYGTMKQOSSCNP 900

Db 841 NCNRLTGECLKCIYNTAGFYCDRCCKDGGFFGNPLAPNPADKCKACNCPYGTMKQOSSCNP 900

QY 901 VTGQCECLPHVTGDCGACDPGFYNLQSGQCERCDCHALGSTNGQCDIRTGQCECQPGI 960

Db 901 VTGQCECLPHVTGDCGACDPGFYNLQSGQCERCDCHALGSTNGQCDIRTGQCECQPGI 960

QY 961 TGOHCERCEVNHFGFEGEGCKPCDCHPEGSLQCKDDGRCECREGVGNRCDCQCEENYF 1020

Db 961 TGOHCERCEVNHFGFEGEGCKPCDCHPEGSLQCKDDGRCECREGVGNRCDCQCEENYF 1020

QY 1021 YNRSWPGCQECPCACYRLVKDKVADHRVKLQELLESILIANLGTGDEMVTDOAFEDRLKEAER 1080

Db 1021 YNRSWPGCQECPCACYRLVKDKVADHRVKLQELLESILIANLGTGDEMVTDOAFEDRLKEAER 1080

QY 1081 EVMDDLREAQDKVDQNLMDRLQRVNNTLSSQISRLQNRNTIETGNLAEQARAHVEN 1140

Db 1081 EVMDDLREAQDKVDQNLMDRLQRVNNTLSSQISRLQNRNTIETGNLAEQARAHVEN 1140

QY 1141 TERLIEIASRELEKAKVAAANVSVTQPESTGDPNNMTLLAEERKLAERHKQEADDIRV 1200

Db 1141 TERLIEIASRELEKAKVAAANVSVTQPESTGDPNNMTLLAEERKLAERHKQEADDIRV 1200

QY 1201 AKTANDTSTEAYNLLRLTLAGENQTAFAIEEELNRKYEQAKNISQDLEKQAARVHEEAKRA 1260

Db 1201 AKTANDTSTEAYNLLRLTLAGENQTAFAIEEELNRKYEQAKNISQDLEKQAARVHEEAKRA 1260

QY 1261 GDKAVEIYASVAQLSPLDSETLENEANNIKMEAEENLEQLIDOKLKDYEDLREDMRGKELE 1320

Db 1261 GDKAVEIYASVAQLSPLDSETLENEANNIKMEAEENLEQLIDOKLKDYEDLREDMRGKELE 1320

QY 1321 VKNLLEKGTQEQTADQQLLARADAAKALAEAAKKGRTDLOEANDILNNLKDFDRRVNDN 1380

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Db 1381 KTAAEELRKIPAINQITITEANEKTRQAQALGSAADATEAKNKAHEAERIAASAVQKNA 1440

QY 1441 TSTKAEARTFAEVTDLNEVNNMLKQLEAEKELKRKQDDADQDMMAGMASQAAQAEAE 1500

Db 1441 TSTKAEARTFAEVTDLNEVNNMLKQLEAEKELKRKQDDADQDMMAGMASQAAQAEAE 1500

QY 1501 INARKAKNSVTSLLSIINDLLEQLGQDVTVDLNLKNEIEGTNLKAKDEMKVSDLDLDRKVSD 1560

Db 1501 INARKAKNSVTSLLSIINDLLEQLGQDVTVDLNLKNEIEGTNLKAKDEMKVSDLDLDRKVSD 1560

QY 1561 LENEAKKQEAAIMDYNRDIIEIMKDIRNLEDIRKTLPSGCFNTPSIEKP 1609

Db 1561 LENEAKKQEAAIMDYNRDIIEIMKDIRNLEDIRKTLPSGCFNTPSIEKP 1609

RESULT 2

US-10-299-058-12
; Sequence 12, Application US/10299058
; Publication No. US20030103975A1
; GENERAL INFORMATION:
; APPLICANT: JONES, JONATHAN C.R.
; APPLICANT: GONZALES, MEREDITH
; TITLE OF INVENTION: MODULATION OF ANGIOGENESIS AND ENDOTHELIALIZATION

; FILE REFERENCE: 1720-1-002 CIP
; CURRENT APPLICATION NUMBER: US/10/299,058
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/706,235
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: 60/163,199
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 12

; LENGTH: 1609

; TYPE: PRT

; ORGANISM: Homo sapien

US-10-299-058-12

Query Match 100.0%; Score 8713; DB 14; Length 1609;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSHRAAPALRPGRLLWPVLAVLAAAAAGCAQAAMDECTDEGGRPQRCMPEFVNAAFN 60

Db 1 MRGSHRAAPALRPGRLLWPVLAVLAAAAAGCAQAAMDECTDEGGRPQRCMPEFVNAAFN 60

QY 61 VTVVATNTCGTPPEEYCVQTGVTGVTKSCHLCDAGQPHLOHGAAFLTDYNNQADTTWWQS 120

Db 61 VTVVATNTCGTPPEEYCVQTGVTGVTKSCHLCDAGQPHLOHGAAFLTDYNNQADTTWWQS 120

QY 121 QTMLAGVQYPPSSINLTLHLGKAFDITYVRLKFHTSRPESFAIYKRTREDGPWIPYQYYS 180

Db 121 QTMLAGVQYPPSSINLTLHLGKAFDITYVRLKFHTSRPESFAIYKRTREDGPWIPYQYYS 180

QY 181 SCENTYSKANRGFIIRTGDEQQALCTDEFSDISPLTGNVAFSTLEGPSAYNFDSN 240

Db 181 SCENTYSKANRGFIIRTGDEQQALCTDEFSDISPLTGNVAFSTLEGPSAYNFDSN 240

QY 241 QEWVTATDIRVTNLNRLNTFGDEVNDPKVLKSYYYAISDAVAGGRCKNCNGHASECMKNEF 300

Db 241 QEWVTATDIRVTNLNRLNTFGDEVNDPKVLKSYYYAISDAVAGGRCKNCNGHASECMKNEF 300

QY 301 DKLVNCKHNTYGVDCCKLPPFFNDRPWRRTAESAASECLPCDCNCRSQECYFDPPELYRS 360
Db 301 DKLVNCKHNTYGVDCCKLPPFFNDRPWRRTAESAASECLPCDCNCRSQECYFDPPELYRS 360
QY 361 TGHGGHCTNCQDNTDGAHCERCRCNFFRLGNNEACSSCHCSPVGLSTQCDSDSYGRCSCKP 420
Db 361 TGHGGHCTNCQDNTDGAHCERCRCNFFRLGNNEACSSCHCSPVGLSTQCDSDSYGRCSCKP 420
QY 421 GVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSDIECNVETGRCVCKDNVEGFNCERCCKPG 480
Db 421 GVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSDIECNVETGRCVCKDNVEGFNCERCCKPG 480
QY 481 FFNLESSNPRGCTPCFCFGHSSVCTNAVGSYVSISSTFQIDEDGWRAEQRDGSEASLEW 540
Db 481 FFNLESSNPRGCTPCFCFGHSSVCTNAVGSYVSISSTFQIDEDGWRAEQRDGSEASLEW 540
QY 541 SSERQDIAVISDSYPPRYFIAPAKFLGKQVLSYQNLFSFRVDRDRTRLRSAEDLVLEGA 600
Db 541 SSERQDIAVISDSYPPRYFIAPAKFLGKQVLSYQNLFSFRVDRDRTRLRSAEDLVLEGA 600
QY 601 GLRVSVPLIAQNSYSPSETTVKYVFRLEHATDYPWRPALTPFEFQKLLNNLTSIKIRGTY 660
Db 601 GLRVSVPLIAQNSYSPSETTVKYVFRLEHATDYPWRPALTPFEFQKLLNNLTSIKIRGTY 660
QY 661 SERSAGYLDVTLASARPGPGVPATWVESCTCPVGYGGQFCMCLSGYRRETPNLGPYSP 720
Db 661 SERSAGYLDVTLASARPGPGVPATWVESCTCPVGYGGQFCMCLSGYRRETPNLGPYSP 720
QY 721 CVLCAACNGHSETCDPETGVNCNRDNTAGPHCEKCSGYYGDSGTAGTSSDCPCPCPGSS 780
Db 721 CVLCAACNGHSETCDPETGVNCNRDNTAGPHCEKCSGYYGDSGTAGTSSDCPCPCPGSS 780
QY 781 CAVVPKTKEVVCTNCPTGTGKRCCLDDGFGDPLGRNGPVLRLCQCSDNIDPNAVG 840
Db 781 CAVVPKTKEVVCTNCPTGTGKRCCLDDGFGDPLGRNGPVLRLCQCSDNIDPNAVG 840
QY 841 NCNRLTGECLCKIYNTAGFYCDRCKDGGFFGNPLAPNPADKCKACNCNFGYTMKQSSCNP 900
Db 841 NCNRLTGECLCKIYNTAGFYCDRCKDGGFFGNPLAPNPADKCKACNCNFGYTMKQSSCNP 900
QY 901 VTGQCECLPHVTGQDCGACDPGFYNLQSGQGCEHCDCHALGSTNGQCDIRTGQCECQPGI 960
Db 901 VTGQCECLPHVTGQDCGACDPGFYNLQSGQGCEHCDCHALGSTNGQCDIRTGQCECQPGI 960
QY 961 TGQHCERCEVNHFGFEGGCKPCDCHPEGSLSLQCKDDGRCECREGFGVGNRCDQCEENYF 1020
Db 961 TGQHCERCEVNHFGFEGGCKPCDCHPEGSLSLQCKDDGRCECREGFGVGNRCDQCEENYF 1020
QY 1021 YNRSWPGCQECPCVRLVKDKVADHRVKLQELSLIANLGTGDEMVTQAFEDRLKEAER 1080
Db 1021 YNRSWPGCQECPCVRLVKDKVADHRVKLQELSLIANLGTGDEMVTQAFEDRLKEAER 1080
QY 1081 EWMDLLREAQDVKDQNLMDRLQVRNNTLSSQISRLQNRNTIETGNLAEQARAHVEN 1140
Db 1081 EWMDLLREAQDVKDQNLMDRLQVRNNTLSSQISRLQNRNTIETGNLAEQARAHVEN 1140
QY 1141 TERLIEIASRELEKAKVAAANVSVTQPESTGDPNNMTLLAEAEARKLAERHKQAEADDIVRV 1200
Db 1141 TERLIEIASRELEKAKVAAANVSVTQPESTGDPNNMTLLAEAEARKLAERHKQAEADDIVRV 1200
QY 1201 AKTANDTSTEAYNLLRTLAGENQTAFEIEELNRKYEQAKNISQDLEKQAARVHEEAKRA 1260
Db 1201 AKTANDTSTEAYNLLRTLAGENQTAFEIEELNRKYEQAKNISQDLEKQAARVHEEAKRA 1260
QY 1261 GDKAVEIYASVAQLSPLDSETLENEANNIKMEAEENLEQLIDQKLDYEDLREDMRGKELE 1320
Db 1261 GDKAVEIYASVAQLSPLDSETLENEANNIKMEAEENLEQLIDQKLDYEDLREDMRGKELE 1320
QY 1321 VKNLLKKGKTEQQTADQLLARADAAKALAEAAKKGRTDLQEAANDILNNLKDfDRRVNDN 1380
Db 1321 VKNLLKKGKTEQQTADQLLARADAAKALAEAAKKGRTDLQEAANDILNNLKDfDRRVNDN 1380
QY 1381 KTAAEALRKIPAINQITTEANEKTRQAQALGSAADAATAEAKNKAHEARIAASAVQKNA 1440

Db 1381 KTAAEALRKIPAINQITTEANEKTRQAQALGSAADAATAEAKNKAHEARIAASAVQKNA 1440
QY 1441 TSTKAEARTFAEVTDLNEVNNMLKQLEAEKELKRKQDDADQDMNMAGMASQAQAEAE 1500
Db 1441 TSTKAEARTFAEVTDLNEVNNMLKQLEAEKELKRKQDDADQDMNMAGMASQAQAEAE 1500
QY 1501 INARKAKNSVTLSLSIINDLLEQLGQDVTDLNKLNEIEGTLNKADEMKVSDLDKRVSD 1560
Db 1501 INARKAKNSVTLSLSIINDLLEQLGQDVTDLNKLNEIEGTLNKADEMKVSDLDKRVSD 1560
QY 1561 LENEAKKQEAAIMDYNRDIEEIMKOIRNLEDIRKTLPSGCFNTPSIEKP 1609
Db 1561 LENEAKKQEAAIMDYNRDIEEIMKOIRNLEDIRKTLPSGCFNTPSIEKP 1609
RESULT 3
US-09-938-275-11
; Sequence 11, Application US/09938275
; Patent No. US20020111309A1
; GENERAL INFORMATION:
; APPLICANT: Gerardo Castillo
; APPLICANT: Alan Snow
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications
; TITLE OF INVENTION: of Laminin and Laminin-Derived Protein Fragments
; FILE REFERENCE: PROTEO.P03
; CURRENT APPLICATION NUMBER: US/09/938,275
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1609
; TYPE: PRT
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Swissprot P11047
; DATABASE ENTRY DATE: 1991-11-01
US-09-938-275-11
Query Match 100.0%; Score 8709; DB 9; Length 1609;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MEGSHRAAPALRPRGRLPVLAVALAAAAAGCAQAAMDECTDEGGRPQRCMPFVNAAFN 60
Db 1 MEGSHRAAPALRPRGRLPVLAVALAAAAAGCAQAAMDECTDEGGRPQRCMPFVNAAFN 60
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Db 61 VTVVATNTCGTPPEEYCVQTVGTGVTGKSCHLCDAGOPHLQGAFLTDYNNQADTTWQOS 120
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Db 121 QTMLAGVQYPPSSINLTHLGKAFDITYVRLKHTSRPESFAIYKRTREDGWPWIPYQYYSG 180
QY 181 SCENTYSKANRGFIRTGGEQQAALCTDEFSDISPLTGGNVAFTLEGRPSAYNFDNSPVL 240
Db 181 SCENTYSKANRGFIRTGGEQQAALCTDEFSDISPLTGGNVAFTLEGRPSAYNFDNSPVL 240
QY 241 QEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSYYYAISDFAVGGRCKCNGHASECMKNEF 300
Db 241 QEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSYYYAISDFAVGGRCKCNGHASECMKNEF 300
QY 301 DKLVNCKHNTYGVDCCKLPPFFNDRPWRRTAESAASECLPCDCNCRSQECYFDPPELYRS 360
Db 301 DKLVNCKHNTYGVDCCKLPPFFNDRPWRRTAESAASECLPCDCNCRSQECYFDPPELYRS 360
QY 361 TGHGGHCTNCQDNTDGAHCERCRCNFFRLGNNEACSSCHCSPVGLSTQCDSDSYGRCSCKP 420
Db 361 TGHGGHCTNCQDNTDGAHCERCRCNFFRLGNNEACSSCHCSPVGLSTQCDSDSYGRCSCKP 420
QY 421 GVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSDIECNVETGRCVCKDNVEGFNCERCCKPG 480

Db 421 GVMGDKCDRCQPGFHSLTEAGCRPCSDPSGSDIECNVETGRVCCKDNVEGFNCERCKPG 480
QY 481 FFNLESSNPRGCTPCFCFGHSSVCTNAVGVSVYSSISSTFOIDEDGWAEQRDGSEASLEW 540
Db 481 FFNLESSNPRGCTPCFCFGHSSVCTNAVGVSVYSSISSTFOIDEDGWAEQRDGSEASLEW 540
QY 541 SSERQDIAVSDSYFPRYFIAPAKFLGKQVLSYQNLSPFRVDRDRLSABDLVLEGA 600
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QY 601 GLRVSVPLIAQNSYPSSETTVKYVFLHEATDYPWRPALTPFEFQKLLNLSIKIRGTY 660
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Db 661 SERSAGYLDVTLASARPGVPATWVESCTCPVGYGGQFCMCLSGYRRETPLNLPYSP 720
QY 721 CVLACNCGHSETCDPETGVCNCRDNTAGPHCEKCSGYYGDSGTAGTSSDCQPCPGSS 780
Db 721 CVLACNCGHSETCDPETGVCNCRDNTAGPHCEKCSGYYGDSGTAGTSSDCQPCPGSS 780
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QY 841 NCNRLTGECLKCIYNTAGFYCDRCXDGFFGNPLAPNADKCKACNPNPYGTMKQSSCNP 900
Db 841 NCNRLTGECLKCIYNTAGFYCDRCXDGFFGNPLAPNADKCKACNPNPYGTMKQSSCNP 900
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Db 901 VTGQCECLPHVTGQDCGACDPGFYNLQSGQGCRCDCCHALGSTNGQCDIRGTQCECQPGI 960
QY 961 TGQHCECERVENHFGFPGEGCKPCDCHPEGSLSLQCKDDGRCEGFGVNRCDQCEENYF 1020
Db 961 TGQHCECERVENHFGFPGEGCKPCDCHPEGSLSLQCKDDGRCEGFGVNRCDQCEENYF 1020
QY 1021 YNRSWPGQCECPACRYLVKQKADHRVKLQELSLIANLGTGDEMVTDOAFEDRLKEAER 1080
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Db 1081 EVMDDLREAGQVDVQNDQNLMDRLQVRNNTLSSQISRLQIRNTIETGNLAEQARAHVEN 1140
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QY 1261 GDKAVEIYASVAQLSPLDSETLENEANNIKMEAEENLEQLIDQKLKDYEDLREDMRGKELE 1320
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Db 1501 INARKAKNSVTSLLSIIINDLEQLGQDQTDVLDNKLNEIEGTNLKAKDEMKVSDLDKRVSD 1560

QY 1561 LENEAKKQEAALMDYNRDIEEIMKDINLEDIRKTLPSGCNTPPSIEKP 1609
Db 1561 LENEAKKQEAALMDYNRDIEEIMKDINLEDIRKTLPSGCNTPPSIEKP 1609

RESULT 4

US-10-372-683-36
; Sequence 36, Application US/10372683
; Publication No. US20040009171A1
; GENERAL INFORMATION:
; APPLICANT: GERRITSEN, MARY E.
; APPLICANT: PEALE JR., FRANKLIN V.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA
; FILE REFERENCE: P1928R1P1
; CURRENT APPLICATION NUMBER: US/10/372,683
; PRIOR APPLICATION NUMBER: US 10/271,690
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/344,534
; PRIOR FILING DATE: 2001-10-18
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 36
; LENGTH: 1609
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-372-683-36

Query Match 100.0%; Score 8709; DB 15; Length 1609;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRGSHRAAPALPRGRLPVLAVALAAAAAGCAQAAMDECTDEGGRPORCMPEFVNAAFN 60
Db 1 MRGSHRAAPALPRGRLPVLAVALAAAAAGCAQAAMDECTDEGGRPORCMPEFVNAAFN 60
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Db 61 VTVVATNTCGTPPEEYCVQGTGVTGKSKCHLDCAGQPHLQHGAAFLTDYNNQADTTWQS 120
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Db 121 QTMLAGVQYPPSSINLTILHLGKAFDITYVRLKFHTSRPESFAIYKRTREDGWPVYQYYS 180
QY 181 SCENTYSKANRGFIRTTGGDEQQAALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFDNSPVL 240
Db 181 SCENTYSKANRGFIRTTGGDEQQAALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFDNSPVL 240
QY 241 QEWVTATDIRVTLNRLNTFGDEVNDPKVLKSYYYAISDFAVGGRCKCNGHASECMKNEF 300
Db 241 QEWVTATDIRVTLNRLNTFGDEVNDPKVLKSYYYAISDFAVGGRCKCNGHASECMKNEF 300
QY 301 DKLVNCKNTYGVDCCKLPFFNDRPWRRATAESASECLPCDCNGRSQECYFDPPELYRS 360
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QY 361 TGHGGHCTNCQDNTDGAHCERCEENFFRLGNNEACSSCHSPVGLSTQCDSYGRCSCKP 420
Db 361 TGHGGHCTNCQDNTDGAHCERCEENFFRLGNNEACSSCHSPVGLSTQCDSYGRCSCKP 420
QY 421 GVMGDKCDRCQPGFHSLTEAGCRPCSDPSGSDIECNVETGRVCCKDNVEGFNCERCKPG 480
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Db 601 GLRVSVPLIAQGNYSYSETTVKYVFRHLHEATDYPWRPALTPFEFQKLLNNLTSIKIRGTY 660
QY 661 SERSAGYLDVTLASARPGVPAWTWVESCTCPVYGGQFCFEMCLSGYRRETPNLGPYSP 720
Db 661 SERSAGYLDVTLASARPGVPAWTWVESCTCPVYGGQFCFEMCLSGYRRETPNLGPYSP 720
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QY 781 CAVVPKTKEVVCTNCPTGTTGKRCELDDGYFGDPLGRNGPVRLCRLCQSDNIDPNAVG 840
Db 781 CAVVPKTKEVVCTNCPTGTTGKRCELDDGYFGDPLGRNGPVRLCRLCQSDNIDPNAVG 840
QY 841 NCNRLTGECLKCIYNTAGFYCDRCKDGFEGNPLAPNADCKKACNCNPNYGTMKQOSSCNP 900
Db 841 NCNRLTGECLKCIYNTAGFYCDRCKDGFEGNPLAPNADCKKACNCNPNYGTMKQOSSCNP 900
QY 901 VTGQCECLPHVTGQDCGACDPGFYNLQSGQGCRCDCCHALGSTNGQCDIRTCQCECQPGI 960
Db 901 VTGQCECLPHVTGQDCGACDPGFYNLQSGQGCRCDCCHALGSTNGQCDIRTCQCECQPGI 960
QY 961 TGQHCECERNHFGFPGEGCKPCDCHPEGSLSLQCKDDGRCECREGFGVGNRCDQCEENYF 1020
Db 961 TGQHCECERNHFGFPGEGCKPCDCHPEGSLSLQCKDDGRCECREGFGVGNRCDQCEENYF 1020
QY 1021 YNRSWPGCQECPCYRLVKDKVADHRVKLQELSLIANLGTGDEMVTDAQFEDRLKEAER 1080
Db 1021 YNRSWPGCQECPCYRLVKDKVADHRVKLQELSLIANLGTGDEMVTDAQFEDRLKEAER 1080
QY 1081 EVMDLLREAQDVKDQVQDNLMDRLQRVNNTLSSQISRLQINRTIETGNLAQARAHVEN 1140
Db 1081 EVMDLLREAQDVKDQVQDNLMDRLQRVNNTLSSQISRLQINRTIETGNLAQARAHVEN 1140
QY 1141 TERLJIASRELEKAKVAAANYSVTQPESTGDPNNMTLLAEARKLAERHKQEADDIVRV 1200
Db 1141 TERLJIASRELEKAKVAAANYSVTQPESTGDPNNMTLLAEARKLAERHKQEADDIVRV 1200
QY 1201 AKTANDTSTEAYNLLRLTLAGENOTAFEIEELNRKYEQAKNISQDLEKQAAARVHEEAKRA 1260
Db 1201 AKTANDTSTEAYNLLRLTLAGENOTAFEIEELNRKYEQAKNISQDLEKQAAARVHEEAKRA 1260
QY 1261 GDKAVEIYASVAQLSPDSEITLNEANNIKMEAEENLEQLIDQKLKDYEDLREDMRGKELE 1320
Db 1261 GDKAVEIYASVAQLSPDSEITLNEANNIKMEAEENLEQLIDQKLKDYEDLREDMRGKELE 1320
QY 1321 VKNLLBKGKTEQQTADQLLARADAAKALAEAAKKGRTDLOEANDILNNLKDFDRRVNDN 1380
Db 1321 VKNLLBKGKTEQQTADQLLARADAAKALAEAAKKGRTDLOEANDILNNLKDFDRRVNDN 1380
QY 1381 KTAABEALRKIPAINQTIITEANEKTREAQOALGSAADATEAKNKAHEAERIAASAVQKNA 1440
Db 1381 KTAABEALRKIPAINQTIITEANEKTREAQOALGSAADATEAKNKAHEAERIAASAVQKNA 1440
QY 1441 TSTKABEAERTFAEVTDLDNVNNMLKQLOEAEKELKRKQDDADQDMMAGMASQAAQAE 1500
Db 1441 TSTKABEAERTFAEVTDLDNVNNMLKQLOEAEKELKRKQDDADQDMMAGMASQAAQAE 1500
QY 1501 INARKAKNSVTSLLSIINDLLEQLGQDQTDVNLNKLNEIEGTLNKADEMKVSDLDKRVSD 1560
Db 1501 INARKAKNSVTSLLSIINDLLEQLGQDQTDVNLNKLNEIEGTLNKADEMKVSDLDKRVSD 1560
QY 1561 LENEAKKQEAAIMDYNRDIEEIMKDIRNLEDIRKTLPSGCFNTPSIEKP 1609
Db 1561 LENEAKKQEAAIMDYNRDIEEIMKDIRNLEDIRKTLPSGCFNTPSIEKP 1609

RESULT 5

US-10-037-182-16

; Sequence 16, Application US/10037182

; Publication No. US2003004899A1

GENERAL INFORMATION:

; APPLICANT: Tryggvason, Karl
; APPLICANT: Doi, Masayuki
; APPLICANT: Thyboll, Jill
; TITLE OF INVENTION: Recombinant Laminin 10
; FILE REFERENCE: 99-274-F
; CURRENT APPLICATION NUMBER: US/10/037,182
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,449
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/279,282
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 1576
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-037-182-16

Query Match 98.1%; Score 8544; DB 14; Length 1576;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 QAAMDECTDEGGRPQRCMPEFVNAAFNVTVAATNCTGPPPEEYCVQTGVTGVTKSHLCD 93
Db 1 QAAMDECTDEGGRPQRCMPEFVNAAFNVTVAATNCTGPPPEEYCVQTGVTGVTKSHLCD 60
QY 94 AGQPHLQHGAAFLTDYNNQADTTWQSQOTMLAGVQYPSSINLTLHLGKAFDITYVRLKFX 153
Db 61 AGQPHLQHGAAFLTDYNNQADTTWQSQOTMLAGVQYPSSINLTLHLGKAFDITYVRLKFX 120
QY 154 TSRPESFAIKYKRTREDGWPIDYQYSGSCENTYSKANRGFIRTTGGDEQQAALCTDEFSDIS 213
Db 121 TSRPESFAIKYKRTREDGWPIDYQYSGSCENTYSKANRGFIRTTGGDEQQAALCTDEFSDIS 180
QY 214 PLTGGNVAFSTLEGRRPSAYNFEDNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSY 273
Db 181 PLTGGNVAFSTLEGRRPSAYNFEDNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSY 240
QY 274 YYAISDFAVGGRCKCNHGHASECMKNEFDKLCVCKNKHNTYGVDCCKLPPFNDRWRRAATA 333
Db 241 YYAISDFAVGGRCKCNHGHASECMKNEFDKLCVCKNKHNTYGVDCCKLPPFNDRWRRAATA 300
QY 334 ESASECLPCDCNRSQECYFDBELYRSTGHGGHCTNCDNTDGAHCERCRENFFRLGNNE 393
Db 301 ESASECLPCDCNRSQECYFDBELYRSTGHGGHCTNCDNTDGAHCERCRENFFRLGNNE 360
QY 394 ACSSCHCSPVGSLSLSTQCDSYGRCSCKPGVMGDKCDRCQPFHSLTEAGCRPCSCDPSGSI 453
Db 361 ACSSCHCSPVGSLSLSTQCDSYGRCSCKPGVMGDKCDRCQPFHSLTEAGCRPCSCDPSGSI 420
QY 454 DECNVETGRCVCKDNVEGFNCERCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGSYVY 513
Db 421 DECNVETGRCVCKDNVEGFNCERCKPGFFNLESSNPRGCTPCFCFGHSSVCTNAVGSYVY 480
QY 514 SISSTFQIDEDGWRAEQORDGSEASLEWSSERQDIAVISDSYFPYFYIAPAKFLGKQVLSY 573
Db 481 SISSTFQIDEDGWRAEQORDGSEASLEWSSERQDIAVISDSYFPYFYIAPAKFLGKQVLSY 540
QY 574 GQNLFSFPRVDRDRTRLASAEDLVLEGAGLRVSVPLIAQGNYSYSETTVKYVFRHLHEATDY 633
Db 541 GQNLFSFPRVDRDRTRLASAEDLVLEGAGLRVSVPLIAQGNYSYSETTVKYVFRHLHEATDY 600
QY 634 PWRPALTPFEFQKLLNNLTSIKIRGTYSERSAGYLDVTLASARPGVPAWTWVESCTCP 693
Db 601 PWRPALTPFEFQKLLNNLTSIKIRGTYSERSAGYLDVTLASARPGVPAWTWVESCTCP 660
QY 694 VGYGGQFCFEMCLSGYRRETPNLGPYSPCVLCACNGHSETCDPETGVCNCRDNTAGPHCEK 753
Db 661 VGYGGQFCFEMCLSGYRRETPNLGPYSPCVLCACNGHSETCDPETGVCNCRDNTAGPHCEK 720
QY 754 CSDGIYGDSTAGTSSDCQPCPCGGSSCAVVPKTKEVVCTNCPTGTTGKRCELDDGYFG 813

Db 721 CSDGYGDSSTAGTSSDCQPCPGSSCAVVPKTKEVVCTNCTGTGTRKCELCDDGYFG 780
QY 814 DPLGRNGPVRCLRCQCSNDIDPNAVGNCRNLTGECCLKCIYNTAGFYCDRCCKDGFNPL 873
Db 781 DPLGRNGPVRCLRCQCSNDIDPNAVGNCRNLTGECCLKCIYNTAGFYCDRCCKDGFNPL 840
QY 874 APNPADKCKACNPNPYGTMKQOSSCNPVGTGQCECLPHVTGQDCGACDPGFYNLQSGQGE 933
Db 841 APNPADKCKACNPNPYGTMKQOSSCNPVGTGQCECLPHVTGQDCGACDPGFYNLQSGQGE 900
QY 934 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCERCEVNHFGFPGEGCKPCDCHPEGSLSL 993
Db 901 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCERCEVNHFGFPGEGCKPCDCHPEGSLSL 960
QY 994 QCKDDGRCECEGFGVGNRCDCQCEENTFYNRSWPGQCECPACRYLLVKQVADHRVKLQELE 1053
Db 961 QCKDDGRCECEGFGVGNRCDCQCEENTFYNRSWPGQCECPACRYLLVKQVADHRVKLQELE 1020
QY 1054 SLIANLTGDEMVTDOAFEDRLKEAREVMDDLREAOQVQVDQNDLMDRLQRVNNTLSSQ 1113
Db 1021 SLIANLTGDEMVTDOAFEDRLKEAREVMDDLREAOQVQVDQNDLMDRLQRVNNTLSSQ 1080
QY 1114 ISRLQIRNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1173
Db 1081 ISRLQIRNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1140
QY 1174 NMVTLAEEARKLAERHKEADDIRVAKTANDTSTEAYNLLRLTLAGENQTAPEIEELN 1233
Db 1141 NMVTLAEEARKLAERHKEADDIRVAKTANDTSTEAYNLLRLTLAGENQTAPEIEELN 1200
QY 1234 RYEQAKNISQLEKQAAARVHEEAKRAGDKAVEIYASVQLSPLDSETLENEANNIKMEA 1293
Db 1201 RYEQAKNISQLEKQAAARVHEEAKRAGDKAVEIYASVQLSPLDSETLENEANNIKMEA 1260
QY 1294 ENLEQLIDQKDYEDLREDMRGKELEVKNLLEKKGTEQQTADQLLARADAAKALAEBA 1353
Db 1261 ENLEQLIDQKDYEDLREDMRGKELEVKNLLEKKGTEQQTADQLLARADAAKALAEBA 1320
QY 1354 KKGRTDQEAANDILNNLKDFDRVNDNKTAAEBALRKIPAINQITITEANEKTRTAAQALG 1413
Db 1321 KKGRTDQEAANDILNNLKDFDRVNDNKTAAEBALRKIPAINQITITEANEKTRTAAQALG 1380
QY 1414 SAAADATEAKNAHEAERIAASVQKNATSTKAEARTFAEVTDLNNEVNNMLKQLOEAEK 1473
Db 1381 SAAADATEAKNAHEAERIAASVQKNATSTKAEARTFAEVTDLNNEVNNMLKQLOEAEK 1440
QY 1474 ELKRKQDDADQDMMAGMASQAAQAEAEINARKAKNSVTSLSIINDLLEQLGQDQDVTDLN 1533
Db 1441 ELKRKQDDADQDMMAGMASQAAQAEAEINARKAKNSVTSLSIINDLLEQLGQDQDVTDLN 1500
QY 1534 KLNEIEGTLNKAKDEMKVSDLRKVSQDLENEAKKQEAAMINDYNRDIEEIMKDINLEDIR 1593
Db 1501 KLNEIEGTLNKAKDEMKVSDLRKVSQDLENEAKKQEAAMINDYNRDIEEIMKDINLEDIR 1560
QY 1594 KTLPSGCFNTPSIEKP 1609
Db 1561 KTLPSGCFNTPSIEKP 1576

RESULT 6
US-09-938-275-10
; Sequence 10, Application US/09938275
; Patent No. US20020111309A1
; GENERAL INFORMATION:
; APPLICANT: Gerardo Castillo
; APPLICANT: Alan Snow
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications
; TITLE OF INVENTION: of Laminin and Laminin-Derived Protein Fragments
; FILE REFERENCE: PROTEO.P03
; CURRENT APPLICATION NUMBER: US/09/938,275
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1607
; TYPE: PRT
; ORGANISM: Mus Musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Swissprot P02468
; DATABASE ENTRY DATE: 1989-07-01
US-09-938-275-10

Query Match 93.7%; Score 8161; DB 9; Length 1607;
Best Local Similarity 92.7%; Pred. No. 0;
Matches 1492; Conservative 61; Mismatches 54; Indels 2; Gaps 1;

QY 1 MEGSHRAAPALRPRGRLPVLAVALAAAGCAQAAMDECTDEGRPQRCMPEFVNAFN 60
Db 1 MTGGRAALALQPRGRLPVLAVAL--AAVAGCVRAAMDECADEGGRPQRCMPEFVNAFN 58
QY 61 VTVVATNTCGTPPEYCVQGTGVTGKSKCHLCLDAGQPHLQHGAAFLTDYNNQADTTWQS 120
Db 59 VTVVATNTCGTPPEYCVQGTGVTGKSKCHLCLDAGQPHLQHGAAFLTDYNNQADTTWQS 118
QY 121 QTMLAGVQYPSINLTILHLGKAFDITYVRLKFHTSRPESPAIKRTREDGFWIPYQYISG 180
Db 119 QTMLAGVQYPSINLTILHLGKAFDITYVRLKFHTSRPESPAIKRTREDGFWIPYQYISG 178
QY 181 SCENTYSKANRGFIRTCGDEQOALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFDNSPVL 240
Db 179 SCENTYSKANRGFIRTCGDEQOALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFDNSPVL 238
QY 241 QEWVTATDIRVTNLRLNTFGDEVNDPKVLKSYYYAISDAVGGRCCKNGHASECMKNEF 300
Db 239 QEWVTATDIRVTNLRLNTFGDEVNDPKVLKSYYYAISDAVGGRCCKNGHASECMKNEF 298
QY 301 DXLVCKNCKHNTYGVDCCKLPLFFNDRPWRRAATAESASECLPCDCNCRSQECYFPELYRS 360
Db 299 DXLMCNCKHNTYGVDCCKLPLFFNDRPWRRAATAESASECLPCDCNCRSQECYFPELYRS 358
QY 361 TGHGGHCTNCODNTDGAHCERCERENFFRLGNNEACSSCHSCPVGSLSTQCDSYGRCSCKP 420
Db 359 TGHGGHCTNCODNTDGAHCERCERENFFRLGNNEACSSCHSCPVGSLSTQCDSYGRCSCKP 418
QY 421 GVMGDKCDRCOPGFHSLTEAGRCPCSDLRGSTDENVTETGRCVCKDNVEGFNCERCKPG 480
Db 419 GVMGDKCDRCOPGFHSLTEAGRCPCSDLRGSTDENVTETGRCVCKDNVEGFNCERCKPG 478
QY 481 FENLESSNPGCTPCFCFHSVCTNAVGSVYSSISSTFOIDEDGWRAEQDGSSEASLEW 540
Db 479 FENLESSNPGCTPCFCFHSVCTNAVGSVYSSISSTFOIDEDGWRAEQDGSSEASLEW 538
QY 541 SSERQDIAVSDSYFFRYFIAPAKFLGKQVLSYQNLNLSFSDVDRDRRLSAEDLVLEGA 600
Db 539 SSERQDIAVSDSYFFRYFIAPAKFLGKQVLSYQNLNLSFSDVDRDRRLSAEDLVLEGA 598
QY 601 GLRVSVPPLIAQNSYSPSETTVKYVFRRLHEATDYPWRPALTPFEFQKLLNLTSTIKIRGTY 660
Db 599 GLRVSVPPLIAQNSYSPSETTVKYVFRRLHEATDYPWRPALTPFEFQKLLNLTSTIKIRGTY 658
QY 661 SERSAGYLDVTLASARPGPGVPATWVESCTCPVGYGGQFCMCLSGYRRETPLNLPYSP 720
Db 659 SERSAGYLDVTLASARPGPGVPATWVESCTCPVGYGGQFCMCLSGYRRETPLNLPYSP 718
QY 721 CVLCAACNGHSETCDPETGVNCRDNTAGPHCEKCSGYYGDSSTAGTSSDCQPCPGGSS 780
Db 719 CVLCAACNGHSETCDPETGVNCRDNTAGPHCEKCSGYYGDSSTAGTSSDCQPCPGGSS 778
QY 781 CAVVPKTEWVCTNCPGTGTTGKRCCELCDGDFGDPILGNGPVRRLCRLCQCSNIDPNAVG 840
Db 779 CAVVPKTEWVCTNCPGTGTTGKRCCELCDGDFGDPILGNGPVRRLCRLCQCSNIDPNAVG 838
QY 841 NCNRLTGECLKCIYNTAGFYCDRCCKDGFNPLAPNPADCKACNPNPYGTMKQOSSCNP 900
Db 839 NCNRLTGECLKCIYNTAGFYCDRCCKDGFNPLAPNPADCKACNPNPYGTMKQOSSCNP 898

QY 1021 YNRSWPGCQCEPACRYLVKDKVADHRVVKLOELESIANLGTGDEMVTDOAFEDRLKEAER 1080
DB 1018 YNRSWPGCQCEPACRYLVKDKAAEHRVVKLOELESIANLGTGDEMVTDOAFEDRLKEAER 1077
QY 1081 EVMDDLREAOQVKDQVNDQNLMDRLQVNNNTLSSQISRLQIRNTIETGNLAQARAHVEN 1140
DB 1078 EVTDLLREAOQVKDQVNDQNLMDRLQVNNNTLSSQISRLQIRNTIETGNLAQARAHVEN 1137
QY 1141 TERLIEIASRELEKAKVAAANVSVTQPESTGDPNNMTLLAEAEARKLAERHKQEAADDIVRV 1200
DB 1138 TEQLIEIASRELEKAKM-AANVSITQPESTGEPNNMTLLAEAEARRLAERHKQEAADDIVRV 1196
QY 1201 AKTANDTSTEAYNLLRLTLAGENQTAPEIEBELNRKYEAKNISQDLEKQAAARVHEEAkra 1260
DB 1197 AKTANETSABAYNLLRLTLAGENQTAPEIEBELNRKYEAKNISQDLEKQAAARVHEEAkra 1256
QY 1261 GDKAVEIVASVAQLSPDSETLENEFANNIKMEAEENLEQIDQKLXDYEDLREDMRGKELE 1320
DB 1257 GDKAVEIVASVAQLTPVDSEALENEANKIKKEAADLRLIDQKLXDYEDLREDMRGKEHE 1316
QY 1321 VKNLLEKGTQEQQTADQLLARADAAKALAEAAKKGRTPLQEAANDILNLLKDFDRRVNDN 1380
DB 1317 VKNLLEKGAEQQTADQLLARADAAKALAEAAKKGRTPLQEAANDILNLLKDFDRRVNDN 1376
QY 1381 KTAEEALRKIPAINQITTEANEKTRAAQALGSAADAAATEAKNKAHEAEERIASAVQKNA 1440
DB 1377 KTAEEALRRIPAINRTIAEANEXTREAAQALGNAADAAATEAKNKAHEAEERIASAAQKNA 1436
QY 1441 TSTKAEAEERFAEVTDLNNEVNNMLKQLOEAEKELKRQDDADQDMMAGMASQAAQAEAE 1500
DB 1437 TSTKAEAEERFGEVTDLDNEVNGMLRQLEEAENELKRQDDADQDMMAGMASQAAQAEAE 1496
QY 1501 INARKAKNSVTSLLSIINDLLEQLGQDQDVTVDLNLKNETEGTLNKADEMVKVSDLDKRVSD 1560
DB 1497 LNARKAKNSVTSLLSQNLNLLDQGLQDQDVTVDLNLKNETEGTLNKADEMVKVSDLDKRVSD 1556
QY 1561 LENEAKKQEAALMDYNDRIEIEIMKDINLEDIRKTLPSCGFNTPSIEKP 1609
DB 1557 LESEARKQEAALMDYNDRIEIEIMKDINLEDIRKTLPSCGFNTPSIEKP 1605

RESULT 8

US-10-037-182-20

; Sequence 20, Application US/10037182

; Publication No. US2003004899A1

; GENERAL INFORMATION:

; APPLICANT: Tryggvason, Karl

; APPLICANT: Doi, Masayuki

; APPLICANT: Thyboll, Jill

; TITLE OF INVENTION: Recombinant Laminin 10

; FILE REFERENCE: 99-274-F

; CURRENT APPLICATION NUMBER: US/10/037,182

; CURRENT FILING DATE: 2001-12-21

; PRIOR APPLICATION NUMBER: 60/257,449

; PRIOR FILING DATE: 2000-12-21

; PRIOR APPLICATION NUMBER: 60/279,282

; PRIOR FILING DATE: 2001-03-28

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 20

; LENGTH: 1572

; TYPE: PRT

; ORGANISM: Mus musculus

US-10-037-182-20

Query Match 92.3%; Score 8038; DB 14; Length 1572;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;

QY 36 AMDECTDEGGRPQRCMPEFVNAAPNVTVAATTCGTPPEEYCVQGTGVTKSKHLCDAG 95

DB 1 AMDECADEGGRPQRCMPEFVNAAPNVTVAATTCGTPPEEYCVQGTGVTKSKHLCDAG 60

QY 96 QPHLQHGAFLTDYNNQADTTWWSQTMLAGVQYPSINLTLHLGKAFDITYVRLKEFHTS 155
DB 61 QPHLQHGAFLTDYNNQADTTWWSQTMLAGVQYPSINLTLHLGKAFDITYVRLKEFHTS 120
QY 156 RPESFAIYKRTREDGPWIPYQYYSGSCENTYSKANRGFIRTGDEQQAALCTDEFSDISPL 215
DB 121 RPESFAIYKRTREDGPWIPYQYYSGSCENTYSKANRGFIRTGDEQQAALCTDEFSDISPL 180
QY 216 TGGNVAFTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSYYY 275
DB 181 TGGNVAFTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSYYY 240
QY 276 AISDFAVGGRCCKNGHASECMKNEFDKLVNCKHNTYGVDCCKCLPFFNDRPWRRAEAS 335
DB 241 AISDFAVGGRCCKNGHASECMKNEFDKLVNCKHNTYGVDCCKCLPFFNDRPWRRAEAS 300
QY 336 ASECLPCDCNGRSQECYFDPPELYRSTGHGGHCTNCQDNTDGAHCRCRNFRLGNNEAC 395
DB 301 ASECLPCDCNGRSQECYFDPPELYRSTGHGGHCTNCQDNTDGAHCRCRNFRLGNNEAC 360
QY 396 SSCHCSPVGSLSLTCQDSYGRCSCKPGVMDKCDRCQPGFHSLTEAGCRPCSCDPSGSIDE 455
DB 361 SPCHCSPVGSLSLTCQDSYGRCSCKPGVMDKCDRCQPGFHSLTEAGCRPCSCDPSGSIDE 420
QY 456 CNVETGRCVCKDNVEGFNCERCCKPGFNFNLESSNPRGCTPCFCFHSVSVCTNAVGSYVSI 515
DB 421 CNVETGRCVCKDNVEGFNCERCCKPGFNFNLESSNPRGCTPCFCFHSVSVCTNAVGSYVSI 480
QY 516 SSTFOIDEDGWRABQRDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSYGQ 575
DB 481 SSTFOIDEDGWRABQRDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSYGQ 540
QY 576 NLSFSFRVDRDRTRLSAEDLVLEGALRVSVPLIAQNSYSPSETTVKYVFRLEATDYPW 635
DB 541 NLSFSFRVDRDRTRLSAEDLVLEGALRVSVPLIAQNSYSPSETTVKYVFRLEATDYPW 600
QY 636 RPALTPFEFQKLLNNLTSLKIRGTYSERSAGYLDVTLASARPGVGPATWVESCTCPVG 695
DB 601 RPALTPFEFQKLLNNLTSLKIRGTYSERSAGYLDVTLASARPGVGPATWVESCTCPVG 660
QY 696 YGQFCFCEMCLSGYRRETPNLGPYSPCVLCAENGHSEICDPETGVNCNRDNTAGPHCEKCS 755
DB 661 YGQFCFCEMCLSGYRRETPNLGPYSPCVLCAENGHSEICDPETGVNCNRDNTAGPHCEKCS 720
QY 756 DGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKVCTNCPTGTTGKRCCLCDDGYFGDP 815
DB 721 DGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKVCTNCPTGTTGKRCCLCDDGYFGDP 780
QY 816 LGRNGPVRCLCCLCQSDNIDPNAVGNCRNLTGECCLKIYNTAGFYCDRCCKDGFNPLAP 875
DB 781 LGRNGPVRCLCCLCQSDNIDPNAVGNCRNLTGECCLKIYNTAGFYCDRCCKDGFNPLAP 840
QY 876 NPADKCKACACN-YPGTVQOQSSCNPTGQCECLPHVTGQDCGACDPPGYNLQSGQCERC 935
DB 841 NPADKCKACACN-YPGTVQOQSSCNPTGQCECLPHVTGQDCGACDPPGYNLQSGQCERC 899
QY 936 DCHALGSTNGQCDIRTGQCECOPGITGQHCERCEVNHFGFEGEGCKPCDCHPEGSLSLQC 995
DB 900 DCHALGSTNGQCDIRTGQCECOPGITGQHCERCEVNHFGFEGEGCKPCDCHPEGSLSLQC 959
QY 996 KDDGRCECEGFGVGNRCDQCEENYFYNRSWPGCQCEPACRYLVKDKVADHRVVKLOELES 1055
DB 960 KDDGRCECEGFGVGNRCDQCEENYFYNRSWPGCQCEPACRYLVKDKVADHRVVKLOELES 1019
QY 1056 IANLGTGDEMVTDOAFEDRLKEAEREVMDLLREAOQVKDQVNDQNLMDRLQVNNNTLSSQIS 1115
DB 1020 IANLGTGDEMVTDOAFEDRLKEAEREVMDLLREAOQVKDQVNDQNLMDRLQVNNNTLSSQIS 1079
QY 1116 RLQNIIRNTIETGNLAQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDPNN 1175
DB 1080 RLQNIIRNTIETGNLAQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDPNN 1138
QY 1176 MTLLEAEARKLAERHKQEAADDIVRVAKTANDTSTEAYNLLRLTLAGENQTAPEIEELNRK 1235

QY 1324 LLEKKGTEQQT-----ADQLLARADAAKALAEAAKKGRTDLOEANDILNNLKDF 1373
Db 1298 QATLRQTEPLTARSRLTATFASQLHQGARAALTOASSSVQAAATVVMGARTLLADLEG 1357
QY 1374 DRRVNDNKTAABEALRKIPAINQITITEANEKTRAQALGSAADATEAKNKAHEAERIA 1433
Db 1358 KLQFPRPKDQALQKADSVSDRLLADTRKKTQKAERMLGNAAPLSSSAKKKGREAELVA 1417
QY 1434 SAVQKNATSTKAEARTFAEVTDLNNEVNNMLKQL-QEAEKELKRKQDDADQDMMAGNA 1492
Db 1418 KDSAKLAKALLERKQAHRRASRLTSQQTALQQAQQVLAASEARRQEELEAEVAGLS 1477
QY 1493 SQAAQEAIEINAKKNSVTSLLSIINDLLEQLGQDLD--VDLNKLNEIEGTLNKADEM- 1549
Db 1478 -----EMEQQIRESRISLEKDIETLSELLARLGSLDTHQAPAQALNETQWALERLRLQLG 1532
QY 1550 KVSDDLKRVSDLENAKKQEAAIMDYNRDIEEIMKDIRNLEDIRKTLPSGC 1600
Db 1533 SPGSLQKLSLLEQESQQELQIQGFESDLAEIRADKQNLKLEAILHSLPENC 1583
RESULT 10
US-10-262-839-210
; Sequence 210, Application US/10262839
; Publication No. US20040038877A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, John,
; APPLICANT: Anderson, David W.,
; APPLICANT: Boldog, Ferenc,
; APPLICANT: Burgess, Catherine,
; APPLICANT: Catterton, Elina,
; APPLICANT: Edinger, Shlomit,
; APPLICANT: Ellerman, Karen,
; APPLICANT: Gerlach, Valerie,
; APPLICANT: Gorman, Linda,
; APPLICANT: Guo, Xiaojia,
; APPLICANT: Ji, Weizhen,
; APPLICANT: Kekuda, Ramesh,
; APPLICANT: Leach, Martin,
; APPLICANT: Li, Li,
; APPLICANT: Miller, Charles,
; APPLICANT: Patturajan, Meera,
; APPLICANT: Reiger, Daniel,
; APPLICANT: Rothenberg, Mark,
; APPLICANT: Shinkets, Richard,
; APPLICANT: Smithson, Glenda,
; APPLICANT: Spytek, Kimberly,
; APPLICANT: Taupier, Raymond, jr.,
; APPLICANT: Vernet, Corine,
; APPLICANT: Voss, Edward,
; APPLICANT: Zerhusen, Brian,
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-462A
; CURRENT APPLICATION NUMBER: US/10/262,839
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,101
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/371,972
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/327,342
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/328,044
; PRIOR FILING DATE: 2001-10-09

; PRIOR APPLICATION NUMBER: 60/328,849
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/374,738
; PRIOR FILING DATE: 2002-04-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 367
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 210
; LENGTH: 1587
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-839-210

Query Match 41.4%; Score 3611; DB 12; Length 1587;
Best Local Similarity 43.5%; Pred. No. 3.8e-197;
Matches 701; Conservative 264; Mismatches 578; Indels 68; Gaps 21;

QY 21 LAVLAAAAAGCAQAAMDECTDEGGRPQRCMPFVNAAFNVTVVATNTCGTPPEEYCVQT 80
Db 10 LALLAPRAAG-----AGMGACYDGAGRPQRCPLPVFENAAFGRLAQAASHTCGSPPEDFCPHV 65
QY 81 GVTGVTKSHLCDAGQPHLQHGAAFLTDYNNQADTTWQSQOTMLAGVQYPSSINLTLLHG 140
Db 66 GAAGAGAHQORCDAADPQRHNASYLTDFHSQDESTWQSPSMAGVQYPTSVNITLRG 125
QY 141 KAFDITYVRLKFTSRPESFAIYKRTREDGPWIPYQYYSGSCENTYSKANRGFIRTTGDE 200
Db 126 KAYEITYVRLKFTSRPESFAIYKRSRADGPWEPYQFYASCCQTYGRPEGQYLRPGEDE 185
QY 201 QQALCTDEFSDISPLTGCNVAFSTLEGRPSAYNFNDNSPVLQEWVTATDIRVTNLRLNTFG 260
Db 186 RVAFCTSEFSDISPLSGGNVAFSTLEGRPSAYNFEESPLQEWVWSTELLISLDRNLNTFG 245
QY 261 DEVFNDPKVLKSYYYAISDFAVGGRCKNGHASECMKNEFDKLVCKCKHNTYGVDCCKCL 320
Db 246 DDIFKDPKVLQSYYYAVSDFSVGGRCKNGHASECGPDVAGQLACRCQHTTGTDCERCL 305
QY 321 PFFNDRPWRRTAASASECLPCDCNGRSQECYFDPPELYRSTGHGHCTNCQDNTDGAHCE 380
Db 306 PFFQDRPWARGTAAAECLPCNCSGRSECTFDRELFRSTGHGRCHCRDHTAGPHCE 365
QY 381 RCRENFFRLGNNEACSSCHCSPVGLSTQDCSYGRCSCKPGVMGDKDRCPQGFHSLTEA 440
Db 366 RCQENFYHWDPRMPCQDCQCSAGSLHLQDQDGTGTACKTPTVTGWKCDRCLPGFHSLSSEG 425
QY 441 GCRPCSDPSGIDECNVETGRCVCKDNVEGFNCERCKPGFFNLESSNPRGCTPCFCFGH 500
Db 426 GCRPCTCNFAGSLDTCPRSGRCPCKENVEGNLDCRCPGTFTNLQPNPAGSCSCFCYGH 485
QY 501 SSVCTNAVGSYVYSISSTFQIDEDGWRAEQDSEASLEWSSERQDIAVISDSYFFRYFI 560
Db 486 SKVCASTAQFQVHHILSDFHQAGEGWARSVGGSEHSPQWSPN----GVLLSPEDEEELT 541
QY 561 APAKFLGKQVLSYGONLSFSFRVDRDRDRLSABDLVLEGAGLRVSVPLIAQNSYPSSETT 620
Db 542 APGKFLGDQRFSGQPLILITFRVPPGDSPLPVQ-LRLEGTGLALS--LRHSSLSGPDAR 598
QY 621 VKYVFRH--EATDYPWRPALTPFEFQKLNLLNLTSIKIRGTYSERSAG--YLDVVTLAS 675
Db 599 ASQGGRAQVPLQETSEDVAPPLPFFHFQRLLANLTSLRLRVSPGPSAGPVFELTEVRLTS 658
QY 676 ARPFGVPATWVESCTCPVGGGQFCCEMCLSGYRRETPNLGPYSPCVLCACNHSETCDP 735
Db 659 ARPGLSPASWVEICSCPTGYTGQFCESCAPGYKREMPQGGPYASCVPCTCNQHG-TCDP 717
QY 736 ETGVCNCRDNTAGPHCEKSDGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTEWVCTNC 795
Db 718 NTGICVCSHHTEGPSCERCLPGFYGNPFPAGQADDQPCPCPGQSACTTIPESGEVVTCH 777
QY 796 PTGTTGKRCELCDGDFGDPPLGRNGVPVRLCRLCQCSNDIDPNAVGNCRNLTBCECLKCIYN 855
Db 778 PPGQRRRCCEVCDGDFGDPPLGLFGHPQPCQCCSGNVDPNAVGNCDPLSGHCLRLHN 837

4

```

; APPLICANT: Patturajan, Meera,
; APPLICANT: Reiger, Daniel,
; APPLICANT: Rothenberg, Mark,
; APPLICANT: Shimkets, Richard,
; APPLICANT: Smithson, Glennda,
; APPLICANT: Spytek, Kimberly,
; APPLICANT: Taupier, Raymond, jr.,
; APPLICANT: Vernet, Corine,
; APPLICANT: Voss, Edward,
; APPLICANT: Zerhusen, Brian,
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD:
; FILE REFERENCE: 21402-462A
; CURRENT APPLICATION NUMBER: US/10/262,839
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,029
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; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,101
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/371,972
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/327,342
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/328,044
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,849
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/374,738
; PRIOR FILING DATE: 2002-04-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 367
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 212
; LENGTH: 1575
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-839-212

Query Match          41.4%; Score 3609; DB 12; Length 1575;
Best Local Similarity 43.7%; Pred. No. 4.9e-197;
Matches 699; Conservative 265; Mismatches 577; Indels 60; Gaps 21;

QY 21 LAVLAAAAAGCAQANDECTDEGGRPQRCMPEFVNAAFNVTVVAINTCGTPPEEYCVQT 80
Db 10 LALLAPRAAG---AGMGACYDGAGRPQRCPLPVFENAAFGRLAQASHTCGSPEDFCPHV 65
QY 81 GVTGVTKSCHLCDAGPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYPSSINLTILHG 140
Db 66 GAAGAGAHQCQRCDADPQRHHNASYLTDFHSQDESTWQSPSMAFGVQYPTSVNITLRLG 125
QY 141 KAFDITYRLKFHTSRPESFAIYKRTREDGPNIPYQYSGSCENTYSKANRGFIRTCGDE 200
Db 126 KAYEITYRLKFHTSRPESFAIYKRSRADGPWEPIQFYASACQKTYGRPEGQYLRGDE 185
QY 201 QQALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFDSNPSVLQEWVTATDIRVTLNRLNFTG 260
Db 186 RVAFTSEFSDISPLSGGNVAFSTLEGRPSAYNFEESPGLQEWVTSTELLISLDRNLNFTG 245
QY 261 DEVENDPKVLKSYVYATISDFAVGGRCKCNGHASECMKNEFDKLVCNCKHNTYGVDCBKCL 320
Db 246 DDIFKDPKVLQSYVYAVDSFVSGGRCKCNGHASECGPDVAGQLACRCQHNTTGTDCERCL 305
QY 321 PFENDRPWRRATAESASECLPCDCNGRSQECYFDPBELYRSTGHGHCTNCQDNTDGAHCE 380
Db 306 PFFQDRPWARGTAEAAHECLPCNCSGRSEECTFRELFRSTGHGGRCHHCRDHTAGHCE 365
QY 381 RCRENFFRLGNNEACSSCHCSPVGLSLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLTEA 440

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Query Match 41.4%; Score 3609; DB 12; Length 1575;
Best Local Similarity 43.7%; Pred. No. 4.9e-197;
Matches 699; Conservative 265; Mismatches 577; Indels 60;

1550 KVSDDLDRKVSDIENEAKKQEEAIMDYNRDIEHIMKDIRNLEDIRKTLPSGC 1600
 1533 SPGSLORKLSLUEQESOOOEOLOIOGFESDIAEIRADKONLEAILHSLPNC 1583

RESULT 11
US-10-262-839-212
; Sequence 212, Application US/10262839
; Publication No. US20040038877A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, John,
; APPLICANT: Anderson, David W.,
; APPLICANT: Boldog, Ferenc,
; APPLICANT: Burgess, Catherine,
; APPLICANT: Catterton, Elina,
; APPLICANT: Edinger, Shlomit,
; APPLICANT: Ellerman, Karen,
; APPLICANT: Gerlach, Valerie,
; APPLICANT: Gorman, Linda,
; APPLICANT: Guo, Xiaojia,
; APPLICANT: Ji, Weizhen,
; APPLICANT: Kekuda, Ramesh,
; APPLICANT: Leach, Martin,
; APPLICANT: Li, Li,
; APPLICANT: Miller, Charles,

Db 366 RCQENFYHWDPRMPCQPCDCQASGSLHLQCDTGTCTACKPTVTGWKCDRCCLPGFHSLSSEG 425
QY 441 GCRPCSDPSPGSDIECNVETGRVCCKDNVEGFNCERCCKPGFFENLESSNPRGCTPCFCFGH 500
Db 426 GCRPCTCNPAGSLDTCDPRSGRCPCKENVEGNLDCRCPGTFLQHPNPAGSSCFYGH 485
QY 501 SSVCTNAVGSYVSYSSSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDYFPPRYFI 560
Db 486 SKVCASTAQFQVHHILSDFHQAGWARSVGGSEHSPQWSPN---GVLLSPDEDEELT 541
QY 561 APAKFLGKQVL SYGQNLFSFRVDRDRDTRL SAEDLVLEGAGLRVSUPLIAQGNYPSETT 620
Db 542 APGKFLGDQRFYSQPLILTFRVPPGDSPLVQ-LRLEGTGLALS--LRHSSLSGPQDAR 598
QY 621 VKYVFRLLH---EATDYPWRPALTPFEFQKLLNNLTSIKIRGTYSERSAG--YLLDDVTLAS 675
Db 599 ASQGRAGVPLQETSEDAVPLPFHFQRLLANLTSRLRVSPGSPAGVPVLTETVRLTS 658
QY 676 ARPGPGVPATWVESCTCPVYGQGFCEMCLSGYRRRETENLGPSPCVLCAACNGHSETCDP 735
Db 659 ARPGLSPASWVEICSCP TGYTGQFCESCAPGYKREMPQGGPYASCVPCTCNQHG-TCDP 717
QY 736 ETGVCNCRDNTAGPHCEKCDGYYGDSTAGTSSDCQPCPCPGSSCAVVPKTKEVVCTNC 795
Db 718 NTGICVCSHHTGSPCERCLPGFYGNPFAGADDQPCPCPGQSACTTIPESGEVVCTHC 777
QY 796 PTGTTGKRCBLCDGDFGDFPLGRNGFVRLCRLCQCSDNIDPNAVGNCRNLTGECCLKIYN 855
Db 778 PPGQRRRCRCEVDDGDFGDFPLGFGHPQPCQCQCSGNVDNAVGNCDPLSGHCLRLHN 837
QY 856 TAGFYCDRCCKDGGFFGNPLAPNPADKCKACACNCPYGTMKQSSCNPNVTGQCECLPHVTGD 915
Db 838 TTGDHCEHCQEGFYGSALAPRPADKCMPCSCHPQGSVSEQMPCDPVTGQCSCLPHVTARD 897
QY 916 CGACDPGFYNLQSGQGCERCDCCHALGSTNGQCDIRTGQCECOPGITGQHCEVNEHFGF 975
Db 898 CSRCYPGFFDLQPGRCRSCKCHPLGSDQDQCHPKTGQCTCRPGVTGACDRCLGFFGS 957
QY 976 GPEGCKPCDCHPEGSLSLQCKDDGRCECREGFGVGNRCDCQCEENFYNRSWPGCQCEPCAC 1035
Db 958 SIKGCRACRCSPLGAASAQCHYNGTCVCRPGFEGYKCDRCHYNFFLTADGTHCQCCPCSY 1017
QY 1036 RLVKDKVADHRVKLQELLES LIANLGTGDEMVTDAQAFEDRLKEAREVMDLLREAAQDVKD 1095
Db 1018 ALVKEETAKLKLTLTTEGLQSGDCGSPW--GPLDILGEAPRG--DVYQGHLLPGA 1072
QY 1096 DONLMDRLQRVNNTLSSQISRLQNRITETGNLAEQARAHVENTERLIEIASRELEKA 1155
Db 1073 REAFLEQMGLGAVKAAREQLRLNKGRFCAQAGSQKTCTQLADLEAVLESSEEEILHA 1132
QY 1156 KVAAANVSVTQPESTGDPNNMTLLAEAEARKLAERHKQEAADDIVRVAKTANDTSTEAYNLL 1215
Db 1133 AAILASLEIPQ-EGPSQPTKWSHLAIEARALARSHRDTATKIAATAWRALLASNTSYALL 1191
QY 1216 LRTLAGEHOTAFEIE-ELNRKYEQAKNISQDLEKQAARVHEEAKRAGDKAVEIYASVAQL 1274
Db 1192 WNLL--EGRVALETORDLEDRYQEVQAAQKALRTAVALPEAE-----SVLATVQOV 1242
QY 1275 SPLDSETL-----ENEANNIKMEAEENLEQLIDQKLKDYEDLREDMRGKELEVKN 1323
Db 1243 GADTAPYLALLASPGALPOKSRaedLGLKAKALEKTV---ASWQHMAE-AARTLQTAA 1297
QY 1324 LLEKKGTEQQTADQLLARADAALAEAEAKKGRDRTLQEAANDILNNLKDfDRRVNDNKTA 1383
Db 1298 QATLRQTEPLT--KLHQEARAALTQASSSVQAAATVVMGARTLLADLEGMKLQFPRPKDQ 1355
QY 1384 ABEALRKIPAINQITTEANEKTRAQALGSAADATEAKNKAHEAERIAASAVQKNATST 1443
Db 1356 AALQRKADSVDRLLADTRKTKQAERMLGNAAPLSSSAKKKGRAEVLAKDSAKLAKAL 1415
QY 1444 KAEABERTFAEVTDLDNVNNMLKQL-QEAEKELKRKQDDADQDMMAGMASQAQAEIN 1502

Db 1416 LRERQAHRRASRLTSQTQATLQOASQOVLASEARRQELEEAEVAGLS-----EMEQQ 1470
QY 1503 ARKAKNSVTSLLSIINDLLBOLGQDLT--VDLNKLNIEIEGTLNKAKDEM-KVSDLDKVS 1559
Db 1471 IRESISLEKDIETLSSELLARGLSLDTHQAPAQALNETQWALERLRLQLGSPGSLQKLS 1530
QY 1560 DLENAKKQEAAMIDYNRDIEIMKDORNLEDIRKTLPSGC 1600
Db 1531 LLEQESQQQELQIQGFESDLAIBRADKQNLAILHSLPENC 1571

RESULT 12
US-10-369-493-6816
; Sequence 6816, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6816
; LENGTH: 1557
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6816

Query Match 37.2%; Score 3240; DB 15; Length 1557;
Best Local Similarity 39.0%; Pred. No. 5.4e-176;
Matches 636; Conservative 289; Mismatches 541; Indels 166; Gaps 32;

QY 40 CTDEGGR-PORCMPEFVNAFNVTVATNTCGTP-PEEYCVQTVGTGVTKSHCLCDAGOP 97
Db 25 CYDRATRQPORCVDFVNAAFNLEVQVNTCGTKRPTKFCVQSGHTGQRSVCETCDDRHE 84

QY 98 HLQGAFLTDYNNQADTTWQSQTMLAGVQYPPSSINLTILHLKAFDITYVRLKFTSRP 157
Db 85 GFSHPAKYLTDFNVGNNETWQSDTMQEGQQYPTTNTLTLVLGKSFDTYVRLKFISRP 144

QY 158 ESFAIYKRTREDGPWIPYQYVSGSCENTYSKANRGFIRTTGGDEQQAALCTDEFSDISPLTG 217
Db 145 ESFTIYKKTHTDSEWEPWQFYSGSCRATYGLSDRAPI-LPGNEATAQCTKEPFSDISPITG 203

QY 218 GNVAFSTLEGPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVNDPKVLKSYVYAI 277
Db 204 GNIAFSTLEGPSAHAFEESEVLQKQWVTASAIRISLNRMTFGDEVFKDPQVLRSYVYAI 263

QY 278 SDFAVGGRCCKNGHASECMKNEF----DKLVNCKHNTYGVDCBKCLPFFNDRPWRRA 333
Db 264 SDFAVGGRCCKNGHASECVGSSVVDGENRLVCRCEHNTQGADCNBCLPFYNDRPWRS 323

QY 334 ESASECLPCDCNGRSQECYFDPPELYRSTGHGGHCTNCQDNTDGAHCCRCRENFRLGNNE 393
Db 324 VEANECIACNCSQLSNRCYFDQQLFEETGHGGHCIDCQNTQGVHCEQCIANHWRRPGEN 383

QY 394 ACSSCHCSPVGSLSSTQCDYSYGRCSCKPGVMGDKCDRCQPGFHSHTAGCRPCSDPSGSI 453
Db 384 YCVACGCNEIGLSLSTQCDNEGKCKQCPGVTRFCQCLDGFYDFSTNGCKNCGCETSGSL 443

QY 454 D---ECNVETGRVCCKDNVEGFNCERCCKPGFPFNLESSNPRGCTPCFCGHSSVCTNAVGY 510
Db 444 NNQPRCDSGSSGSCSKLNVEGRQCDKCKPGYFDLSTENQFGCTPCFCFGHSSICNTADGY 503

QY 511 SVYSISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDYFPPRYFIAPAKFLGKQV 570

Db	504	FAMNVSSVFDQDKQKWAGQNRIGLQ-DTQWAELDKAVAVSDTDNSPVYFVAPEQFLGDQR	562
Qy	571	LSYGQNLFSFRVDRDTRLAEDLVLEGAGLR-VSVPLIAQNSYSPSETTVKXVFLHE	629
Db	563	SSYNQDLVFTLKAKHVNTQDVKDIIVGADRQELSTSTAQGNPFPPTTEAQTYRFRVHA	622
Qy	630	ATDYPWRPALTPFEFQKLNNLTSIKIRGYSERSAGYLDVTLASARPGPV---PAT	685
Db	623	DPYFGWYPRINELDFIGILSNITAIKIRGYSYKDIGYLSNVNLGTAGVAPSAANPKQAT	682
Qy	686	WVESCTCPVGYGGOFCEMCLSGYRRETNLGPYSPCVLCACNGHSETCDPETGVNCNRDN	745
Db	683	WIEHCECLPGFVGQFCESCESGFRRETKEGPFNFHCHIKDCDCHNHSNCSCEAESGSCICEHN	742
Qy	746	TAGPHCEKCSGXYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKEVVCTNCPTGTGKRCE	805
Db	743	TAGDTCERCARGYGDALQGTEDCQKPCPNDBGPC-ILHADGDVICTECPNGYTGRRCD	801
Qy	806	LCDDGYFGDPLGRNGPVRLCRLCQCSDNIDPNAVGNCRNLTGECCLKCIYNTAGFYCDRCK	865
Db	802	ECSDGYFGNP--KDGTE--CVECACSGNTDPNSIGNCDKITGECKKICIFNTHGFCENCK	857
Qy	866	DGFFGNPLAPNPADKCKACNCNPYGMTKQOS-----SCNPVTGQCECLPHVTGQDCGACD	920
Db	858	PGYWGDAI-EPKGNCSGCGFAAGTRRPNDYTLLECNOQDGCDCCLPNVIGIQDQCA	916
Qy	921	PGFYNLQSGQGCERCDCCHALGSTNGQCDIRTGQCEQPGITGOHCERCEVNHFGFBEGC	980
Db	917	HGFYNTSLGLCQCECNCDPLGSEGNTCDVNTGQCCQKPGVTGQRCDCADYHFGFSANGC	976
Qy	981	KPCDCHPEGSLSLQCK-DDGRCECREGVGNRCDOCEENYFYNRSWPGCQCECPACVRLVK	1039
Db	977	QPCDCEYIGSENQCCDVNSGQCLCKENVEGRRCDQCAENRY--GITQGCLPCDDCYTLIQ	1034
Qy	1040	DKVADHRVKLOELESILIANLGTGDEMVTQAFEDRLKEAER--EVMDLLREAQDVKDVD	1096
Db	1035	SRVNVFREKVKSLDNLTBQEIENPAPVNDTKFDEKVKETSRAASEVWEAVK--QKTKEGG	1092
Qy	1097	QNLMDRLQRVNNTLSSQISRLQNRINTIETGNLAEQARAHVENTERLIEIASREL----	1152
Db	1093	GTIKTKSKAIKDEIIVAALKLTSIDESVAQAKVGADAENDMKRWEIIENARREIENVL	1152
Qy	1153	-----EKAKVAAANVSVTQPESTGDPNNMTLLABEARKLAERHKQEAADDIVRVAKTA	1204
Db	1153	HYLETEGEERAQI-AYNASQYGEQS--KRMSELASTREEAEKHLKQASEIEQLSEQA	1208
Qy	1205	NDTSTEAYNLLRLTAGENOTAFEIEELNRKYEQ-AKNISQDLEKQAAARVHEEAKRAGDK	1263
Db	1209	IANATOANKEASDAIYGGEQISKQIAELKEKQNLNESIHTLTD----LAEEQKKSAD	1263
Qy	1264	AVEIYA-----SVAQISPLDSETLENEANNIKMEAEENLEQLIDQKLKDD--YEDLREDM	1314
Db	1264	ANLAAVSLTNVEAVKIPSPVDPKELRNDVAGVLESEN--LVDSSVKENSANDELDFEV	1320
Qy	1315	RGKELEVKNLLEKGTQEQOTADOLLARADAAKALAEAAKGRDRTLQEAANDILNNLKDFD	1374
Db	1321	NRSVADARNELQSSDQQRVSDQMLMLEKSRERIVDSVSTADKTLKDAAEALQVLEEF	1380
Qy	1375	RRVNDNKTAEEBALRKIPAINQ---TITEANEKTREA---QOALGSAADATEAKNAH	1427
Db	1381	AKIEKSRNDAAVEAFAGVEGINQRDLDDIIDAQDKRRNSULPIDKQFVIDYRKSDAVLLNETH	1440
Qy	1428	E-AERIASAVQKNA-TSTKAEAEARTFAEVTDLDNEVNNMLKQLOEAEKELKXKQDDADQD	1485
Db	1441	ALADRYKDIIHSDVTRDSTEA-----VOYDIEQLMEELTDSNENLOYQYKKQAEDD	1491
Qy	1486	MMMAGMASQ-----AAQEAEINARKAKNSVTSLLSIINDLLEQLGQLDVTDLNKLUN	1536
Db	1492	KOMATEAVRKQLPLRILPSKQMLPFSLRKMKSRKSSILWVL-----	1532
Qy	1537	EIEGTLNKAKOEMKVSILDRKVSLENEAKKQEAAMINDYNRDIIEIMKDIRNLEDIRKTL	1596
Db	1533	-----NLEEIRDNL	1541

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QY      1597 PSGCFNTPSIEK 1608
      :||| :|:
Db      1542 PTKCFNVINLEQ 1553

RESULT 13
US-09-756-071B-13
; Sequence 13, Application US/09756071B
; Patent No. US20020052307A1
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
;           Kallunki, Pekka
;           Pyke, Charles
; TITLE OF INVENTION: Laminin Chains: Diagnostic Uses
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fay Sharpe Fagan Minnich & McKee
; STREET: 1100 Superior Ave, Suite 700
; CITY: Cleveland
; STATE: Ohio
; COUNTRY: USA
; ZIP: 44114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/756,071B
; FILING DATE: 08-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/663,147
; FILING DATE: 150-September 2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Minnich, Richard, J.
; REGISTRATION NUMBER: 24,175
; REFERENCE/DOCKET NUMBER: TRV 20014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 216-861-5582
; TELEFAX: 216-241-1666
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1193 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-756-071B-13

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Query Match	30.3%;	Score 2637;	DB 9;	Length 1193;
Best Local Similarity	39.4%;	Pred. No. 9.4e-142;		
Matches 515;	Conservative 235;	Mismatches 418;	Indels 138;	Gaps 12;

Qy	319	CLPFFNDPWRRTAAESASECLPCDCNGRSQECYFDPELYRSTGHGHCNQCNDTDGAH	378
Db	9	CLCFSLLLPAARATSRE---VCDGCKSRQCFIDRELHRQTGNGFRCLNCNDNTDGIH	64
Qy	379	CERCRENFFRLGNNEACSSCHCSPVGSILSTQCDSYGRCSCKPGVMGDKDCRCQPGFHSLT	438
Db	65	CEKCKNGFYRHRERDRCLPCNCNKGSLSARCDSNGRCSCKPGVTGARCDCLPGFHMILT	124
Qy	439	EAGC-----RPCSDPSGSIDECNVETGRVCVKDNVEGFNCERCCKPGFFNLESSNPR	490
Db	125	DAGCTQDQRLDLSKDCDCDPAGIAGPC--DAGRCVCKPAVTGERCDRCRSGYNLDGNGPE	182
Qy	491	GCTPCFCFGHSSVCTNAVGYSVYSISSTTFQIDEDGWRAEQRDGSEASLEWSERQDIAVI	550
Db	183	GCTQCFCYGHASACRSSAEYSVHKITSTFHQDVGWKAVQRNGSPAKLQWSQRHQDVFS	242
Qy	551	SDSYFFRYFIAPAKFLGQVLSYGQNLSSFSFRVDRDRTRLSEAEDLVLEGAGLRVSVPLIA	610

Query Match 30.3%; Score 2637; DB 9; Length 1193;

Best Local Similarity 39.4%; Pred. No. 9.4e-142;
Matches 515; Conservative 235; Mismatches 418; Indels 138; Gaps 12;

QY	319	CLPFFNDPWRRTAAESASECLPCDNGRSQECYFDP	ELYRSTGHGGHCTNCQDNTDGAH	378	
Db	9	CLCFSLLLPAARATSRR-----VCD	CNGKSRQCFDRELHRQTGNGFRCLNCNDNTDGIH	64	
QY	379	CERRENFFRLGNNEACSSCHCSPVGSILSTQ	CDSYGRCSCKPGVMGDKDCRCQPGFHSLT	438	
Db	65	CEKCKNGPYRHRERDRCLPCNCNKGSL	SARCDNSGRCSCKPGVTGARCDCPLPGFHM	124	
QY	439	EAGC-----RPCSDPSGSI	DECNVETGRVCCKDNVEGFNCERCKPGFFNLESSNPR	490	
Db	125	DAGCTQORLLDSKCDCDPAGIAGPC--	DAGRCVCKPAVTGERCDRCRSGYINLDG	182	
QY	491	GCTPCFCFGHSSVCTNAVGYSVY	YSISSTFQIDEDGWRAEQRDGSEASLEWSERQDIAVI	550	
Db	183	GCTQCFCYGHASACR	SSAEYSVHKITSTFHQDVGWKAVORNGSPAKLQWSORHQDV	242	
QY	551	SDSYFRRFYIAPAKFLGQVLSYGQNL	SFSFRVDRDRTRL	SAEDLVLEGAGLRVSVPLIA	610

Db 243 AQRLLDPVYFVAPAKFLGNQQVSYGOSLSFDYRVDGRGHRPSAHDVILEGAGLRITAPLMP 302

QY 611 QGNSYPSETTVKYVFRLEHATDYPWRPALTPFEFQKLNLTISIKIRGTYSERSAGYLDLDD 670

Db 303 LGKTLPCGLTKTYTFRLNEHPSNNWSPQLSYFEYRRLRLNLTALRIRATYGEYSTGYIDN 362

QY 671 VTLASARPGVPATWVESCTCPVYGQGFCEMCLSGYRRETPNLGPSPCVLCACNGHS 730

Db 363 VTLISARPVSGAPAPWVEQCICPVYKGQFCQDCASGYKDSARLPGFTCIPCNCQG-G 421

QY 731 ETCDPETGVCNCRDNTAGPHCEKCSDDGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKEV 790

Db 422 GACDPDTGDCYSGDENPDIEACDCPIGFYNDPHDPRS--CKPCCHNGFSCSVIPETEEV 479

QY 791 VCTNCPTGTTGKRCCLCDDGYFGDPLGRNGPVRRLCRLCQCSNIDPNVAGNCNRLTGECL 850

Db 480 VCNNCPGVTGARCELCAADGYFGDPFGEHGPVPCQPCQCNNSVDPSPASGNCDRLTGRCL 539

QY 851 KCIYNTAGFYCDRCKDGFPGNPLAPNADKCKACNCPYGTMKQQSSCNPTGTQCECLPH 910

Db 540 KCIHNTAGIYCDQCKAGYFGDPLAPNADKCRACNCPMGS----- 580

QY 911 VTGQDCGACDPGFYNLQSGQGCRCRCDHALGSTNGQCDIRTGQCECQPGITGQHCEV 970

Db 581 ----- 580

QY 971 NHFGFGECKPCDCHPEGSLSLQCKDDRCCECREGFVGNRCDQCEENFYFNRSWPCQE 1030

Db 581 -----EPVG-----CRSDGTCVCKPGFGGPNCEH-----GAFS 608

QY 1031 CPACYRLVKDVADHRVKLQELSLJANLGTGDEMVTQAFEDRLKEAEREVMDLLEBAQ 1090

Db 609 CPACYNQVKIQMDQFMQQLQRMELISKAQGGDGVVPDTELEGRMQQAEALQDILRDAQ 668

QY 1091 DVKDVQDNLMDRLQRVNNTLSSQISRLQNRNTIETGNLAEQARAHVENTERLIEIASR 1150

Db 669 ISEGASRSLGLQAKVRSQENSYSQSRDLDKMTVERVRLGSGYQNRVRDTHRLITQML 728

QY 1151 ELEKAKVAAANVSVTQPESTGDPNNMTLLABEARKLAERHKBADDIRVAKTANDISTE 1210

Db 729 SLAESEASLGNTNIPASDHYVGPNGFKSLAQEAATRLAESHVESASNMEOQLTRETEDYSKQ 788

QY 1211 AYNLLRLTL-----AGENQTAFEIEELNRKYEQAKNISQDLEKQAARVHEEAKRAGDK 1263

Db 789 ALSLVRKALHEGVSGSGSPDGAV-VQGLVEKLEKTKSLAQQLTREATQAEIEADRSYQH 847

QY 1264 AVEIYASVAQLSPDLSETLE-NEANNIKMEAELENLEQLIDQKLKDYEDLREDMRGKELEVK 1322

Db 848 SLRLDSDSVSPLOGVSDQSFQVEEAKRIKQKADSLSLVTRHMEFFKRTQKNLGNWKEEAQ 907

QY 1323 NLEKKGTEQQQTADQLLARADAALAEAAKKGRTDLOEANDILNNLKDFDRRVNDNKT 1382

Db 908 QLLQNGKSGREKSDQLLSRANLAKSRAQEAALSMGNATFYEVESILKNLREFDLQVDNRKA 967

QY 1383 ABEEALRKIPAINQITITEANEKTRQAALGSAADATEAKNKAHEAERIAASAVQKNATS 1442

Db 968 EAEEAMKRLSYISQKVSADSKTQQAERALGSAADAAQRAKNGAGEALEISIEIEQETGS 1027

QY 1443 TKAEAEERTFAEVTDLDNEVNNMLKQLOEAEKELKRKQDDADQDMMAGMASQAAQAEIN 1502

Db 1028 LNLEANVTADGALAMEKGLASLKSEMREVEGELEKLEFEFTNMDAVQMVITEAQKVDTR 1087

QY 1503 ARKAKNSVTSLLSIINDLLEQLGLDQTDVLDNKLNEIEGTLNKADEMKSVDLDRKVSLE 1562

Db 1088 AKNAGVTIQDTLNTLDGLHLMDQPLSVDEGLVLLEQKLSRAKTQIN-SQLRPFMMSELE 1146

QY 1563 NEAKKQEAAIMDYNRDIEEIMKDNRNLEDIRKTLPSGCFNTPSIEK 1608

Db 1147 ERARQQRGHLHLLETSIDGILADVKNLENIRDNLPFGCYNTQALEQ 1192

; Sequence 14, Application US/10392113
; Publication No. US20030224993A1
; GENERAL INFORMATION:
; APPLICANT: Land, Hartmut
; APPLICANT: Deleu, Laurent
; TITLE OF INVENTION: COMPOSITIONS THAT INHIBIT PROLIFERATION
; FILE REFERENCE: 21108.0005U3
; CURRENT APPLICATION NUMBER: US/10/392,113
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: 60/365,078
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: PCT/US01/32127
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/239,705
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1193
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
; OTHER INFORMATION: Synthetic Construct
US-10-392-113-14

Query Match 30.3%; Score 2637; DB 12; Length 1193;
Best Local Similarity 39.4%; Pred. No. 9.4e-142;
Matches 515; Conservative 237; Mismatches 416; Indels 138; Gaps 12;

QY 319 CLPFFNDPRWRATAESASECLPCDNGRSQECYFDPPELVRSTGHGHCNTNQDNTDGAH 378

Db 9 CLCFSLLLPAARATSRRE---VCDNGKSRQCIFDRELHRTQNGFRCLNCNNDNTDGIH 64

QY 379 CERCRENFFRLGNNEACSSCHSCPVSLSLSTQCDSDYGRCSCKPVGMDKCDRCQPGHSLT 438

Db 65 CEKCKNGFYRHRERDRCLPCNCNSKGLSARCDNSGRCSCKPVGVTGARCDRCLPGFHMLT 124

QY 439 EAGC-----RPCSDPSSIDECNVETGRVCCKDNVEGFNCERCKPGFFNLESSNPR 490

Db 125 DAGCTQDQRLDLSKDCDPAIAGPC--DAGRCVCKPAVTGERCDRCRSGYNNLDGGNPE 182

QY 491 GCTPCFCFGHSSVCTNAVGSVYSSISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAMI 550

Db 183 GCTQCFCYGHASACRSSEAEYSVHKITSTFPHQDVQVWGKAVQRNGSPAKLQWSQRHQDVFS 242

QY 551 SDSYFPYRPIAPAKFLGKQVLSYGNLSFSPFRVDRDRTRLRLSAEDLVLEGAGLRVSVPLIA 610

Db 243 AQRLLDPVYFVAPAKFLGNQQVSYGOSLSFDYRVDGRGHRPSAHDVILEGAGLRITAPLMP 302

QY 611 QGNSYPSETTVKYVFRLEHATDYPWRPALTPFEFQKLNLTISIKIRGTYSERSAGYLDLDD 670

Db 303 LGKTLPCGLTKTYTFRLNEHPSNNWSPQLSYFEYRRLRLNLTALRIRATYGEYSTGYIDN 362

QY 671 VTLASARPGVPATWVESCTCPVYGQGFCEMCLSGYRRETPNLGPSPCVLCACNGHS 730

Db 363 VTLISARPVSGAPAPWVEQCICPVYKGQFCQDCASGYKDSARLPGFTCIPCNCQG-G 421

QY 731 ETCDPETGVCNCRDNTAGPHCEKCSDDGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKEV 790

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Db 480 VCNNCPGVTGARCELCAADGYFGDPFGEHGPVPCQPCQCNNSVDPSPASGNCDRLTGRCL 539

QY 851 KCIYNTAGFYCDRCKDGFPGNPLAPNADKCKACNCPYGTMKQQSSCNPTGTQCECLPH 910

Db 540 KCIHNTAGIYCDQCKAGYFGDPLAPNADKCRACNCPMGS----- 580

QY 911 VTGQDCGACDPGFYNLQSGQGCRCRCDHALGSTNGQCDIRTGQCECQPGITGQHCEV 970

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Db 581 ----- 580
QY 971 NHFGFPEGCKPCDCHPEGSLSLQCKDDGRCEGFGVGNRCDOCEENFYNRSWPGCQE 1030
Db 581 -----EPVG-----CRSDGTCVCKPGFGGPNCEH-----GAFS 608
QY 1031 CPACYRLVKDKVADHRVKLQELLESILIANLGTGDEMVTDOAFEDRLKEAEREVMDLLREAQ 1090
Db 609 CPACYNQVKIQMDQFMQQLORMEALISKAQGGDGVVPDTELEGRMQAEQALQDILRDAQ 668
QY 1091 DVKDVDQNLMDRLQVRNNTLSSQISRLQNRNIRNTIETGNLAEQARAHVENTERLIEIASR 1150
Db 669 ISEGASRSLGLQAKVRSQENSYSQSLDDLKMTIVERVRLGSGYQYQNRVDRDTHRLITQMQL 728
QY 1151 ELEKAKVAAANVSVTQPESTGDPNNMTLLAEAEARKLAERHKQAEADDIVRVAKTANDTSTE 1210
Db 729 SLAESEASLGNNTNIPASDHVVGPNFGFKSLAQEATRLAESHVESASNMEQLTRETEDYSKQ 788
QY 1211 AYNLLRLTL-----AGENQTAFEIEELNRKYEQAKNISODLEKQAAARVHEEAKRAGDK 1263
Db 789 ALSLVKALHEGVGSGSGSPDGAV-VQGLVEKLEKTKSLAQQLTREATQAEIADRYSQH 847
QY 1264 AVEIYASVAQLSPDLSETLE-NEANNIKMEAEENLEQLIDOKLXDYEDLPEDMRGKELEVK 1322
Db 848 SLRLLDVSRLOQVSDQSFQVEEAKRIKQKADSLSTLVTRHMDFFKRTQKNLGNWKEEAQ 907
QY 1323 NLEKKGTEQQTADQLLARADAAKALAEAAKKGRTLOEANDILNLLKDFDRRVNDNKT 1382
Db 908 QLLQNGKSGREKSDQLLSRANLAKSRAQEAALSMGNATFYEVEISILKNLREFDLQVDNRKA 967
QY 1383 ABEALRKIPAINQITITEANEKTRAQOALGSAADATEAKNKAHEAERIAASAVQKNATS 1442
Db 968 EABEAMKRLSYISKVSDASDKTQQAERALGSAADAQRAKNKGAGEALEISSEIEQEIGS 1027
QY 1443 TKBAERTFAEVTDLNNEVNMMLKQLOEAEKELKRQDDADQDMMAGMASQAAQAEIN 1502
Db 1028 LNLEAVNTADGALAMEKGLASLKSEMREVEGELERKELEFDTNMDAVQMVITEAQKVDT 1087
QY 1503 ARKAKNSVTSLLSIINDLLEQLGQDQTDVNLKNEIEGTLNKADEMKSVDLDRKVSdle 1562
Db 1088 AKNAGVTIQDTLNTLDGLHMDQPLSVDEEGLVLEQKLSRAKTQIN-SQLRPMVSELE 1146
QY 1563 NEAKKQEAAIMDYNRDIIEIMKDIRNLEDIRKTLPSGCFNTPSIEK 1608
Db 1147 ERARQQRGHLHLETSIDGILADVKNLENIRDNLPFGCYNTQALEQ 1192

RESULT 15
US-10-171-311-115
; Sequence 115, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoerish, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF CERVICAL CANCER
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 115
; LENGTH: 1193
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-311-115

Query Match      30.3%; Score 2637; DB 14; Length 1193;
Best Local Similarity 39.4%; Pred. No. 9.4e-142;
Matches 515; Conservative 237; Mismatches 416; Indels 138; Gaps 12;

QY 319 CLPFFNDRPWRRAATAESASECLPCDCNGRSQECYFDPPELYRSTGHGHTNCQDNTDGAH 378
Db 9 CLCFSLLLPAARATSRRE----VCDGNGKSRQCIFDRELHRQTGNGFRCLNCNDTDGIH 64
QY 379 CERCENFERLGNNEACSSCHSPVGSLSLSTQCDYSGRCSCKPGVMGDKCDRCQPGFHSLT 438
Db 65 CEKCKNGFYRHRERDRCLPCNCNSKGSLSARCDNSGRCSCKPGVTGARCDRCILPGFHMILT 124
QY 439 EAGC-----RPCSCDPSGSIDECNVETGRCVCKDNVEGECERCKPGFFNLESSNPR 490
Db 125 DAGTQDQORLLDSKCDPCDAGIAGPC--DAGRCVCKPAVTGERCDRCRSGYVNLDDGNPE 182
QY 491 GCTPCFCFGHSSVCTNAVGSYVSYSSISSTFQIDEDGWRAEQRDGSEASLEWSSERQDI 550
Db 183 GCTQCFYGHSAACRSASAEYSVHKITSTFHQDQVDGWKAVQNRNGSPAKLQWSQRHQDVFS 242
QY 551 SDSYFPRYFIAPAKFLGKQVLSYQNLFSFSFRVDRDRDTRLAEDLVLEGALRVSVPLIA 610
Db 243 AQRLDVYFVAPAKFLGNQOVSYGQSLSFYDRVDRGGRHPSAHDVILEGALRLITAPLMP 302
QY 611 QGNSYPSSETTVKYVFRLEHATDYPWRPALTPFEFQKLLNNLTSIKIRGTYSERSAGYLD 670
Db 303 LGKTLPCGLTKYTFRLNEHPSNNWSPQLSYFEYRLLRLNLTLRIRATYGEYSTGYIDN 362
QY 671 VTLASARPPGVPATWVESCTCPVGYGGQFCMCLSGYRRRETNLGPYSPCVLCAACNGHS 730
Db 363 VTLISARPPVSGAPAPWVEQICPVGYKGQFCQDCASGYKRDSARLPPFGTCIPCNCGQ-G 421
QY 731 ETCDEPTEGVCNCRDNTAGPHCEKCSGYGSDTAGTSSDCCQPCPGGSSCAVVPKTKEV 790
Db 422 GACDPTGDCYSGDENPDIECADCPIGFYNDPHDPRS--CKPCCHNGFSCSVMPETE 479
QY 791 VCTNCTPTGTTKRCCELCDGDFGDPGLGRNGFVRLCRLCQCSNDIDPNVAGNCNRLTGECL 850
Db 480 VCNNCPPGVTGARCELCAADGYFGDPFGEHGFVRPCQPCQNNNVDPASAGNCDRLTGRCL 539
QY 851 KCIYNTAGFYCDRCCKDGGFFGNPLAPNPADKCKACNCPYGTMMKQQSSCNVPTGQCECLPH 910
Db 540 KCIHNTAGIYCDQCKAGYFGDPLAPNPADKCRACNCPMGS----- 580
QY 911 VTGQDCGACDPGFYNLQSGGGERCDCHALGSTNGQCDIRTGQCECQPGITGQHCEV 970
Db 581 ----- 580
QY 971 NHFGFPEGCKPCDCHPEGSLSLQCKDDGRCEGFGVGNRCDOCEENFYNRSWPGCQE 1030
Db 581 -----EPVG-----CRSDGTCVCKPGFGGPNCEH-----GAFS 608
QY 1031 CPACYRLVKDKVADHRVKLQELLESILIANLGTGDEMVTDOAFEDRLKEAEREVMDLLREAQ 1090
Db 609 CPACYNQVKIQMDQFMQQLORMEALISKAQGGDGVVPDTELEGRMQAEQALQDILRDAQ 668
QY 1091 DVKDVDQNLMDRLQVRNNTLSSQISRLQNRNIRNTIETGNLAEQARAHVENTERLIEIASR 1150
Db 669 ISEGASRSLGLQAKVRSQENSYSQSLDDLKMTIVERVRLGSGYQYQNRVDRDTHRLITQMQL 728
QY 1151 ELEKAKVAAANVSVTQPESTGDPNNMTLLAEAEARKLAERHKQAEADDIVRVAKTANDTSTE 1210
Db 729 SLAESEASLGNNTNIPASDHVVGPNFGFKSLAQEATRLAESHVESASNMEQLTRETEDYSKQ 788
QY 1211 AYNLLRLTL-----AGENQTAFEIEELNRKYEQAKNISODLEKQAAARVHEEAKRAGDK 1263
Db 789 ALSLVKALHEGVGSGSGSPDGAV-VQGLVEKLEKTKSLAQQLTREATQAEIADRYSQH 847
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Search completed: May 18, 2004, 15:42:52
Job time : 47.9344 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:58 ; Search time 14.8077 Seconds
(without alignments)
10452.141 Million cell updates/sec

Title: US-10-037-182-14
Perfect score: 8713
Sequence: 1 MRGSHRAAPALPRGRWLV.....EDIRKTLPSGCFNTPSIEKP 1609

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8709	100.0	1609	1 MMHUB2	laminin gamma-1 ch
2	8161	93.7	1607	1 MMMSB2	laminin gamma-1 ch
3	3433	39.4	1639	1 MMFE2	laminin gamma-1 ch
4	3240	37.2	1557	2 T28811	hypothetical prote
5	2637	30.3	1193	2 A44018	laminin B2t chain
6	2454.5	28.2	1192	2 S69000	laminin gamma 2 ch
7	1782.5	20.5	3084	1 MMMSA	laminin alpha-1 ch
8	1774.5	20.4	3106	1 S53868	laminin alpha-2 ch
9	1739.5	20.0	3075	2 S14458	laminin alpha-1 ch
10	1680.5	19.3	1786	1 MMHUB1	laminin beta-1 cha
11	1669.5	19.2	1790	1 MMFB1	laminin beta-1 cha
12	1651	18.9	1786	1 MMMSB1	hypothetical prote
13	1626.5	18.7	2823	2 T23064	protein T22A3.8 [i
14	1626.5	18.7	2823	2 F87908	laminin alpha ch
15	1626.5	18.7	3102	2 T43291	laminin beta-2 cha
16	1613.5	18.5	1801	1 MMRTS	hypothetical prote
17	1608	18.5	1808	2 T15099	laminin beta-2 cha
18	1598.5	18.3	1798	2 S53869	laminin beta-2 cha
19	1496	17.2	1797	2 A55677	laminin alpha-1 ch
20	1486.5	17.1	3712	2 S18253	hypothetical prote
21	1394	16.0	3672	2 T23433	probable laminin a
22	1394	16.0	3704	2 T37316	laminin alpha 5 ch
23	1327.5	15.2	3635	2 T10053	netrin-1 precursor
24	1173	13.5	606	2 A54665	netrin-2 precursor
25	1070	12.3	581	2 B54665	laminin-related pr
26	989	11.4	612	2 JH0799	laminin B1k chain
27	923	10.6	1170	2 A53612	kalinin B1 - mouse
28	887.5	10.2	1168	2 I56985	perlecan precursor
29	880	10.1	4391	2 A38096	

30	867.5	10.0	3707	2	S18252	heparan sulfate pr
31	630	7.2	1751	1	MMHUMH	laminin alpha-2 ch
32	609	7.0	1160	2	F88369	protein unc-52 [im
33	609	7.0	2295	2	C88369	protein unc-52 [im
34	609	7.0	3375	2	T19821	hypothetical prote
35	591	6.8	1620	2	T27283	hypothetical prote
36	574.5	6.6	1111	2	T26972	hypothetical prote
37	572.5	6.6	1816	1	S68960	laminin alpha-4 ch
38	549	6.3	1574	2	T13954	MEGF6 protein - ra
39	510	5.9	1713	2	A53347	adhesive ligand ep
40	485	5.6	303	2	B45067	laminin B1 chain -
41	483	5.5	2524	2	A35844	Xotch protein - Af
42	479	5.5	400	2	T46383	hypothetical prote
43	454.5	5.2	2437	2	S42612	transmembrane prot
44	452.5	5.2	2703	1	A24420	notch protein - fr
45	450.5	5.2	2318	2	S45306	notch 3 protein -

ALIGNMENTS

RESULT 1

MMHUB2
laminin gamma-1 chain precursor - human
N;Alternate names: laminin chain B2
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text change 10-Dec-1999
C;Accession: S13548; A28158; S13549; B34961; S14664; S23567
R;Pikkarainen, T.; Ikonen, J.; Chow, L.T.; Kallunki, P.; Tryggvason, K.
J. Biol. Chem. 266, 221-228, 1991
A;Title: Structure of the human laminin B2 chain gene reveals extensive divergence from t
A;Reference number: S13548; MUID:91093128; PMID:1985895
A;Accession: S13548
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1609 <KAL>
A;Cross-references: GB:M55217; NID:gl86937
A;Note: the nucleotide sequence was submitted to GenBank, February 1991
R;Pikkarainen, T.; Kallunki, T.; Tryggvason, K.
J. Biol. Chem. 263, 6751-6758, 1988
A;Title: Human laminin B2 chain. Comparison of the complete amino acid sequence with the
A;Reference number: A28158; MUID:88198245; PMID:3360804
A;Accession: A28158
A;Molecule type: mRNA
A;Residues: 1-211,'I',213-1609 <PIK>
A;Cross-references: EMBL:J03202; NID:gl86916; PIDN:AAA59488.1; PID:G307107
R;Fukushima, Y.; Pikkarainen, T.; Kallunki, T.; Eddy, R.L.; Byers, M.G.; Haley, L.L.; Her
cyogenet. Cell Genet. 48, 137-141, 1988
A;Title: Isolation of a human laminin B2 (LAMB2) cDNA clone and assignment of the gene to
A;Reference number: S13549; MUID:89169663; PMID:3234037
A;Accession: S13549
A;Molecule type: mRNA
A;Residues: 1393-1609 <FUK>
A;Cross-references: EMBL:M27654; NID:gl86923; PIDN:AAA59489.1; PID:gl86924
R;Olsen, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki, T
Lab. Invest. 60, 772-782, 1989
A;Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 cha
A;Reference number: A34961; MUID:89280632; PMID:2733383
A;Accession: B34961
A;Molecule type: mRNA
A;Residues: 868-1551,'N',1553-1609 <OLS>
R;Santos, C.L.S.; Sabbaga, J.; Brentani, R.
DNA Seq. 1, 275-277, 1991
A;Title: Differences in human laminin B2 sequences.
A;Reference number: S14664; MUID:92216129; PMID:1806043
A;Accession: S14664
A;Molecule type: mRNA
A;Residues: 1282-1609 <SAN>
A;Cross-references: EMBL:X13939; NID:G34237; PIDN:CAA32122.1; PID:G34238
R;Vuolteenaho, R.; Kallunki, T.; Chow, L.; Ikonen, J.; Pikkarainen, T.; Tryggvason, K.
in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp. 175-193, Academic P
A;Title: Genes for the human laminin B1 and B2 chains.
A;Reference number: S23566

A:Accession: S23567
A:Molecule type: DNA
A:Residues: 801-1481, R', 1483-1609 <VUO>
A:Note: mRNA was also sequenced
C:Genetics:
A:Gene: GDB:LAMC1; LAMB2
A:Cross-references: GDB:120136; OMIM:150290
A:Map position: 1q31-1q31
A:Introns: 140/1; 241/3; 285/2; 341/1; 404/1; 443/2; 476/2; 522/1; 563/1; 626/2; 664/1; 73; 1525/1
A:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C:Function:
A:Description: interact with cells and with other basement membrane proteins to promote
C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular
F:1-33/Domain: signal sequence #status predicted <SIG>
F:34-1609/Product: laminin gamma-1 chain #status predicted <MAT>
F:34-285/Domain: VI <DOM6>
F:286-504/Domain: V <DOM5>
F:286-339/Domain: laminin-type EGF-like homology <LE01>
F:342-395/Domain: laminin-type EGF-like homology <LE02>
F:398-442/Domain: laminin-type EGF-like homology <LE03>
F:445-492/Domain: laminin-type EGF-like homology <LE04>
F:495-504/Domain: laminin-type EGF-like homology #status atypical <LE05>
F:505-689/Domain: IV <DOM4>
F:690-1034/Domain: III <DOM3>
F:690-721/Domain: laminin-type EGF-like homology #status atypical <LE06>
F:724-770/Domain: laminin-type EGF-like homology <LE07>
F:773-825/Domain: laminin-type EGF-like homology <LE08>
F:828-881/Domain: laminin-type EGF-like homology <LE09>
F:884-932/Domain: laminin-type EGF-like homology <LE10>
F:935-980/Domain: laminin-type EGF-like homology <LE11>
F:983-1028/Domain: laminin-type EGF-like homology <LE12>
F:1035-1609/Domain: II/I <DOM1>
F:1035-1609/Region: heptad repeats
F:40-50/Disulfide bonds: #status predicted
F:60,134,576,650,1022,1107,1161,1175,1205,1223,1241,1380,1395,1439/Binding site: carboxy
F:1031,1034,1600/Disulfide bonds: interchain #status predicted

Query Match 100.0%; Score 8709; DB 1; Length 1609;
Best Local Similarity 99.9%; Pred. No. 4e-314;
Matches 1608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MRGSHRAAPALPRGRLLWPVLAVLAAAAAAGCAQAA	DECTDEGGRPQRCMPEFVNAAFN	60
DB	1	MRGSHRAAPALPRGRLLWPVLAVLAAAAAAGCAQAA	DECTDEGGRPQRCMPEFVNAAFN	60
QY	61	VTVVAATNTCGTPEEYCVQGTGVTGTSKCHL	CDAGQPHLQHGAAFLTDYNNQADTTWQS	120
DB	61	VTVVAATNTCGTPEEYCVQGTGVTGTSKCHL	CDAGQPHLQHGAAFLTDYNNQADTTWQS	120
QY	121	QTMLAGVQYPPSSINLTHLGKAFDITYVRLKFHT	SRPESFAIYKRTREDDGPWIPYQYYS	180
DB	121	QTMLAGVQYPPSSINLTHLGKAFDITYVRLKFHT	SRPESFAIYKRTREDDGPWIPYQYYS	180
QY	181	SCENTYSKANRGFIRTTGGDEQQAALCTDEFS	DISPLTGGNVAFSTLEGRPSAYNFDNSPVL	240
DB	181	SCENTYSKANRGFIRTTGGDEQQAALCTDEFS	DISPLTGGNVAFSTLEGRPSAYNFDNSPVL	240
QY	241	QEWVTATDIRVTILNRLNTFGDEVNDPKVLKSY	YYYAISDFAVGGRCKCNHGASECMKNEF	300
DB	241	QEWVTATDIRVTILNRLNTFGDEVNDPKVLKSY	YYYAISDFAVGGRCKCNHGASECMKNEF	300
QY	301	DKLVCNCKHNTYGVDCCKLPPFNDRPWRRTA	ESASECLPCDCNGRSQECYFDPPELYRS	360
DB	301	DKLVCNCKHNTYGVDCCKLPPFNDRPWRRTA	ESASECLPCDCNGRSQECYFDPPELYRS	360
QY	361	TGHGGHCTNCQDNTDGAHCRCRENFFRLGN	NEACSSCHCSPVGLSTQCDSYGRCSCKP	420
DB	361	TGHGGHCTNCQDNTDGAHCRCRENFFRLGN	NEACSSCHCSPVGLSTQCDSYGRCSCKP	420
QY	421	GWMDKCDRCQPGFHSLTEAGRCPCSDPSG	SIDECNVETGRCVCKDNVEGFNCERCKPG	480

Db	421	GVMDKCDRCQPGFHSLTEAGRCPCSDPSG	SIDECNVETGRCVCKDNVEGFNCERCKPG	480
QY	481	FFNLESSNPRGCTPCFCFGHSSVCTNAVG	YSVYSSISSTFQIDEDGWRAEQDSEASLEW	540
Db	481	FFNLESSNPRGCTPCFCFGHSSVCTNAVG	YSVYSSISSTFQIDEDGWRAEQDSEASLEW	540
QY	541	SSERQDIAVISDSYFFRYFIAPAKFLGKQ	VLSYGQNLVSFPRVDRDRTRLSEAEDLVLEGA	600
Db	541	SSERQDIAVISDSYFFRYFIAPAKFLGKQ	VLSYGQNLVSFPRVDRDRTRLSEAEDLVLEGA	600
QY	601	GLRVSVPLIAQNSYPSETTVKTVFRLHEA	TDYPWRPALTPFEFQKLLNLTISIKIRTY	660
Db	601	GLRVSVPLIAQNSYPSETTVKTVFRLHEA	TDYPWRPALTPFEFQKLLNLTISIKIRTY	660
QY	661	SERSAGYLDVTLASARPGVGPATWVESCT	CPVGYGGQFCMCLSGYRRETNPNGPYSP	720
Db	661	SERSAGYLDVTLASARPGVGPATWVESCT	CPVGYGGQFCMCLSGYRRETNPNGPYSP	720
QY	721	CVLCACNGHSETCDPETGVCNCRDNTAG	PHCEKCSGDIYGDSTAGTSSDCQPCPCGGSS	780
Db	721	CVLCACNGHSETCDPETGVCNCRDNTAG	PHCEKCSGDIYGDSTAGTSSDCQPCPCGGSS	780
QY	781	CAVVPKTKBVVCTNCPTGTTGKRCCLCDD	GYFGDPLGRNGPVRLCRLCQCSNDIDPNAVG	840
Db	781	CAVVPKTKBVVCTNCPTGTTGKRCCLCDD	GYFGDPLGRNGPVRLCRLCQCSNDIDPNAVG	840
QY	841	NCNRLTGECLKCIYNTAGFYCDRCCKDGF	FGNPLAPNPADKCAKNCNPGYTMKQSSCNP	900
Db	841	NCNRLTGECLKCIYNTAGFYCDRCCKDGF	FGNPLAPNPADKCAKNCNPGYTMKQSSCNP	900
QY	901	VTGQCECLPHVTGQDCGACDPGFYNLQ	SGQGCERCDCCHALGSTNGQCDIRTGQCECQPGI	960
Db	901	VTGQCECLPHVTGQDCGACDPGFYNLQ	SGQGCERCDCCHALGSTNGQCDIRTGQCECQPGI	960
QY	961	TGQHCEVNEHFGFGEKPCDCHPEGSL	LSLQCKDGRCEGREGVGNRCDCQCEENYF	1020
Db	961	TGQHCEVNEHFGFGEKPCDCHPEGSL	LSLQCKDGRCEGREGVGNRCDCQCEENYF	1020
QY	1021	YNRSWPGCQCPACRYLVKQKADHRVKL	QLESLIANLGTGDEMVTDAQAFEDRLKEAER	1080
Db	1021	YNRSWPGCQCPACRYLVKQKADHRVKL	QLESLIANLGTGDEMVTDAQAFEDRLKEAER	1080
QY	1081	EVMDLLREAQDVKDQNLMDRLQRVNNT	LSSSQISRLQNIIRNTIETGNLAEQARAHVEN	1140
Db	1081	EVMDLLREAQDVKDQNLMDRLQRVNNT	LSSSQISRLQNIIRNTIETGNLAEQARAHVEN	1140
QY	1141	TERLIEIASRELEKAKVAAANVS	VTQPESTGDPNNMTLLAEBAERKQAEADIVRV	1200
Db	1141	TERLIEIASRELEKAKVAAANVS	VTQPESTGDPNNMTLLAEBAERKQAEADIVRV	1200
QY	1201	AKTANDTSTEAYNLLRLTAGENQTA	FEIEELNRKYEQAQKNSQDLEKQAARVHEEAKRA	1260
Db	1201	AKTANDTSTEAYNLLRLTAGENQTA	FEIEELNRKYEQAQKNSQDLEKQAARVHEEAKRA	1260
QY	1261	GDKAVEIYASVAQLSPLDSETLE	NEANNIKWEAENLEQLIDQKLKDYEDLREDMRGKELE	1320
Db	1261	GDKAVEIYASVAQLSPLDSETLE	NEANNIKWEAENLEQLIDQKLKDYEDLREDMRGKELE	1320
QY	1321	VKNLLEKGTQEQOTADQLLARADA	AKALAEAAKKGRDITLQEANDILNNLKDFDNRVNDN	1380
Db	1321	VKNLLEKGTQEQOTADQLLARADA	AKALAEAAKKGRDITLQEANDILNNLKDFDNRVNDN	1380
QY	1381	KTAAEEALRKIPAINQTI	TEANEKTRAQQAALGSAADATEAKNKAHEAERIA	1440
Db	1381	KTAAEEALRKIPAINQTI	TEANEKTRAQQAALGSAADATEAKNKAHEAERIA	1440
QY	1441	TSTKAAEAERTFAEVTDL	DNEVNNMLKQLQEAELKRRKQDDADQDMMAGMASQAQAE	1500
Db	1441	TSTKAAEAERTFAEVTDL	DNEVNNMLKQLQEAELKRRKQDDADQDMMAGMASQAQAE	1500
QY	1501	INARKAKNSVTSLLSI	IINDLLEQLGLDITVDLNLKNEIEGTLNKADEM	KVSD1560
Db	1501	INARKAKNSVTSLLSI	IINDLLEQLGLDITVDLNLKNEIEGTLNKADEM	KVSD1560

RESULT 2
MMMSB2

laminin gamma-1 chain precursor - mouse
N; Alternate names: laminin chain B2
C; Species: Mus musculus (house mouse)
C; Date: 28-Feb-1986 #sequence revision 30-Jun-1991 #text change 10-Dec-1999
C; Accession: A28469; A27729; A28082; S02680; S05327; S02037; A02870; S13544; S14552
R; Sasaki, M.; Yamada, Y.
J. Biol. Chem. 262, 17111-17117, 1987
A; Title: The laminin B2 chain has a multidomain structure homologous to the B1 chain.
A; Reference number: A28469; MUID:88059118; PMID:3680290
A; Accession: A28469
A; Molecule type: mRNA
A; Residues: 1-1607 <SAS>
A; Cross-references: EMBL:J03484; NID:G198694; PIDN:AAA39405.1; PID:G293688
R; Durkin, M.E.; Barros, B.B.; Liu, S.H.; Phillips, S.L.; Chung, A.E.
Biochemistry 27, 5198-5204, 1988
A; Title: Primary structure of the mouse laminin B2 chain and comparison with laminin B1
A; Reference number: A27729; MUID:89000737; PMID:3167041
A; Accession: A27729
A; Molecule type: mRNA
A; Residues: 1-263, 'D', 265-336, 'C', 338-446, 'PS', 449-661, 'S', 663-885, 887-1155, 1157-1433, 'A'
A; Cross-references: EMBL:J02930; NID:G198702; PIDN:AAA39408.1; PID:G293691
A; Note: the authors translated the codon TAT for residue 544 as Asp and GCG for residue
R; Ogawa, K.; Burbelo, P.D.; Sasaki, M.; Yamada, Y.
J. Biol. Chem. 263, 8384-8389, 1988
A; Title: The laminin B2 chain promoter contains unique repeat sequences and is active in
A; Reference number: A28082; MUID:88228071; PMID:2836421
A; Accession: A28082
A; Molecule type: DNA
A; Residues: 1-215, 'A', 217-239 <OGA>
A; Cross-references: EMBL:J03749; NID:G198704; PIDN:AAA39409.1; PID:G554184
R; Fujiwara, S.; Shinkai, H.; Deutzmann, R.; Paulsson, M.; Timpl, R.
Biochem. J. 252, 453-461, 1988
A; Title: Structure and distribution of N-linked oligosaccharide chains on various domain
A; Reference number: S02678; MUID:88326259; PMID:2458101
A; Accession: S02680
A; Molecule type: protein
A; Residues: 227-238 <FUJ>
R; Hartl, L.; Oberbaeumer, I.; Deutzmann, R.
Eur. J. Biochem. 173, 629-635, 1988
A; Title: The N terminus of laminin A chain is homologous to the B chains.
A; Reference number: S00624; MUID:88225080; PMID:3267223
A; Accession: S05327
A; Molecule type: protein
A; Residues: 227-238; 387-393, 'F', 395-405; 881-912; 1022-1034 <HAR>
R; Deutzmann, R.; Huber, J.; Schmetz, K.A.; Oberbaeumer, I.; Hartl, L.
Eur. J. Biochem. 177, 35-45, 1988
A; Title: Structural study of long arm fragments of laminin. Evidence for repetitive C-ter
A; Reference number: S01790; MUID:89030693; PMID:3181157
A; Accession: S02037
A; Molecule type: protein
A; Residues: 1362-1377, 'X', 1379-1392, 'X', 1394-1406 <DEU>
R; Barlow, D.P.; Green, N.M.; Kurkinen, M.; Hogan, B.L.M.
EMBO J. 3, 2355-2362, 1984
A; Title: Sequencing of laminin B chain cDNAs reveals C-terminal regions of coiled-coil a
A; Reference number: A02870; MUID:85051302; PMID:6209134
A; Accession: A02870
A; Molecule type: mRNA
A; Residues: 1391-1474, 'K', 1476-1575, 'N', 1577-1607 <BAR>
A; Cross-references: EMBL:X05211; NID:G52862; PIDN:CAA28838.1; PID:G817975
R; Paulsson, M.; Deutzmann, R.; Timpl, R.; Dalzoppo, D.; Odermatt, E.; Engel, J.
EMBO J. 4, 309-316, 1985
A; Title: Evidence for coiled-coil alpha-helical regions in the long arm of laminin.
A; Reference number: S13543; MUID:85257455; PMID:3848400
A; Accession: S13544
A; Molecule type: protein

Db 359 TGHGGHCTNCRDNTDGA KCERCRCRNFRLGNTEACSPCHCSPVGSLSLTQCDSYGRCSCKP 418
QY 421 GVMGDKDRCPQGFHSLTEAGCRPCSDPSGSIDECNVETGRVCVKDNVEGFNCRCCKPG 480
Db 419 GVMGDKDRCPQGFHSLTEAGCRPCSDLRGSTDECNVETGRVCVKDNVEGFNCRCCKPG 478
QY 481 FFNLESNPRGCTPCFCFGHSSVCTNAVGYSVYSSISSTFOIDEDGWRAEQRDGSEASLEW 540
Db 479 FFNLESNPKGCTPCFCFGHSSVCTNAVGYSVYDISSTFFQIDEDGWRVEQRDGSSEASLEW 538
QY 541 SSERQDIAVISDSYFPRYFIAPAKELGKQVLSYGQNLSEFPRVDRDRTRLSEAEDLVLEGA 600
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Db 599 GLRVSVPLIAQNSYPSETTVKYIFRLHEATDYPWRPALSPPEFQKLLNNLTSIKIRGTY 658
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QY 781 CAVVPKTKEVVCTNCPTGTTGKRCELDDGYFGDPLGRNGPVRLCRLCQCSDNIDENAVG 840
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QY 841 NCNRLTGECLKCIYNTAGFYCDRCCKDGFFGNPLAPNPADKCKACNCNYPYGTMKQQSSCNP 900
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QY 1021 YNRSWPGQCECPACVRLVKDVAHRVKLQLES LIANLGTGDEMVTDDQAFEDRLKEAER 1080
Db 1019 YNRSWPGQCECPACVRLVKDKAAEHRVKLQLES LIANLGTGDDMTDQAFEDRLKEAER 1078
QY 1081 EVMDLLREAOQVKVDQNLMDRLQRVNNLTSSQISRLQNRINTTIEETGNLAEQARAHVEN 1140
Db 1079 EVTDLLREAOQVKVDQNLMDRLQRVNSSLHQSISRLQNRINTTIEETGILAEARSRVES 1138
QY 1141 TERLIEIASRELEKAKVAAANVSVTQPESTGDPNNMTLLAEERKLAERHKQEAADDIVRV 1200
Db 1139 TEQLIEIASRELEKAKVAAANVSITQPESTGEPNNMTLLAEERLAEERHKQEAADDIVRV 1198
QY 1201 AKTANDTSTEAYNLLRTLAGEHOTAFEIEELNRKYEQAKNISQDLEKQAARVHEEAKRA 1260
Db 1199 AKTANETSAEAYNLLRTLAGEHOTALEIEELNRKYEQAKNISQDLEKQAARVHEEAKRA 1258
QY 1261 GDKAVEIYASVAQLSPDSETLENEANNIKMEAEENLEQLIDQKLKDYEDLREDMRGKELE 1320
Db 1259 GDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLDRLLIDQKLKDYEDLREDMRGKEHE 1318
QY 1321 VKNLLEKKGTEQQTADQLLARADA AKALAEAAKKGRDTLQEAANDILNNLKDFDRRVNDN 1380
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QY 1381 KTAABEALRKIPAINQITTEANEKTRTAQQAALGSAADATEAKNKAHEAERIA SAVQKNA 1440
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QY 1441 TSTKAAEARTFAEVTDLNVEVNNMLKQLOEAEKELKRQDDADQDMMAGMASQAQAEAE 1500
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QY 1501 INARKAKNSVTLSLSIINDLLEQLGQLDVTDLNKLNEIEGTINKAKDEMKVSDLRKVSD 1560
Db 1499 LNARKAKNSVSSLLSQNLNLLDQLGQLDVTDLNKLNEIEGSLNKAKDEMKASDLDRKVSD 1558
QY 1561 LENEAKQOEAAIMDYNRDIEEIMKDIRNLEDIRKTLPSGCFNTPPSIEKP 1609
Db 1559 LESEARKOEAAIMDYNRDIAEIIKDIHNLEDIKKTLPTGCFNTPPSIEKP 1607
RESULT 3
NMFFB2
laminin gamma-1 chain precursor - fruit fly (Drosophila melanogaster)
N/Alternate names: laminin chain B2
C/Species: Drosophila melanogaster
C/Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jun-2000
C/Accession: A31483; A33737; S01733; A40502
R/Chi, H.C.; Hui, C.F.
J. Biol. Chem. 264, 1543-1550, 1989
A/Title: Primary structure of the Drosophila laminin B2 chain and comparison with human,
A/Reference number: A31483; MUID:89109164; PMID:2912972
A/Accession: A31483
A/Molecule type: mRNA
A/Residues: 1-1639 <CHI>
A/Cross-references: EMBL:M25063; NID:g157803; PIDN:AAA28664.1; PID:g157804
R/Montell, D.J.; Goodman, C.S.
J. Cell Biol. 109, 2441-2453, 1989
A/Title: Drosophila laminin: sequence of B2 subunit and expression of all three subunits
A/Reference number: A33737; MUID:90037237; PMID:2808533
A/Accession: A33737
A/Molecule type: mRNA
A/Residues: 1-39, 'T', '41-891, 'L', 893-1106, 'T', 1108-1459, 'HV', 1462-1581, 'G', 1583-1639 <MON
A/Note: 831-Tyr was also found
R/Chi, H.C.; Hui, C.F.
Nucleic Acids Res. 16, 7205-7206, 1988
A/Title: cDNA and amino acid sequences of Drosophila laminin B2 chain.
A/Reference number: S01733; MUID:88303364; PMID:3405777
A/Accession: S01733
A/Molecule type: mRNA
A/Residues: 344-1639 <CH2>
A/Cross-references: EMBL:X07806; NID:98179; PIDN:CAA30665.1; PID:g1335618
A/Note: the authors translated the codon GGC for residue 409 as Phe
R/Chi, H.C.; Juminaga, D.; Wang, S.Y.; Hui, C.F.
DNA Cell Biol. 10, 451-466, 1991
A/Title: Structure of the Drosophila gene for the laminin B2 chain.
A/Reference number: A40502; MUID:91299161; PMID:1840513
A/Accession: A40502
A/Molecule type: DNA
A/Residues: 1-891, 'L', 893-1639 <CH3>
A/Cross-references: GB:M58417; NID:g157805; PIDN:AAA28665.1; PID:g157806
C/Genetics:
A/Gene: lamb2
A/Cross-references: FlyBase:FBgn0002528
A/Map position: 3L 67C
A/Introns: 65/3; 110/2; 153/1; 358/1; 495/2; 1357/2; 1469/3; 1570/1
C/Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C/Function:
A/Description: interact with cells and with other basement membrane proteins to promote
C/Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C/Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular
F;1-33/Domain: signal sequence #status predicted <SIG>
F;34-1639/Product: laminin gamma-1 chain #status predicted <MAT>
F;34-297/Domain: VI <DOM6>
F;298-528/Domain: V <DOM5>
F;299-356/Domain: laminin-type EGF-like homology <LE01>
F;359-411/Domain: laminin-type EGF-like homology <LE02>
F;414-458/Domain: laminin-type EGF-like homology <LE03>
F;461-511/Domain: laminin-type EGF-like homology <LE04>
F;514-523/Domain: laminin-type EGF-like homology #status atypical <LE05>
F;529-705/Domain: IV <DOM4>
F;706-1057/Domain: III <DOM3>
F;710-741/Domain: laminin-type EGF-like homology #status atypical <LE06>
F;744-790/Domain: laminin-type EGF-like homology <LE07>

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:26:08 ; Search time 9.14821 Seconds
(without alignments)
9158.169 Million cell updates/sec

Title: US-10-037-182-14
Perfect score: 8713
Sequence: 1 MRGSHRAAPALRPRGRLWPV.....EDIRKTLPSGCFNTPSIEKP 1609

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Swissprot_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8709	100.0	1609	1 LMG1_HUMAN	P11047 homo sapien
2	8161	93.7	1607	1 LMG1_MOUSE	P02468 mus musculus
3	3611	41.4	1587	1 LMG3_HUMAN	Q9Y6N6 homo sapien
4	3492.5	40.1	1581	1 LMG3_MOUSE	Q9R0B6 mus musculus
5	3440	39.5	1639	1 LMG1_DROME	P15215 drosophila
6	3222	37.0	1535	1 LML1_MOUSE	Q18823 caenorhabdi
7	2637	30.3	1193	1 LMG2_HUMAN	Q13753 homo sapien
8	2529	29.0	1191	1 LMG2_MOUSE	Q61092 mus musculus
9	1782.5	20.5	3084	1 LMA1_MOUSE	P19137 mus musculus
10	1782.5	20.5	3110	1 LMA2_HUMAN	P24043 homo sapien
11	1774.5	20.4	3106	1 LMA2_MOUSE	Q60675 mus musculus
12	1739.5	20.0	3075	1 LMA1_HUMAN	P25391 homo sapien
13	1680.5	19.3	1786	1 LMB1_HUMAN	P07942 homo sapien
14	1669.5	19.2	1790	1 LMB1_DROME	P11046 drosophila
15	1651	18.9	1786	1 LMB1_MOUSE	P02469 mus musculus
16	1613.5	18.5	1801	1 LMB2_RAT	P15800 rattus norv
17	1592.5	18.3	1798	1 LMB2_HUMAN	P55268 homo sapien
18	1572	18.0	1799	1 LMB2_MOUSE	Q61292 mus musculus
19	1486.5	17.1	3712	1 LMA_DROME	Q00174 drosophila
20	1394	16.0	3672	1 LML2_MOUSE	Q21313 caenorhabdi
21	1373.5	15.8	3718	1 LMA5_MOUSE	Q61001 mus musculus
22	1318	15.1	3695	1 LMA5_HUMAN	O15230 homo sapien
23	1174	13.5	604	1 NET1_MOUSE	O09118 mus musculus
24	1173	13.5	604	1 NET1_HUMAN	O95631 homo sapien
25	1173	13.5	606	1 NET1_CHICK	Q90922 gallus gall
26	1141.5	13.1	3333	1 LMA3_MOUSE	Q61789 mus musculus
27	1070	12.3	581	1 NET2_MOUSE	Q90923 gallus gall
28	989	11.4	612	1 UNCE_MOUSE	P34710 caenorhabdi
29	930	10.7	1172	1 LMB3_HUMAN	Q13751 homo sapien
30	887	10.2	727	1 NETA_DROME	Q24567 drosophila
31	886.5	10.2	1168	1 LMB3_MOUSE	Q61087 mus musculus
32	880	10.1	4391	1 PGBM_HUMAN	P98160 homo sapien
33	867.5	10.0	793	1 NETB_DROME	Q24568 drosophila

34	867.5	10.0	3707	1 PGBM_MOUSE	Q05793 mus musculus
35	640.5	7.4	539	1 NTG1_MOUSE	Q8r4g0 mus musculus
36	609	7.0	3375	1 UN52_MOUSE	Q06561 caenorhabdi
37	581	6.7	530	1 NTG2_HUMAN	Q96cw9 homo sapien
38	571.5	6.6	1816	1 LMA4_HUMAN	Q16363 homo sapien
39	554.5	6.4	1816	1 LMA4_MOUSE	P97927 mus musculus
40	545	6.3	589	1 NTG2_MOUSE	Q8r4f1 mus musculus
41	510	5.9	1713	1 LMA3_HUMAN	Q16787 homo sapien
42	485	5.6	303	1 LMB1_CHICK	Q01635 gallus gall
43	474.5	5.4	2524	1 NOTC_XENLA	P21783 xenopus lae
44	454.5	5.2	2437	1 NTC1_BRARE	P46530 brachydanio
45	453.5	5.2	2703	1 NTC1_DROME	P07207 drosophila

ALIGNMENTS

RESULT 1
LMG1_HUMAN
ID LMG1_HUMAN STANDARD; PRT; 1609 AA.
AC P11047;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Laminin gamma-1 chain precursor (Laminin B2 chain).
GN LAMC1 OR LAMB2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91093128; PubMed=1985895;
RA Kallunki T., Ikonen J., Chow L.T., Kallunki P., Tryggvason K.;
RT "Structure of the human laminin B2 chain gene reveals extensive
divergence from the laminin B1 chain gene.";
RL J. Biol. Chem. 266:221-228(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88198245; PubMed=3360804;
RA Pikkariainen T., Kallunki T., Tryggvason K.;
RT "Human laminin B2 chain. Comparison of the complete amino acid
sequence with the B1 chain reveals variability in sequence homology
between different structural domains.";
RL J. Biol. Chem. 263:6751-6758(1988).
RN [3]
RP SEQUENCE OF 1393-1609 FROM N.A.
RX MEDLINE=89169663; PubMed=3234037;
RA Fukushima Y., Pikkariainen T., Kallunki T., Eddy R.L., Byers M.G.,
RT "Isolation of a human laminin B2 (LAMB2) cDNA clone and assignment of
the gene to chromosome region 1q25-->q31.";
RL Cytogenet. Cell Genet. 48:137-141(1988).
RN [4]
RP SEQUENCE OF 1282-1609 FROM N.A.
RX TISSUE=Endothelial cells;
MEDLINE=92216129; PubMed=1806043;
RA Santos C.L.S., Sabbaga J., Brentani R.;
RT "Differences in human laminin B2 sequences.";
RL DNA Seq. 1:275-277(1991).
RN [5]
RP CARBOHYDRATE-LINKAGE SITE ASN-650.
RX MEDLINE=22660472; PubMed=12754519;
RA Zhang H., Li X.-J., Martin D.B., Aebersold R.;
RT "Identification and quantification of N-linked glycoproteins using
hydrazide chemistry, stable isotope labeling and mass spectrometry.";
RL Nat. Biotechnol. 21:660-666(2003).
CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
is thought to mediate the attachment, migration and organization
of cells into tissues during embryonic development by interacting
with other extracellular matrix components.
CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
different polypeptide chains (alpha, beta, gamma), which are bound

to each other by disulfide bonds into a cross-shaped molecule comprising one long and three short arms with globules at each end. The gamma-1 chain is a subunit of laminin-1 (EHS laminin), laminin-2 (merosin), laminin-3 (S-laminin), laminin-4 (S-merosin), laminin-6 (K-laminin) and laminin-7 (KS-laminin).

-!- SUBCELLULAR LOCATION: Extracellular.

-!- TISSUE SPECIFICITY: Found in the basement membranes (major component).

-!- DOMAIN: The alpha-helical domains I and II are thought to interact with other laminin chains to form a coiled coil structure.

-!- DOMAIN: Domains VI and IV are globular.

-!- SIMILARITY: Contains 1 laminin N-terminal domain.

-!- SIMILARITY: Contains 11 laminin EGF-like domains.

-!- SIMILARITY: Contains 1 laminin IV domain.

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EMBL; M55210; AAA59492.1; JOINED.
EMBL; M55217; AAA59492.1; JOINED.
EMBL; M55201; AAA59492.1; JOINED.
EMBL; M55211; AAA59492.1; JOINED.
EMBL; M55212; AAA59492.1; JOINED.
EMBL; M55213; AAA59492.1; JOINED.
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EMBL; M55215; AAA59492.1; JOINED.
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EMBL; M55202; AAA59492.1; JOINED.
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EMBL; M55208; AAA59492.1; JOINED.
EMBL; M55209; AAA59492.1; JOINED.
EMBL; J03202; AAA59488.1; -.
EMBL; M27654; AAA59489.1; -.
EMBL; X13939; CAA32122.1; -.
PIR; S13548; MGHUB2.
HSSP; P02468; 1TLE.
Genew; HGNC:6492; LAMC1.
MIM; 150290; -.
GO; GO:0005604; C:basement membrane; TAS.
GO; GO:0007492; P:endoderm development; TAS.
GO; GO:0006461; P:protein complex assembly; TAS.
InterPro; IPR006209; EGF-like.
InterPro; IPR008212; Lam_N2.
InterPro; IPR000034; Laminin_B.
InterPro; IPR002049; Laminin_EGF.
InterPro; IPR008211; LamNT.
Pfam; PF00052; laminin_B; 1.
Pfam; PF00053; laminin_EGF; 9.
Pfam; PF00055; laminin_Nterm; 1.
PRINTS; PR00011; EGF_LAMININ.
ProDom; PD002082; Lam_N2; 1.
SMART; SM00180; EGF_Lam; 8.
SMART; SM00281; LamB; 1.
SMART; SM00136; LamNT; 1.
PROSITE; PS00022; EGF_1; 8.

DR PROSITE; PS01186; EGF 2; 2.
DR PROSITE; PS01248; LAMININ TYPE_EGF; 11.
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal; Polymorphism.
FT SIGNAL 1 33
FT CHAIN 34 1609 LAMININ GAMMA-1 CHAIN.
FT DOMAIN 34 285 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 286 341 LAMININ EGF-LIKE 1.
FT DOMAIN 342 397 LAMININ EGF-LIKE 2.
FT DOMAIN 398 444 LAMININ EGF-LIKE 3.
FT DOMAIN 445 494 LAMININ EGF-LIKE 4.
FT DOMAIN 495 504 LAMININ EGF-LIKE 5 (N-TERMINAL).
FT DOMAIN 505 689 LAMININ DOMAIN IV.
FT DOMAIN 690 723 LAMININ EGF-LIKE 5 (C-TERMINAL).
FT DOMAIN 724 772 LAMININ EGF-LIKE 6.
FT DOMAIN 773 827 LAMININ EGF-LIKE 7.
FT DOMAIN 828 883 LAMININ EGF-LIKE 8.
FT DOMAIN 884 934 LAMININ EGF-LIKE 9.
FT DOMAIN 935 982 LAMININ EGF-LIKE 10.
FT DOMAIN 983 1030 LAMININ EGF-LIKE 11.
FT DOMAIN 1030 1609 DOMAIN II AND I.
FT DOMAIN 1038 1609 COILED COIL (POTENTIAL).
FT DISULFID 286 295 BY SIMILARITY.
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FT DISULFID 1003 1012 BY SIMILARITY.
FT DISULFID 1015 1028 BY SIMILARITY.
FT DISULFID 1031 1031 INTERCHAIN (PROBABLE).
FT DISULFID 1034 1034 INTERCHAIN (PROBABLE).
FT DISULFID 1600 1600 INTERCHAIN (PROBABLE).
FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 576 576 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 650 650 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1022 1022 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1107 1107 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1161 1161 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1175 1175 N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match 100.0%; Score 8709; DB 1; Length 1609;
Best Local Similarity 99.9%; Pred. No. 1.5e-315;
Matches 1608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MRGSHRAAPALPRGRRLWPVLAVLAAAAAGCAQAAMDECTDEGGRPQRCMPEFVNAAFN	60
Db	1	MRGSHRAAPALPRGRRLWPVLAVLAAAAAGCAQAAMDECTDEGGRPQRCMPEFVNAAFN	60
QY	61	VTVVATNTCGTPPEEYCVQGTGVTGKSKCHLCDAGQPHLQHGAAFLTDYNNQADTTWQOS	120
Db	61	VTVVATNTCGTPPEEYCVQGTGVTGKSKCHLCDAGQPHLQHGAAFLTDYNNQADTTWQOS	120
QY	121	QTMLAGVQYPPSSINLTLLHLGKAFDITYVRLKFHTSRPESFAIYKRTREDGPNTPYQYYS	180
Db	121	QTMLAGVQYPPSSINLTLLHLGKAFDITYVRLKFHTSRPESFAIYKRTREDGPNTPYQYYS	180
QY	181	SCENTYSKANRGFIRTTGGDEQALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFDNSPVL	240
Db	181	SCENTYSKANRGFIRTTGGDEQALCTDEFSDFSPLTGGNVAFSTLEGRPSAYNFDNSPVL	240
QY	241	QEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSYYYAISDFAVGGRCKCNGHASECMKNEF	300
Db	241	QEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSYYYAISDFAVGGRCKCNGHASECMKNEF	300
QY	301	DKLVCNCKHNTYGVDCCKLCPFENDRPWRRATAESASECLPCDCNGRSQECYFDPPELYRS	360
Db	301	DKLVCNCKHNTYGVDCCKLCPFENDRPWRRATAESASECLPCDCNGRSQECYFDPPELYRS	360
QY	361	TGHGGHCTNCQDNTDGAHCERCENFFRLGNNEACSSCHCSPVGSLSSTQCDSYGRCSCKP	420
Db	361	TGHGGHCTNCQDNTDGAHCERCENFFRLGNNEACSSCHCSPVGSLSSTQCDSYGRCSCKP	420
QY	421	GVMGDKDRCPQGFHSLTEAGRPCSCDPSGSIDECNVETGRVCVKONVEGFNCERCKPG	480
Db	421	GVMGDKDRCPQGFHSLTEAGRPCSCDPSGSIDECNVETGRVCVKONVEGFNCERCKPG	480
QY	481	FFNLESSNPRGCTPCFCFGHSSVCTNAVGSYVSISSFTQIDEDGWRAEQRDGSEASLEW	540
Db	481	FFNLESSNPRGCTPCFCFGHSSVCTNAVGSYVSISSFTQIDEDGWRAEQRDGSEASLEW	540
QY	541	SSERQDIAVISDSYFPRYFIAPAKFLGKQVLSYGQNLSPFRVDRRLTSLAEDLVLEGA	600
Db	541	SSERQDIAVISDSYFPRYFIAPAKFLGKQVLSYGQNLSPFRVDRRLTSLAEDLVLEGA	600
QY	601	GLRVSVPILIAQNSYSPSETTVKYVRLHEATDYPWRPALTPPEFQKLLNLTSTKIRGTY	660
Db	601	GLRVSVPILIAQNSYSPSETTVKYVRLHEATDYPWRPALTPPEFQKLLNLTSTKIRGTY	660
QY	661	SERSAGYLDVDTLASARPGPGVPATWVESCTCPVGYGGGFCFEMCLSGYRRETNLGPYSP	720
Db	661	SERSAGYLDVDTLASARPGPGVPATWVESCTCPVGYGGGFCFEMCLSGYRRETNLGPYSP	720
QY	721	CVLCAACNGHSETCDPETGVNCNCRDNTAGPHCEKCSGDIYGDSTAGTSSDCQPCPCPGSS	780
Db	721	CVLCAACNGHSETCDPETGVNCNCRDNTAGPHCEKCSGDIYGDSTAGTSSDCQPCPCPGSS	780
QY	781	CAVVPKTKEVVCTNCPTGTTGKRCCLCDDGYFGDPLGRNGPVRLLCRLCQCSNDIDPNAVG	840
Db	781	CAVVPKTKEVVCTNCPTGTTGKRCCLCDDGYFGDPLGRNGPVRLLCRLCQCSNDIDPNAVG	840
QY	841	NCNRLTGECLKCIYNTAGFYCDRCCKDGGFFGNPLAPNPADKCKACNCNPNYGTMKQSSCNP	900
Db	841	NCNRLTGECLKCIYNTAGFYCDRCCKDGGFFGNPLAPNPADKCKACNCNPNYGTMKQSSCNP	900
QY	901	VTGQCECLPHVTGQDCGACDPGFYNLQSGQGCERCDCHALGSTNGQCIRTGQCECQPGI	960
Db	901	VTGQCECLPHVTGQDCGACDPGFYNLQSGQGCERCDCHALGSTNGQCIRTGQCECQPGI	960
QY	961	TGQHCECEVNHFGFPGEGCKPCDCHPEGSLSLQCKDDGRCECREGVGNRCDCQCEENYF	1020
Db	961	TGQHCECEVNHFGFPGEGCKPCDCHPEGSLSLQCKDDGRCECREGVGNRCDCQCEENYF	1020

QY	1021	YNRSWPCCQCECPACYRLVKDKVADHRVKLQELLESILIANLGTGDEMVTDAQAFEDRLKEAER	1080
Db	1021	YNRSWPCCQCECPACYRLVKDKVADHRVKLQELLESILIANLGTGDEMVTDAQAFEDRLKEAER	1080
QY	1081	EVMDLLREAQDVQKVDQNLMDRLQRVNNTLSSQISRLQIRNTIETGNLAEQARAHVEN	1140
Db	1081	EVMDLLREAQDVQKVDQNLMDRLQRVNNTLSSQISRLQIRNTIETGNLAEQARAHVEN	1140
QY	1141	TERLIEIASRELEKAKVAAANVSVTQPESTGDPNNMTLLAEARKLAERHKQEAADDIVRV	1200
Db	1141	TERLIEIASRELEKAKVAAANVSVTQPESTGDPNNMTLLAEARKLAERHKQEAADDIVRV	1200
QY	1201	AKTANDTSTEAYNLLLRTLAGEQTAFIEEELNRKYEQAKNISQDLEKQAAARVHEEAKRA	1260
Db	1201	AKTANDTSTEAYNLLLRTLAGEQTAFIEEELNRKYEQAKNISQDLEKQAAARVHEEAKRA	1260
QY	1261	GDKAVEIYASVAQLSPLDSETLENEANNIKMEAEENLEQLIDQKLKDYEDLREDMRGKELE	1320
Db	1261	GDKAVEIYASVAQLSPLDSETLENEANNIKMEAEENLEQLIDQKLKDYEDLREDMRGKELE	1320
QY	1321	VKNLLEKGKTEQQTADQLLARADAALAEAAKKGRTDQLQEANDILNNLKDFDRRVNDN	1380
Db	1321	VKNLLEKGKTEQQTADQLLARADAALAEAAKKGRTDQLQEANDILNNLKDFDRRVNDN	1380
QY	1381	KTAEEEEALRKIPAINQITITEANEKTRTAAQALGSAADAAATEAKNKAHEAERIAASAVQKNA	1440
Db	1381	KTAEEEEALRKIPAINQITITEANEKTRTAAQALGSAADAAATEAKNKAHEAERIAASAVQKNA	1440
QY	1441	TSTKAEABERTFAEVTDLNEVNNMLKQLEAEKELKRKQDDADQDMMAGMASQAAQEA	1500
Db	1441	TSTKAEABERTFAEVTDLNEVNNMLKQLEAEKELKRKQDDADQDMMAGMASQAAQEA	1500
QY	1501	INARKAKNSVTSLLSIINDLLEQLGQDVTVDLNLKLEIEGTNLKAKDEMKSVDLDRKYS	1560
Db	1501	INARKAKNSVTSLLSIINDLLEQLGQDVTVDLNLKLEIEGTNLKAKDEMKSVDLDRKYS	1560
QY	1561	LENEAKKQEAAMIDYNRDIEEIMKDINLEDIRKTLPSGCFNTPSIEKP	1609
Db	1561	LENEAKKQEAAMIDYNRDIEEIMKDINLEDIRKTLPSGCFNTPSIEKP	1609

RESULT 2

LMG1	MOUSE	STANDARD;	PRT;	1607	AA.
ID	LMG1	MOUSE			
AC	P02468;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	01-JUL-1989 (Rel. 11, Last sequence update)				
DT	15-MAR-2004 (Rel. 43, Last annotation update)				
DE	Laminin gamma-1 chain precursor (Laminin B2 chain).				
GN	LAMC1 OR LAMC-1 OR LAMB-2.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=88059118; PubMed=3680290;				
RA	Sasaki M., Yamada Y.;				
RT	"The laminin B2 chain has a multidomain structure homologous to the				
RT	B1 chain.";				
RL	J. Biol. Chem. 262:17111-17117(1987).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=89000737; PubMed=3167041;				
RA	Durkin M.E., Bartos B.B., Liu S.-H., Phillips S.L., Chung A.E.;				
RT	"Primary structure of the mouse laminin B2 chain and comparison with				
RT	laminin B1.";				
RL	Biochemistry 27:5198-5204 (1988).				
RN	[3]				
RP	SEQUENCE OF 1-239 FROM N.A.				
RX	MEDLINE=88228071; PubMed=2836421;				
RA	Ogawa K., Burbello P.D., Sasaki M., Yamada Y.;				
RT	"The laminin B2 chain promoter contains unique repeat sequences and				

RT is active in transient transfection.";
RL J. Biol. Chem. 263:8384-8389(1988).
RN [4]
RP SEQUENCE OF 1391-1607 FROM N.A.
RX MEDLINE=85051302; PubMed=6209134;
RA Barlow D.P., Green N.M., Kurkinen M., Hogan B.L.M.;
RT "Sequencing of laminin B chain cDNAs reveals C-terminal regions of
PT coiled-coil alpha-helix.";
RL EMBO J. 3:2355-2362(1984).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 771-932.
RX MEDLINE=96196434; PubMed=8648630;
RA Stetefeld J., Mayer U., Timpl R., Huber R.;
RT "Crystal structure of three consecutive laminin-type epidermal growth
PT factor-like (LE) modules of laminin gammal chain harboring the
RT nidogen binding site.";
RL J. Mol. Biol. 257:644-657(1996).
RN [6]
RP STRUCTURE BY NMR OF 824-881.
RX MEDLINE=96196435; PubMed=8648631;
RA Baumgartner R., Czisch M., Mayer U., Poeschl E., Huber R.,
RA Timpl R., Holak T.A.;
RT "Structure of the nidogen binding LE module of the laminin gammal
RT chain in solution.";
RL J. Mol. Biol. 257:658-668(1996).
RN [7]
RP FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components.
CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC different polypeptide chains (alpha, beta, gamma), which are bound
CC to each other by disulfide bonds into a cross-shaped molecule
CC comprising one long and three short arms with globules at each
CC end. The gamma-1 chain is a subunit of laminin-1 (EHS laminin),
CC laminin-2 (merosin), laminin-3 (S-laminin), laminin-4 (S-merosin),
CC laminin-6 (K-laminin) and laminin-7 (KS-laminin).
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Found in the basement membranes (major
CC component).
CC -!- DOMAIN: The alpha-helical domains I and II are thought to interact
CC with other laminin chains to form a coiled coil structure.
CC -!- DOMAIN: Domains VI and IV are globular.
CC -!- SIMILARITY: Contains 1 laminin N-terminal domain.
CC -!- SIMILARITY: Contains 11 laminin EGF-like domains.
CC -!- SIMILARITY: Contains 1 laminin IV domain.

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CC or send an email to license@isb-sib.ch).

DR EMBL; X05211; CAA28838.1; -;
DR EMBL; J03484; AAA39405.1; -;
DR EMBL; J02930; AAA39408.1; -;
DR EMBL; J03749; AAA39409.1; -;
DR PIR; A28469; MMSB2.
DR PDB; 1KLO; 20-AUG-97.
DR PDB; 1TLE; 12-FEB-97.
DR MGD; MGI:99914; Lamcl.
DR GO; GO:0005604; C:basement membrane; IDA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR008212; Lam_N2.
DR InterPro; IPR000034; Laminin_B.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR008211; LamNT.
DR Pfam; PF00052; laminin_B; 1.
DR Pfam; PF00053; laminin_EGF; 9.
DR Pfam; PF00055; laminin_Nterm; 1.
DR PRINTS; PR00011; EGFLAMININ.
DR ProDom; PD002082; Lam_N2; 1.

DR SMART; SM00180; EGF_Lam; 8.
DR SMART; SM00281; LamB; 1.
DR SMART; SM00136; LamNT; 1.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 10.
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal; 3D-structure.
FT SIGNAL 1 33
FT CHAIN 34 1607 LAMININ GAMMA-1 CHAIN.
FT DOMAIN 34 283 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 284 339 LAMININ EGF-LIKE 1.
FT DOMAIN 340 395 LAMININ EGF-LIKE 2.
FT DOMAIN 396 442 LAMININ EGF-LIKE 3.
FT DOMAIN 443 492 LAMININ EGF-LIKE 4.
FT DOMAIN 493 502 LAMININ EGF-LIKE 5 (N-TERMINAL).
FT DOMAIN 503 687 LAMININ DOMAIN IV.
FT DOMAIN 688 721 LAMININ EGF-LIKE 5 (C-TERMINAL).
FT DOMAIN 722 770 LAMININ EGF-LIKE 6.
FT DOMAIN 771 825 LAMININ EGF-LIKE 7.
FT DOMAIN 826 881 LAMININ EGF-LIKE 8 (NIDOGEN-BINDING).
FT DOMAIN 882 932 LAMININ EGF-LIKE 9.
FT DOMAIN 933 980 LAMININ EGF-LIKE 10.
FT DOMAIN 981 1028 LAMININ EGF-LIKE 11.
FT DOMAIN 1029 1607 DOMAIN II AND I.
FT DOMAIN 1034 1594 COILED COIL (POTENTIAL).
FT DISULFID 340 349 BY SIMILARITY.
FT DISULFID 342 365 BY SIMILARITY.
FT DISULFID 368 377 BY SIMILARITY.
FT DISULFID 380 393 BY SIMILARITY.
FT DISULFID 396 408 BY SIMILARITY.
FT DISULFID 398 414 BY SIMILARITY.
FT DISULFID 416 425 BY SIMILARITY.
FT DISULFID 428 440 BY SIMILARITY.
FT DISULFID 443 454 BY SIMILARITY.
FT DISULFID 445 461 BY SIMILARITY.
FT DISULFID 463 472 BY SIMILARITY.
FT DISULFID 475 490 BY SIMILARITY.
FT DISULFID 722 731 BY SIMILARITY.
FT DISULFID 724 738 BY SIMILARITY.
FT DISULFID 740 749 BY SIMILARITY.
FT DISULFID 752 768 BY SIMILARITY.
FT DISULFID 771 779
FT DISULFID 773 790
FT DISULFID 793 802
FT DISULFID 805 823
FT DISULFID 826 840
FT DISULFID 828 847
FT DISULFID 850 859
FT DISULFID 862 879
FT DISULFID 882 896
FT DISULFID 884 903
FT DISULFID 905 914
FT DISULFID 917 930
FT DISULFID 933 945
FT DISULFID 935 952
FT DISULFID 954 963
FT DISULFID 966 978
FT DISULFID 981 993
FT DISULFID 983 999
FT DISULFID 1001 1010
FT DISULFID 1013 1026
FT DISULFID 1029 1029
FT DISULFID 1032 1032
FT DISULFID 1598 1598 INTERCHAIN (PROBABLE).
FT CARBOHYD 58 58 INTERCHAIN (WITH BETA-1 CHAIN).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 574 574 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 648 648 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1020 1020 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1105 1105 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1159 1159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1173 1173 N-LINKED (GLCNAC. . .) (POTENTIAL).

RESULT 3		
LMG3_HUMAN		
ID	LMG3_HUMAN	STANDARD; PRT; 1587 AA.
AC	Q9Y6N6;	
DT	28-FEB-2003	(Rel. 41, Created)
DT	28-FEB-2003	(Rel. 41, Last sequence update)
DT	15-MAR-2004	(Rel. 43, Last annotation update)
DE	Laminin gamma-3 chain precursor (Laminin 12 gamma 3).	

GN LAMC3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=99242614; PubMed=10225960;
RA Koch M., Olson P.F., Albus A., Jin W., Hunter D.D., Brunken W.J.,
RA Burgeson R.E., Champlaud M.F.;
RT "Characterization and expression of the laminin gamma3 chain: a novel,
RT non-basement membrane-associated, laminin chain.";
RL J. Cell Biol. 145:605-618(1999).
CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components.
CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC different polypeptide chains (alpha, beta, gamma), which are bound
CC to each other by disulfide bonds into a cross-shaped molecule
CC comprising one long and three short arms with globules at each
CC end. The gamma-3 chain is a subunit of laminin-12.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Broadly expressed in: skin, heart, lung, and
CC the reproductive tracts.
CC -!- DOMAIN: The alpha-helical domains I and II are thought to interact
CC with other laminin chains to form a coiled coil structure.
CC -!- DOMAIN: Domain IV is globular.
CC -!- SIMILARITY: Contains 1 laminin N-terminal domain.
CC -!- SIMILARITY: Contains 11 laminin EGF-like domains.
CC -!- SIMILARITY: Contains 1 laminin IV domain.
CC -----
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CC -----
CC EMBL; AF041835; AAD36991.1; --
DR HSSP; P02468; 1TLE.
DR Genew; HGNC:6494; LAMC3.
DR MIM; 604349; --
DR GO; GO:0005578; C:extracellular matrix; TAS.
DR GO; GO:0016020; C:membrane; TAS.
DR GO; GO:0005198; F:structural molecule activity; TAS.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR008212; Lam_N2.
DR InterPro; IPR000034; Laminin_B.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR008211; LamNT.
DR Pfam; PF00052; laminin_B; 1.
DR Pfam; PF00053; laminin_EGF; 9.
DR Pfam; PF00055; laminin_Nterm; 1.
DR PRINTS; PR00011; EGF_LAMININ.
DR PRODOM; PD002082; Lam_N2; 1.
DR SMART; SM00180; EGF_Lam; 9.
DR SMART; SM00136; LamNT; 1.
DR PROSITE; PS00022; EGF_1; 7.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01248; LAMININ TYPE_EGF; 10.
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 1587 LAMININ GAMMA-3 CHAIN.
FT DOMAIN 20 270 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 271 326 LAMININ EGF-LIKE 1.
FT DOMAIN 327 382 LAMININ EGF-LIKE 2.
FT DOMAIN 383 429 LAMININ EGF-LIKE 3.
FT DOMAIN 430 479 LAMININ EGF-LIKE 4.
FT DOMAIN 480 489 LAMININ EGF-LIKE 5 (N-TERMINAL).

FT	DOMAIN	490	672	LAMININ DOMAIN IV.
FT	DOMAIN	673	706	LAMININ EGF-LIKE 5 (C-TERMINAL).
FT	DOMAIN	707	754	LAMININ EGF-LIKE 6.
FT	DOMAIN	755	809	LAMININ EGF-LIKE 7.
FT	DOMAIN	810	865	LAMININ EGF-LIKE 8.
FT	DOMAIN	866	916	LAMININ EGF-LIKE 9.
FT	DOMAIN	917	964	LAMININ EGF-LIKE 10.
FT	DOMAIN	965	1013	LAMININ EGF-LIKE 11.
FT	DOMAIN	1014	1587	DOMAIN II AND I.
FT	DOMAIN	1071	1141	COILED COIL (POTENTIAL).
FT	DOMAIN	1200	1229	COILED COIL (POTENTIAL).
FT	DOMAIN	1424	1504	COILED COIL (POTENTIAL).
FT	DOMAIN	1535	1579	COILED COIL (POTENTIAL).
FT	SITE	1059	1061	CELL ATTACHMENT SITE (POTENTIAL).
FT	CARBOHYD	87	87	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	119	119	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	295	295	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	328	328	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	631	631	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	837	837	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	980	980	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1185	1185	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1518	1518	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	1587 AA;	172051 MW;	3CB6E09B5F203319 CRC64;

Query Match 41.4%; Score 3611; DB 1; Length 1587;
Best Local Similarity 43.5%; Pred. No. 8e-127;
Matches 701; Conservative 264; Mismatches 578; Indels 68; Gaps 21;

QY	21	LAVLAAAAAGCAQAAMDECTDEGRRPQRCMPFVNAAFNVTVATNTCGTPPEEYCVQT	80
Db	10	LALLAPRAAG---AGMGACYDAGRPQRCPLVFENAAFGRLAQASHTCGSPPEDFCPHV	65
QY	81	GVTGVTYKCHLCDAGQPHLQGAFLTDYNNQADTTWQSQTMLAGVQYSSINLTILHG	140
Db	66	GAAGAGAHQRCDAADPQRHNASYLTDFHSQDESTWQSPSMAFGVQYPTSVNITRLG	125
QY	141	KAFDITYVRLKFHTSRPESPAIKRTREDGPWIPYQYISGSCENTYSKANRGFIRTCGDE	200
Db	126	KAYEITYVRLKFHTSRPESPAIKRSRADGPWEYPYQFYASCCQTYGRPEGQYLRGCEDE	185
QY	201	QALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFNDSPLVQEWVTATDIRVTLRNLNTFG	260
Db	186	RVAFCTSEFSDISPLSGGNVAFSTLEGRPSAYNFEEPSGLQEWVTSTELLISLDRNLNTFG	245
QY	261	DEVFNDPKVLKSYYYAISDFAVGGRCKNGHASECMKNEFDKLVNCKKHNTYGVDCCKCL	320
Db	246	DDIFKDPKVLQSYYYAVSDFSVGGRCKNGHASECGPDVAGQLACRCQHTTGTDCERCL	305
QY	321	PFNDPRWRATAESAECPLDCNCRSQECYFDPPELYRSTGHGCHTCNQDNTDGAHCE	380
Db	306	PFQDRPWARGTAAEAHECLPCNCSGRSEECTFDRELFRSTGHGGRCHCRDHTAGPHCE	365
QY	381	RCRENFFRLGNNEACSSCHCSPVGSLSQCDSDSYGRCSCKPGVMGDKDCRCQPGFHSLTEA	440
Db	366	RCQENFYHWDPRMPCQPCDCQCSAGSLHLQCDTGTCACTVTGKCDRCCLPGFHSLSSEG	425
QY	441	GCRPCSCDPSGSDIECNVETGRVCVKDNVEGFNCERCCKPGFFNLESSNPRGCTPCFCFGH	500
Db	426	GCRPCTCNPAGSLDTCDRSGRCPCKEVGNLDCRCRPGTFLQPHNPAGCSCFCYGH	485
QY	501	SSVCTNAVGVSYYSISSTFQIDEDGNRAEQRDGSEASLEWSSERQDIIVISDSYFPRYFI	560
Db	486	SKVCASTAQFQVHHILSDFHQAGEGWARSVGGSEHSPQWSPN----GVLLSPEDEEELT	541
QY	561	APAKFLGKQVLSYQNLFSFRVDRDRTRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETT	620
Db	542	APGKFLGDQRFSGQPLILTFRVPPGDSPLPVQ-LRLEGTGLALS--LRHSSLGPDQAR	598
QY	621	VKIVFRLH---EATDYPWRPALTPFEFQKLLNNLTISKIRGTYSERSAG--YLDDEVTLAS	675
Db	599	ASQGGRAQVPLQETSEDVAPPLPPFHFQRLANLTSLRLRVSPGSPAGVPVFLTEVRLTS	658

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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:28 ; Search time 43.6478 Seconds
(without alignments)
11631.021 Million cell updates/sec

Title: US-10-037-182-14
Perfect score: 8713
Sequence: 1 MRGSHRAAPALPRGRLWPV.....EDIRKTLPSGCFNTPTSEKP 1609

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- SPTREMBL 25:*
 - 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6217	71.4	1593	13 Q8JHV8	Q8j hv6 brachydanio
2	4789	55.0	1007	13 Q90ZN3	Q90zn3 gallus gall
3	3533.5	40.6	1623	5 Q9U3U7	Q9u3u7 anopheles g
4	2614.5	30.0	1190	6 Q8HZI9	Q8hzi9 equus cabal
5	2612.5	30.0	1196	6 Q867A2	Q867a2 canis famil
6	1719.5	19.7	1785	13 Q8JHV7	Q8j hv7 brachydanio
7	1716	19.7	529	4 Q8N2D6	Q8n2d6 homo sapien
8	1687.5	19.4	1792	13 Q57484	Q57484 gallus gall
9	1652	19.0	1761	4 Q86XN2	Q86xn2 homo sapien
10	1626.5	18.7	3102	5 O45614	O45614 caenorhabdi
11	1580.5	18.1	1799	11 Q8R0Y0	Q8r0y0 mus musculu
12	1566	18.0	319	4 Q96BH6	Q96bh6 homo sapien
13	1517	17.4	351	11 P97552	P97552 rattus norv
14	1506.5	17.3	2731	5 Q9VJT5	Q9vjt5 drosophila
15	1506.5	17.3	3367	5 Q9XZC9	Q9xzc9 drosophila
16	1506.5	17.3	3375	5 Q8IP51	Q8ip51 drosophila

17	1485.5	17.0	1631	4 Q9Y6U6	Q9y6u6 homo sapien
18	1485.5	17.0	3712	5 Q9VRW0	Q9vrw0 drosophila
19	1477.5	17.0	1827	13 Q8JHV6	Q8j hv6 brachydanio
20	1394	16.0	3704	5 P91904	P91904 caenorhabdi
21	1317	15.1	3695	4 Q8TDF8	Q8tdf8 homo sapien
22	1197	13.7	1168	5 Q967S8	Q967s8 schistocerc
23	1172	13.5	604	11 Q924Z9	Q924z9 rattus norv
24	1151.5	13.2	603	13 Q42140	Q42140 brachydanio
25	1139.5	13.1	602	13 Q42203	Q42203 brachydanio
26	1137.5	13.1	569	13 Q57339	Q57339 xenopus lae
27	1136	13.0	1026	5 Q8SWY0	Q8swy0 drosophila
28	1131.5	13.0	464	11 Q61965	Q61965 mus musculu
29	1096	12.6	555	5 Q9NFW6	Q9nfw6 branchiosto
30	1086.5	12.5	1069	5 Q9BPS2	Q9bps2 bombyx mori
31	1071	12.3	1086	4 Q8TAS6	Q8tas6 homo sapien
32	1056	12.1	1067	5 O44565	O44565 caenorhabdi
33	1053.5	12.1	610	5 Q96659	Q96659 hirudo medi
34	1034	11.9	1546	4 Q9NS27	Q9ns27 homo sapien
35	1031	11.8	1461	11 Q9JLP3	Q9jlp3 mus musculu
36	1030	11.8	1546	4 O75445	O75445 homo sapien
37	979	11.2	1512	11 Q8K3K1	Q8k3k1 rattus norv
38	962.5	11.0	984	11 Q8K271	Q8k271 mus musculu
39	934.5	10.7	1486	4 O14637	O14637 homo sapien
40	918.5	10.5	695	11 Q8C9J2	Q8c9j2 mus musculu
41	905.5	10.4	1168	11 Q91V90	Q91v90 mus musculu
42	896	10.3	911	11 Q9CRX6	Q9crx6 mus musculu
43	879	10.1	667	5 Q9VY25	Q9vy25 drosophila
44	870	10.0	580	4 O00634	O00634 homo sapien
45	870	10.0	580	11 Q9R1A3	Q9ria3 mus musculu

ALIGNMENTS

RESULT 1

Q8JHV8	ID	Q8JHV8	PRELIMINARY;	PRT; 1593 AA.
AC	Q8JHV8;			
DT	01-OCT-2002 (Tremblrel. 22, Created)			
DT	01-OCT-2002 (Tremblrel. 22, Last sequence update)			
DT	01-JUN-2003 (Tremblrel. 24, Last annotation update)			
DE	Laminin gamma 1.			
GN	LAMC1.			
OS	Brachydanio rerio (Zebrafish) (Danio rerio).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;			
OC	Cyprinidae; Danio.			
OX	NCBI_TaxID=7955;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22065263; PubMed=12070089;			
RA	Parsons M.J., Pollard S.M., Saude L., Feldman B., Coutinho P.,			
RA	Hirst E.M., Stemple D.L.;			
RT	"Zebrafish mutants identify an essential role for laminins in			
RT	notochord formation."			
RL	Development 129:3137-3146(2002).			
DR	EMBL; AF468048; AAM61766.1; -.			
DR	GO; GO:0005198; C:extracellular matrix; IEA.			
DR	GO; GO:0005578; C:structural molecule activity; IEA.			
DR	InterPro; IPR006209; EGF like.			
DR	InterPro; IPR000034; Laminin B.			
DR	InterPro; IPR002049; Laminin_EGF.			
DR	InterPro; IPR008211; LamNT.			
DR	InterPro; IPR008212; Lam_N2.			
DR	Pfam; PF00052; laminin B; 1.			
DR	Pfam; PF00053; laminin_EGF; 10.			
DR	Pfam; PF00055; laminin_Nterm; 1.			
DR	PRINTS; PR00011; EGFLAMININ.			
DR	ProDom; PD002082; Lam N2; 1.			
DR	SMART; SM00180; EGF_Lam; 11.			
DR	SMART; SM00281; LamB; 1.			
DR	SMART; SM00136; LamNT; 1.			
DR	PROSITE; PS00022; EGF_1; 7.			

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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:28 ; Search time 48.4494 Seconds
(without alignments)
11631.021 Million cell updates/sec

Title: US-10-037-182-10
Perfect score: 9758
Sequence: 1 MGLQVAFGVLALWGTRVC.....EVRSLKDISKAVYSTCL 1786

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6781.5	69.5	1785	13 Q8JHV7	Q8jvh7 brachydanio
2	5434	55.7	1086	4 Q8TAS6	Q8tas6 homo sapien
3	5323	54.6	1792	13 Q57484	Q57484 gallus gall
4	5195	53.2	984	11 Q8K271	Q8k271 mus musculus
5	5086.5	52.1	1799	11 Q8R0Y0	Q8roY0 mus musculus
6	4790	49.1	911	11 Q9CRX6	Q9cix6 mus musculus
7	3813.5	39.1	1761	4 Q86XN2	Q86xn2 homo sapien
8	3743.5	38.4	1827	13 Q8JHV6	Q8jvh6 brachydanio
9	3607.5	37.0	1631	4 Q9Y6U6	Q9y6u6 homo sapien
10	2837.5	29.1	1067	5 Q44565	Q44565 caenorhabdi
11	2271.5	23.3	1168	5 Q967S8	Q967s8 schistocerc
12	2015	20.6	761	4 Q9UHI2	Q9uhi2 homo sapien
13	1936	19.8	1026	5 Q8SWY0	Q8swy0 drosophila
14	1832	18.8	1069	5 Q9BPS2	Q9bps2 bombyx mori
15	1751	17.9	3704	5 P91904	P91904 caenorhabdi
16	1671	17.1	3712	5 Q9VRW0	Q9vrw0 drosophila

17	1644.5	16.9	1593	13 Q8JHV8	Q8jvh8 brachydanio
18	1636.5	16.8	1623	5 Q9U3U7	Q9u3u7 anopheles 9
19	1572.5	16.1	3695	4 Q8TDF8	Q8tdf8 homo sapien
20	1531.5	15.7	1168	11 Q91V90	Q91v90 mus musculus
21	1342	13.8	1007	13 Q90ZN3	Q90zn3 gallus gall
22	1305.5	13.4	3102	5 Q45614	Q45614 caenorhabdi
23	1243	12.7	2731	5 Q9VJT5	Q9vjt5 drosophila
24	1243	12.7	3367	5 Q9XZC9	Q9xzc9 drosophila
25	1243	12.7	3375	5 Q8IP51	Q8ip51 drosophila
26	1110.5	11.4	1546	4 Q9NS27	Q9ns27 homo sapien
27	1108.5	11.4	1546	4 Q75445	Q75445 homo sapien
28	1083	11.1	1486	4 Q14637	Q14637 homo sapien
29	1041	10.7	1461	11 Q9JLP3	Q9jlp3 mus musculus
30	1032	10.6	750	4 Q86TP7	Q86tp7 homo sapien
31	987.5	10.1	628	4 Q9HB63	Q9hb63 homo sapien
32	987.5	10.1	628	4 Q9BZP1	Q9bzip1 homo sapien
33	986.5	10.1	628	11 Q9J133	Q9ji33 mus musculus
34	978.5	10.0	616	4 Q15483	Q15483 homo sapien
35	972.5	10.0	605	4 Q7Z5B6	Q7z5b6 homo sapien
36	971	10.0	1512	11 Q8K3K1	Q8k3k1 rattus norv
37	875.5	9.0	1190	6 Q8HZI9	Q8hzi9 equus cabal
38	872.5	8.9	1196	6 Q867A2	Q867a2 canis famil
39	692.5	7.1	529	4 Q8N2D6	Q8n2d6 homo sapien
40	690.5	7.1	604	11 Q924Z9	Q924z9 rattus norv
41	683.5	7.0	1664	5 Q9TVQ2	Q9tvq2 caenorhabdi
42	683	7.0	603	13 Q42140	Q42140 brachydanio
43	680	7.0	1574	11 Q88281	Q88281 rattus norv
44	679	7.0	569	13 Q57339	Q57339 xenopus lae
45	675	6.9	602	13 Q42203	Q42203 brachydanio

ALIGNMENTS

RESULT 1

Q8JHV7
ID Q8JHV7 PRELIMINARY; PRT; 1785 AA.
AC Q8JHV7;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, last sequence update)
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE Laminin beta 1.
GN LAMB1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;

[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=22065263; PubMed=12070089;
RX Parsons M.J., Pollard S.M., Saude L., Feldman B., Coutinho P.,
RA Hirst E.M., Stemple D.L.;
RT "Zebrafish mutants identify an essential role for laminins in
notochord formation."
RL Development 129:3137-3146(2002).
DR EMBL; AF468049; AAM61767.1; .
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR008211; LamNT.
DR Pfam; PF00053; laminin_EGF; 13.
DR Pfam; PF00055; laminin_Nterm; 1.
DR PRINTS; PR00011; EGFLAMININ.
DR SMART; SM00180; EGF_Lam; 13.
DR SMART; SM00136; LamNT; 1.
DR PROSITE; PS00022; EGF_1; 10.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 12.
KW Laminin EGF-like domain.
SQ SEQUENCE 1785 AA; 197279 MW; 1BD338A0B6AB9F26 CRC64;

Query Match	69.5%;	Score 6781.5;	DB 13;	Length 1785;	
Best local similarity	67.0%;	Pred. No. 5.9e-290;			
Matches 1198;	Conservative 246;	Mismatches 335;	Indels 9;	Gaps 7;	
QY	3	LLQVAFGLALWGRVCAQAEBSYCAEGSCYPATGDLILIGRAQKLSVTSTCGLHKPE	62		
Db	2	LLQLAALSILGAN--ALADVPGLDVCTEGSCYPATGDLILIGRAQKLSVTSTCGLHKPE	58		
QY	63	PYCIIVSHLOEDKCFICDSRDPYHETLNP-DSHLIENVVTTTAPNRLKIWQSENGVENV	121		
Db	59	PFCIVSHLOEKCFVCDSRQAYNETAHQVTSIENVVTTTAPNRLKIWQSENGLENV	118		
QY	122	TIQDLAEAFHFTLIMTFKTRPAPAMLIERSSDPGKTGWVRYFYAYDCSSFPGISTGP	181		
Db	119	TIQDLAEAFHFTLIMTFKTRPAPAMVIERSADFGNTWQVRYFYAYDCSSFPVSHGP	178		
QY	182	MKKVDDIICDSRYSIDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLLKITNLRKFVKLH	241		
Db	179	MTKVDDVICDTRYSDIEPSTEGEVIFRVLDPAFRIEDPSPRIQNMLKITNLRVKFTKLH	238		
QY	242	TLGDNLLDSRMEIREKYYIAYVDMVVRGNCFCYGHASECAPVDGVNEEVEGMVGHCMCR	301		
Db	239	TLGDNLLDSRIEIKYYIAYIYDMVVRGNCFCYGHASECAPVDGTGEAVEGMVGHCMCN	298		
QY	302	HNTKGLNCELMDYFHDLPWPAEGRNSNACKKNCNEHSSSCHFDNAVFLATGNVSGGV	361		
Db	299	HNTIGLNCERCQDFYHDLWPAEGRNTNACKKCHNHSHSCHFDNAVYRAGNVSGGV	358		
QY	362	CDNCQHNWGRNCEOCKPFYFQHPERDIRDNLCEPCTCDPAGSENGICDGYTDFSVGL	421		
Db	359	CDDCQHNWGNHCEOCKPFYFQHPERDIRDNLCEPCTCDPAGSENGICDGYTDFSVGL	418		
QY	422	IAGQCRCKLHVEGERCDVCKEFGFYDLSAEDPYGCKSCACNPLGTIPGPNPCDSETGYCYC	481		
Db	419	ISGQCRCKPNVEGERCDVCKEFGFYDLSAEDPYGCKSCACNPLGTIPGPNPCDSETGYCYC	477		
QY	482	KRLVTGRCQDCLPQHWGLSNDLDCRCPDCLDGLGALNNSCEDSGQCSCLPHMIGRCQN	541		
Db	478	KRLVTGRCQDCLPQHWGLSNDLDCRCPDCLDGLGALNNSCEDSGQCSCLPHMIGRCQN	537		
QY	542	EVEGSGYFTTLDHYIYEAEANLPGVWVVERQYIQRIPSWTGPFGVVRVPEGAYLEFFI	601		
Db	538	QVESGFFIADHYTYEAEAKFGPGVTVPVPRNHPQDRSPTWTGIGFVNVPEGAFLFESI	597		
QY	602	DNIPYSMEYELIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTPVDDNQVSLSPGS	661		
Db	598	DNIPYSMEYDLIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTPVDDNQVSLSPGS	657		
QY	662	RYVLPVPVCFEKGMYTVRLPQYTAGSDVESPYTFIDSLVLMFYCKSLDIFTVGS	721		
Db	658	RYVLPVPVCFEGLNYTVRLSLSLYSAL-SDVQSPYTLIDSIVLMPHCKNLDIFSGST	716		
QY	722	GDGE-VTNSAWETFORVRCLENSRSVWKTMTDVCNRIIFSISALIHOTGLACECDPQS	780		
Db	717	EGGNLVTNSAWENFORVRCLENSQAVVKTMTDVCNRIIFSISALIHOTGLACECDPQS	776		
QY	781	LSSVCDPNGGQCCQCRPNVVRGTCNRCPATGTFGPGNGCKPCDCHLQGSASAFCDAITGC	840		
Db	777	LSTVCDPNSGGQCCQCRPNVVRGTCNRCPATGTFGPGNGCKPCDCHLQGSASAFCDAITGC	836		
QY	841	HCFQGIYARQCDRLPGYWGFPSCQPCQCNHGLDCTVTGECILSCDYTTGHNRCERCLA	900		
Db	837	ECIAGAYGRQCDRLPGYWGFPNCRPCTCNHGLDCTVTGECILSCDYTTGHNRCERCLA	896		
QY	901	GYGDPPIIGSGDHCRPCPCPDGPDGSGRQFARSCYQDPVTLQACVDPYIGSRCDDCAS	960		
Db	897	GYGDPVVLGSGDHCRPCPCPDGPDGSGRQFARSCYQDPVTLQACVDPYIGSRCDDCAS	956		
QY	961	GFFGNPSDFGSGCQPCQCHNIDTTPDCAKDTGRCLKCLYHTEGDHQCQLCYGYVGA	1020		
Db	957	GYGNPHEVGECRQPCQCHNIDTTPDCAKDTGRCLKCLYHTEGDHQCQLCYGYVGA	1016		
QY	1021	LQDCRCVCNVLGTVKEHC-NGSDCHCDKATGQCSCLPNVIGQNCDCRCAPTWQLASGT	1079		

RESULT 2

Q8TAS6

ID	Q8TAS6	PRELIMINARY;	PRT;	1086	AA.
AC	Q8TAS6;				
DT	01-JUN-2002 (Tremblrel. 21, Created)				
DT	01-JUN-2002 (Tremblrel. 21, Last sequence update)				
DT	01-JUN-2003 (Tremblrel. 24, Last annotation update)				
DE	Similar to laminin, beta 1 (Fragment).				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Muscle;				
RA	Strausberg R.;				
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; BC026018; AAH26018.1; -				
DR	GO; GO:0005198; F:structural molecule activity; IEA.				
DR	InterPro; IPR006209; EGF-like.				
DR	InterPro; IPR002049; Laminin_EGF.				

Db	1017	LTQSCRKVCNQMGTVEEMCPSPGNCNCDLTSGQCLPLNVVGHCDCQCAPDTWNMASGK	1076		
QY	1080	CGPCNCAAHSGFSPSCNEFTGQCQCPGFGGRTSCSQELFWGDPDVECRACDCDPRGI	1139		
Db	1077	GCEDCDPNHSGFSSCNEIMGQSCCKPGFGGRTSCRELFWGNPEVKCHACDCDPRGI	1136		
QY	1140	ETPQCQSTQOCVCEGVEGPRCDKCTRGYSGVFPDCTPCHQCFALWDAIIGELTNRTHK	1199		
Db	1137	AEQCNKVTGHCVCEGVEGPRCDTCARGYTGEFPQCHQCFAEWDIIIGDLTNQTHR	1196		
QY	1200	FLEKAKALKISGVIGPYRETVDSEKKNVNEIKOILAQSPAAEPLKNIGILFEAEKLTKD	1259		
Db	1197	LVQKVNTIKATGITGYPQATINNVENANSIRNLAQNPAOTPLTEIQGLLEQATALMAE	1256		
QY	1260	VTEKMAQVEVKLTDTASQSNSTAGELGALQAEASLDKTVKELAEQLEFIKNSDIQGALD	1319		
Db	1257	MNSNLNLTBEETLSEISSDNNSTDTKLKSLKEEAQKLEQTVKDLREQVEFVKNSDIRGARA	1316		
QY	1320	SITKYFOMSLAEAKRVNASTTDPNSTVEQSALTTRDRVEDLMLERESPFEQOEQARLLD	1379		
Db	1317	SVTRYEQSQNAEIRANASTTDPNVLNVSQATLRTTEELMNQTKKEEFNQRODEFKSLD	1376		
QY	1380	ELAGKQLSLDLSAAAQMTCTGTPPGAD-CSESECGGNCRTDEGEKKCGGPGGGLVTVAH	1438		
Db	1377	NLAGQLETLDLSELSEKTCGSPAGSENCADSRCCGSLSCVDMQSGRCKCGEGCDGLTTLAH	1436		
QY	1439	SAWQKAMDFDRDVLSEALAEVQLSKMVSEAKVRADRAKQNAQDVLKTNATKEKVKDSNE	1498		
Db	1437	NAWQKAFDLEIIISAMEEVDKLSKVSEAKVKADEAKLNAQAEVLAKTNETKRVDSNE	1496		
QY	1499	DLRLIKOIRNFLTEDSADLDSIEAVANEVLKSGNASTPQQLQNLNLTEDIRERVETLSQVE	1558		
Db	1497	ELRLIKOIRNFLTQDGLDLESIEAVANEVLQMQMPTTQAQLQNLNLTEDIRERVETLSQVE	1556		
QY	1559	VILQSAADILRAEALLLEAKRASKSATDVKVTADMVKEALEAEAKQVAAEKAKIQAAD	1618		
Db	1557	DILNQSAADILRAEALLLEAKRASKSATDVKVTADMVKEALEAEAKQVAAEKAKIQAAD	1616		
QY	1619	DIQGTQNLTSIESETAASEETLTNASQRIKERNVEELKRAAKAAQNSGEAEYIEKVVS	1678		
Db	1617	DIQGTQNLTSIESETAASEETLTNASQRIKERNVEELKRAAKAAQNSGEAEYIEKVVS	1676		
QY	1679	VKQADVDVKTLDGELDEKVKKVESLIAQKTESADARRKAEALLQNEAKTLLAQANSKLQ	1738		
Db	1677	INALAEQKKDLSELKDKYSTVEELITQKAEQVAAEKRAEKLEAEARNLLQASEKLQ	1736		
QY	1739	LLEDLEKVEDNQKYLEDKAQELVRLGEVRSLLKDISEKAVYSTCL	1786		
Db	1737	LLKNLEKVEDNQKYLEDKAQELVRLGEVRSLLKDISEKAVYSTCL	1784		

OM protein - protein search, using sw model

Run on: May 18, 2004, 14:26:08 ; Search time 10.1546 Seconds
(without alignments)
9158.169 Million cell updates/sec

Title: US-10-037-182-10
Perfect score: 9758
Sequence: 1 MGLLQVFAFGVLAALWGTRVC.....EVRSLKDISEKVAVYSTCL 1786

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9758	100.0	1786	1 LMB1_MOUSE	P02469 mus musculu
2	9144	93.7	1786	1 LMB1_HUMAN	P07942 homo sapien
3	5087.5	52.1	1801	1 LMB2_RAT	P15800 rattus norv
4	5066.5	51.9	1799	1 LMB2_MOUSE	Q61292 mus musculu
5	5031.5	51.6	1798	1 LMB2_HUMAN	P55268 homo sapien
6	3859.5	39.6	1790	1 LMB1_DROME	P11046 drosophila
7	1751	17.9	3672	1 LMB2_CAEEL	Q21313 caenorhabdi
8	1708	17.5	1639	1 LMG1_DROME	P15215 drosophila
9	1675	17.2	3712	1 LMA_DROME	Q00174 drosophila
10	1647	16.9	1609	1 LMG1_HUMAN	P11047 homo sapien
11	1645.5	16.9	1535	1 LML1_CAEEL	Q18823 caenorhabdi
12	1634.5	16.8	1607	1 LMG1_MOUSE	P02468 mus musculu
13	1602.5	16.4	3718	1 LMA5_MOUSE	Q61001 mus musculu
14	1575	16.1	303	1 LMB1_CHICK	Q01635 gallus gall
15	1573.5	16.1	3075	1 LMA1_HUMAN	P25391 homo sapien
16	1566.5	16.1	3695	1 LMA5_HUMAN	O15230 homo sapien
17	1555	15.9	3110	1 LMA2_HUMAN	P24043 homo sapien
18	1551.5	15.9	1172	1 LMB3_HUMAN	Q13751 homo sapien
19	1525.5	15.6	1581	1 LMG3_MOUSE	Q9r0b6 mus musculu
20	1524	15.6	3106	1 LMA2_MOUSE	Q60675 mus musculu
21	1519.5	15.6	1168	1 LMB3_MOUSE	Q61087 mus musculu
22	1513	15.5	1587	1 LMG3_HUMAN	Q9y6n6 homo sapien
23	1510	15.5	3084	1 LMA1_MOUSE	P19137 mus musculu
24	1353	13.9	3333	1 LMA3_MOUSE	Q61789 mus musculu
25	875	9.0	1191	1 LMG2_MOUSE	Q61092 mus musculu
26	862.5	8.8	1193	1 LMG2_HUMAN	Q13753 homo sapien
27	693	7.1	604	1 NET1_HUMAN	O95631 homo sapien
28	691.5	7.1	604	1 NET1_MOUSE	O09118 mus musculu
29	686	7.0	606	1 NET1_CHICK	Q90922 gallus gall
30	656	6.7	3707	1 PGBM_MOUSE	Q05793 mus musculu
31	647.5	6.6	4391	1 PGBM_HUMAN	P98160 homo sapien
32	617	6.3	612	1 UNC6_CAEEL	P34710 caenorhabdi
33	608.5	6.2	581	1 NET2_CHICK	Q90923 gallus gall

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EMBL; M15525; AAA39407.1; ALT_INIT.
EMBL; X05212; CAA28839.1; --
PIR; A26413; MMSB1.
HSSP; P02468; 1KLO.
MGD; MGI:96743; Lamb1-1.
InterPro; IPR006209; EGF like.
InterPro; IPR002049; Laminin_EGF.
InterPro; IPR008211; LamNT.
Pfam; PF00053; laminin_EGF; 13.
Pfam; PF00055; laminin_Nterm; 1.
PRINTS; PR00011; EGFLAMININ.
SMART; SM00180; EGF_Lam; 11.
SMART; SM00136; LamNT; 1.
PROSITE; PS00022; EGF_1; 9.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01248; LAMININ_TYPE_EGF; 11.
Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
SIGNAL 1 21
CHAIN 22 1786 LAMININ BETA-1 CHAIN.
DOMAIN 22 270 LAMININ N-TERMINAL (DOMAIN VI).
DOMAIN 271 334 LAMININ EGF-LIKE 1.
DOMAIN 335 397 LAMININ EGF-LIKE 2.
DOMAIN 398 457 LAMININ EGF-LIKE 3.
DOMAIN 458 509 LAMININ EGF-LIKE 4.
DOMAIN 510 540 LAMININ EGF-LIKE 5 (INCOMPLETE).
DOMAIN 541 772 LAMININ DOMAIN IV.
DOMAIN 773 820 LAMININ EGF-LIKE 6.
DOMAIN 821 866 LAMININ EGF-LIKE 7.
DOMAIN 867 916 LAMININ EGF-LIKE 8.
DOMAIN 917 975 LAMININ EGF-LIKE 9.
DOMAIN 976 1027 LAMININ EGF-LIKE 10.
DOMAIN 1028 1083 LAMININ EGF-LIKE 11.
DOMAIN 1084 1131 LAMININ EGF-LIKE 12.
DOMAIN 1132 1178 LAMININ EGF-LIKE 13.
DOMAIN 1179 1397 DOMAIN II.
DOMAIN 1398 1430 DOMAIN ALPHA.
DOMAIN 1431 1786 DOMAIN I.
DOMAIN 1216 1315 COILED COIL (POTENTIAL).
DOMAIN 1368 1388 COILED COIL (POTENTIAL).
DOMAIN 1448 1778 COILED COIL (POTENTIAL).
DISULFID 271 280 BY SIMILARITY.
DISULFID 273 298 BY SIMILARITY.
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DISULFID 806 818 BY SIMILARITY.
DISULFID 821 833 BY SIMILARITY.
DISULFID 823 840 BY SIMILARITY.
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DISULFID 854 864 BY SIMILARITY.
DISULFID 867 876 BY SIMILARITY.
DISULFID 869 883 BY SIMILARITY.
DISULFID 886 895 BY SIMILARITY.

FT DISULFID 898 914 BY SIMILARITY.
FT DISULFID 917 933 BY SIMILARITY.
FT DISULFID 919 944 BY SIMILARITY.
FT DISULFID 946 955 BY SIMILARITY.
FT DISULFID 958 973 BY SIMILARITY.
FT DISULFID 976 990 BY SIMILARITY.
FT DISULFID 978 997 BY SIMILARITY.
FT DISULFID 1000 1009 BY SIMILARITY.
FT DISULFID 1012 1025 BY SIMILARITY.
FT DISULFID 1084 1096 BY SIMILARITY.
FT DISULFID 1086 1103 BY SIMILARITY.
FT DISULFID 1105 1114 BY SIMILARITY.
FT DISULFID 1117 1129 BY SIMILARITY.
FT DISULFID 1132 1144 BY SIMILARITY.
FT DISULFID 1134 1151 BY SIMILARITY.
FT DISULFID 1153 1162 BY SIMILARITY.
FT DISULFID 1165 1176 BY SIMILARITY.
FT DISULFID 1179 1179 INTERCHAIN (PROBABLE).
FT DISULFID 1182 1182 INTERCHAIN (PROBABLE).
FT DISULFID 1785 1785 INTERCHAIN (PROBABLE).
FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 519 519 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 677 677 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1041 1041 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1195 1195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1279 1279 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1336 1336 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1343 1343 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1487 1487 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1533 1533 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1542 1542 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1643 1643 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 1531 1534 SGNA -> MEMP (IN REF. 2).
FT CONFLICT 1749 1749 D -> N (IN REF. 2).
SQ SEQUENCE 1786 AA; 196904 MW; 846671B7BF41A474 CRC64;
Query Match 100.0%; Score 9758; DB 1; Length 1786;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLLQVFAFGVLALWGTRVCAQEPEFSYGAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60
DB 1 MGLLQVFAFGVLALWGTRVCAQEPEFSYGAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60
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QY 181 PMKKVDDIIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLLKITNLRKFVKL 240
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DB 301 RHNTKGLNCELMDFYHDLPRPAEGRNSNACKKCNCSHSSCHFDMAVFLATGNVSGG 360
QY 361 VCDNCQHTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVG 420
DB 361 VCDNCQHTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVG 420
QY 421 LIAGQCRCKLHVEGERCDVCKEGFYDLSEAEDPYGCKSCACNPLGTIPGGNCPDSETGYCY 480
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721 SGdgeVtNSAwETfQRYrCLenSRsvvKtPMTdVCRNIIFsISALIHQTGLACECDPQGS 780
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1501 RNLIKQIRNFELTSADLDSIEAVANEVLKSGNASTPQQLQNLTDIRERVETLSQVEVI 1560
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1561 LQQSAADIARAEALLLEAKRASKSATDVKVTADMVKEALEEAERAKAIAKQADEDI 1620

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1621 QGTQNLTSIESETAASEETLTNASQRIKSLERNVEELKRKAQNSGEAEYIEKVVSVK 1680
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1681 QNADDVKKTLdGELdEKYKkVESLIaQKTEESADARRKAEllQNEAKTLlAQANSKLQll 1740
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1741 EDLERKYEDNQKYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1786
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RESULT 2
LMB1_HUMAN STANDARD; PRT; 1786 AA.
ID LMB1_HUMAN
AC P07942;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Laminin beta-1 chain precursor (Laminin B1 chain).
GN LAMB1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90368768; PubMed=1975589;
RA Vuolteenaho R., Chow L.T., Tryggvason K.;
RT "Structure of the human laminin B1 chain gene.";
RL J. Biol. Chem. 265:15611-15616(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87280097; PubMed=3611077;
RA Pikkariainen T., Eddy R., Fukushima Y., Byers M., Shows T.,
RA Pihlajaniemi T., Saraste M., Tryggvason K.;
RT "Human laminin B1 chain. A multidomain protein with gene (LAMB1)
RT locus in the q22 region of chromosome 7.";
RL J. Biol. Chem. 262:10454-10462(1987).
RN [3]
RP SEQUENCE OF 1276-1709 FROM N.A.
RX MEDLINE=88021029; PubMed=3661559;
RA Jaye M., Modi W.S., Ricca G.A., Mudd R., Chiu I.M., O'Brien S.J.,
RA Drohan W.N.;
RT "Isolation of a cDNA clone for the human laminin-B1 chain and its
RT gene localization.";
RL Am. J. Hum. Genet. 41:605-615(1987).
CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components.
CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC different polypeptide chains (alpha, beta, gamma), which are bound
CC to each other by disulfide bonds into a cross-shaped molecule
CC comprising one long and three short arms with globules at each
CC end. The beta-1 chain is a subunit of laminin-1 (EHS laminin),
CC laminin-2 (merosin), and laminin-6 (K-laminin).
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Found in the basement membranes (major
CC component).
CC -!- DOMAIN: The alpha-helical domains I and II are thought to interact
CC with other laminin chains to form a coiled coil structure.
CC -!- DOMAIN: Domains VI and IV are globular.
CC -!- SIMILARITY: Contains 1 laminin N-terminal domain.
CC -!- SIMILARITY: Contains 13 laminin EGF-like domains.
CC -!- SIMILARITY: Contains 1 laminin IV domain.

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----

CC EMBL; M61951; AAA59486.1; JOINED.
CC EMBL; M58147; AAA59486.1; JOINED.
CC EMBL; M61917; AAA59486.1; JOINED.
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CC EMBL; M61916; AAA59482.1; JOINED.
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DR EMBL; M20206; AAA59487.1; --
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DR HSSP; P02468; 1KLO.
DR Genew; HGNC:6486; LAMB1.
DR MIM; 150240; --
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR008211; LamNT.
DR Pfam; PF00053; laminin_EGF; 13.
DR Pfam; PF00055; laminin_Nterm; 1.
DR PRINTS; PR00011; EGFLAMININ.
DR SMART; SM00180; EGF_Lam; 12.
DR SMART; SM00136; LamNT; 1.
DR PROSITE; PS00022; EGF_1; 9.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01248; LAMININ TYPE EGF; 11.
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal; Polymorphism.
FT SIGNAL 1 21
FT CHAIN 22 1786 LAMININ BETA-1 CHAIN.
FT DOMAIN 22 270 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 271 334 LAMININ EGF-LIKE 1.
FT DOMAIN 335 397 LAMININ EGF-LIKE 2.
FT DOMAIN 398 457 LAMININ EGF-LIKE 3.
FT DOMAIN 458 509 LAMININ EGF-LIKE 4.
FT DOMAIN 510 540 LAMININ EGF-LIKE 5 (INCOMPLETE).
FT DOMAIN 541 771 LAMININ DOMAIN IV.
FT DOMAIN 773 820 LAMININ EGF-LIKE 6.
FT DOMAIN 821 866 LAMININ EGF-LIKE 7.
FT DOMAIN 867 916 LAMININ EGF-LIKE 8.
FT DOMAIN 917 975 LAMININ EGF-LIKE 9.
FT DOMAIN 976 1027 LAMININ EGF-LIKE 10.
FT DOMAIN 1028 1083 LAMININ EGF-LIKE 11.
FT DOMAIN 1084 1131 LAMININ EGF-LIKE 12.
FT DOMAIN 1132 1178 LAMININ EGF-LIKE 13.
FT DOMAIN 1179 1397 DOMAIN II.
FT DOMAIN 1398 1430 DOMAIN ALPHA.
FT DOMAIN 1431 1786 DOMAIN I.
FT DOMAIN 1216 1315 COILED COIL (POTENTIAL).
FT DOMAIN 1353 1388 COILED COIL (POTENTIAL).
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Query Match		93.7%;	Score 9144;	DB 1;	Length 1786;
Best Local Similarity		92.7%;	Pred. No. 0;		
Matches 1655;		Conservative	72;	Mismatches	59; Indels 0; Gaps 0;
QY	1	MGLLQVFAFGVLAALMGTRVCAQEPESYGCAGSCYPATGDLIGRAQKLSVTSTCGLHK	60		
Db	1	MGLLQVFAFGVLAALMGTRVCAQEPESYGCAGSCYPATGDLIGRAQKLSVTSTCGLHK	60		
QY	61	PEPYCIVSHLQEDKCFICDSRDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVEN	120		
Db	61	PEPYCIVSHLQEDKCFICDSRDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVEN	120		
QY	121	VTIQLDLAEFHTHLIMTFKTRPAAMLIERSSDFGKTGWVRYFAYDCESSFPGISG	180		
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QY	181	PMKKVDDIICDSRYSDIEPSTEGEVIFRALDPFAFKIEDPYSPRIQNLLKITNLRIKFVKL	240		
Db	181	PMKKVDDIICDSRYSDIEPSTEGEVIFRALDPFAFKIEDPYSPRIQNLLKITNLRIKFVKL	240		
QY	241	HTLGDNLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGVNEEVEGMVGHCMC	300		
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Db	361	VCDNCQHTMGRNCECKPFYFOHPERDIRPNLCEPCTCDPAGSENGGICDGYTDFSVG	420		
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QY	481	CKRLVTGQRCDQCLPOHFWGLSNDLDGCRPCDCLGGALNNSCSEDSGQCSCLPHMIGRQC	540		
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QY	1381	LAGKLQSLDLSAAQMTCTGTPPGADCSSECGPNCRCTDEGEKCGGCGGLVTVAHSA	1440		
Db	1381	LAGKLQSLDLSAAQMTCTGTPPGADCSSECGPNCRCTDEGEKCGGCGGLVTVAHSA	1440		
QY	1441	WQKAMDFDRDVLALAEVEQLSKMVSEAKVRADEAKQNAQDVLTKNATKEKVDKSNEDL	1500		
Db	1441	WQKAMDFDRDVLALAEVEQLSKMVSEAKVRADEAKQNAQDVLTKNATKEKVDKSNEDL	1500		
QY	1501	RNLIKQIRNFELTDSADLDSIEAVANEVLKSGNASTPQQLQNLNLTEDIRERVETLSQVEVI	1560		
Db	1501	RNLIKQIRNFELTDSADLDSIEAVANEVLKSGNASTPQQLQNLNLTEDIRERVETLSQVEVI	1560		
QY	1561	LQOASADIARAEALLLEAKRASKSATDVKTADVMVKEALEEAEKAQVAEKAQKQADEDI	1620		
Db	1561	LQOASADIARAEALLLEAKRASKSATDVKTADVMVKEALEEAEKAQVAEKAQKQADEDI	1620		
QY	1621	QGTQNLTSIESETAASEETLTNASQRISELRNVEELKRKAAQNSGEAEVIEKVYSVK	1680		
Db	1621	QGTQNLTSIESETAASEETLTNASQRISELRNVEELKRKAAQNSGEAEVIEKVYSVK	1680		
QY	1681	QNAADVKKTLGDELDEKYKKVESLIAQKTESADARRKAEALLQNEAKTLAQANSKLQLL	1740		
Db	1681	QNAADVKKTLGDELDEKYKKVESLIAQKTESADARRKAEALLQNEAKTLAQANSKLQLL	1740		
QY	1741	EDLERKYEDNQYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL	1786		
Db	1741	EDLERKYEDNQYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL	1786		

RESULT 3
LMB2 RAT
ID LMB2_RAT STANDARD; PRT; 1801 AA.
AC P15800;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Laminin beta-2 chain precursor (S-laminin) (Laminin chain B3).
GN LAMB2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89159410; PubMed=2922051;
RA Hunter D.D., Shah V., Merlie J.P., Sanes J.R.;
RT "A laminin-like adhesive protein concentrated in the synaptic cleft of the neuromuscular junction."
RL Nature 338:229-234 (1989).

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:25:32 ; Search time 46.7946 Seconds

(without alignments)

10415.614 Million cell updates/sec

Title: US-10-037-182-12

Perfect score: 9429

Sequence: 1 EPYCIVSHLQEDKKCFICDS.....EVRSLKDISEKVAVYSTCL 1725

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_29Jan04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9429	100.0	1725	3 AAB19800	Aab19800 Mouse lam
2	9429	100.0	1725	3 AAB48451	Aab48451 Mouse lam
3	9429	100.0	1725	5 ABB81593	Abb81593 Mouse lam
4	9429	100.0	1786	3 AAB19799	Aab19799 Mouse lam
5	9429	100.0	1786	3 AAB48450	Aab48450 Mouse lam
6	9429	100.0	1786	5 ABB81592	Abb81592 Mouse lam
7	9363	99.3	1776	2 AAW50894	Aaw50894 Mouse lam
8	9307.5	98.7	1764	1 AAP91672	Aap91672 Primary a
9	8873	94.1	1765	3 AAB19798	Aab19798 Human lam
10	8873	94.1	1765	3 AAB48449	Aab48449 Human lam
11	8873	94.1	1765	5 ABB81591	Abb81591 Human lam
12	8873	94.1	1786	2 AAW50893	Aaw50893 Human lam
13	8873	94.1	1786	3 AAB16522	Aab16522 Human lam
14	8873	94.1	1786	3 AAB19797	Aab19797 Human lam
15	8873	94.1	1786	3 AAB48448	Aab48448 Human lam
16	8873	94.1	1786	4 AAB90788	Aab90788 Human she
17	8873	94.1	1786	5 ABB81590	Abb81590 Human lam
18	8860	94.0	1786	5 AAM48896	Aam48896 Laminin p
19	8837.5	93.7	1785	2 AAY15461	Aay15461 Human lam
20	4936	52.3	1801	2 AAW50895	Aaw50895 Rat lamin
21	4936	52.3	1801	7 ADE60383	Ade60383 Rat Prote
22	4914	52.1	1799	5 AAM50359	Aam50359 Mouse lam
23	4890	51.9	1798	2 AAW50896	Aaw50896 Human lam
24	4890	51.9	1798	7 ADE60385	Ade60385 Human Pro
25	4778	50.7	1798	5 AAU84346	Aau84346 Protein L

26	4778	50.7	1798	5 AAM50360	Aam50360 Human lam
27	3736.5	39.6	1788	4 ABB62995	Abb62995 Drosophil
28	3712.5	39.4	1761	2 AAY15457	Aay15457 Human lam
29	3616	38.3	822	5 AAM48897	Aam48897 Laminin p
30	3506.5	37.2	1670	7 ADE07851	Ade07851 Novel pro
31	2967.5	31.5	1101	7 ADE28641	Ade28641 Human NOV
32	2945.5	31.2	1105	2 AAY15459	Aay15459 SEQ ID 5
33	2640	28.0	466	2 AAR07447	Aar07447 Human lam
34	2154	22.8	527	3 AAB58995	Aab58995 Breast an
35	1940	20.6	434	1 AAP60109	Aap60109 Human B1
36	1682.5	17.8	1639	4 ABB59807	Abb59807 Drosophil
37	1681	17.8	315	6 ABU70520	Abu70520 Human adi
38	1645	17.4	3712	4 ABB64954	Abb64954 Drosophil
39	1637.5	17.4	1572	3 AAB19806	Aab19806 Mouse lam
40	1637.5	17.4	1572	3 AAB48455	Aab48455 Mouse lam
41	1637.5	17.4	1572	5 ABB81597	Abb81597 Mouse lam
42	1637.5	17.4	1605	3 AAB19805	Aab19805 Mouse lam
43	1637.5	17.4	1605	3 AAB48454	Aab48454 Mouse lam
44	1637.5	17.4	1605	5 ABB81596	Abb81596 Mouse lam
45	1622.5	17.2	1576	3 AAB19802	Aab19802 Human lam

ALIGNMENTS

RESULT 1

AAB19800

ID AAB19800 standard; protein; 1725 AA.

XX AAB19800;

XX 05-MAR-2001 (first entry)

XX Mouse laminin 2 mature beta-1 chain.

XX Laminin 2; mouse; nerve regeneration; angiogenic; cell adhesion;

XX degenerative muscle disorder; muscular dystrophy; cell therapy.

XX Mus musculus.

XX WO200066730-A2.

XX 09-NOV-2000.

XX 28-APR-2000; 2000WO-US011378.

XX 30-APR-1999; 99US-0131720P.

XX 15-JUN-1999; 99US-0139198P.

XX 12-JUL-1999; 99US-0143289P.

XX 24-SEP-1999; 99US-0155945P.

XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.

XX Yurchenco P;

XX WPI; 2000-687537/67.

XX N-PSDB; AAA88900.

XX Claim 5; Page 236-232; 305pp; English.

XX The present sequence is that of the mouse laminin 2 beta-1 chain mature

XX protein. Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and

XX gamma-1 (100 kDa) chains. It is thought to be specifically required for

XX stabilizing myotubes during skeletal muscle development, and for

XX preventing apoptosis. Genetic defects in human laminin 2 structure or

XX expression are associated with a major type of congenital muscular

XX dystrophy. Laminin 2 is also thought to be important in Schwann

XX cell/basal lamina interactions. The invention provides laminin 2 alpha-2,

XX beta-1 and gamma-1 chain polypeptides (see AAB19791-806) and the

CC	polynucleotides encoding them (see AAA88891-906), methods for making									
CC	recombinant laminin 2, cells that express recombinant laminin 2, and									
CC	methods for using purified laminin 2 for research and therapeutic									
CC	purposes including peripheral nerve regeneration, treatment of									
CC	degenerative muscle disorders, angiogenesis regulation, promoting cell									
CC	attachment and migration, ex vivo cell therapy, improving the take of									
CC	grafts, improving the biocompatibility of medical devices and preparing									
CC	improved culture devices and media									
XX										
SQ	Sequence 1725 AA;									
	Query Match	100.0%;	Score 9429;	DB 3;	Length 1725;					
	Best Local Similarity	100.0%;	Pred. No. 0;							
	Matches 1725;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;					
QY	1	EPYCIIVSHLOEDKCKFCIDSRDPYHETLNPD	SHLIENVVTFPAPNRLKIWWQSENGVENV	60						
Db	1	EPYCIIVSHLOEDKCKFCIDSRDPYHETLNPD	SHLIENVVTFPAPNRLKIWWQSENGVENV	60						
QY	61	TIQLDLEAEFHTLIMTFKTRPAAMLIERSSD	FGKTGWVRYFYAYDCSSFPFGISTGP	120						
Db	61	TIQLDLEAEFHTLIMTFKTRPAAMLIERSSD	FGKTGWVRYFYAYDCSSFPFGISTGP	120						
QY	121	MKKVDDIICDSRYSIDIEPSTEGEVI	FRALDPAFKIEDPYSPIQNLLKITNRIKFVKLH	180						
Db	121	MKKVDDIICDSRYSIDIEPSTEGEVI	FRALDPAFKIEDPYSPIQNLLKITNRIKFVKLH	180						
QY	181	TLGDNLLDSRMEIREKYYAYVYDMVVRGNC	FCYGHASECAPVDGWNVEEVEGMVHGCMCR	240						
Db	181	TLGDNLLDSRMEIREKYYAYVYDMVVRGNC	FCYGHASECAPVDGWNVEEVEGMVHGCMCR	240						
QY	241	HNTKGLNCEL	CMDFYHDL	PWRPAEGRNSACKKNCNEHSSSCHFDMAVFLATGNVSGV	300					
Db	241	HNTKGLNCEL	CMDFYHDL	PWRPAEGRNSACKKNCNEHSSSCHFDMAVFLATGNVSGV	300					
QY	301	CDNCQHTMGRNCEQCKPFYFQHPERDIR	PNLCEPCTCDPAGSENGGICDGYTDFS	360						
Db	301	CDNCQHTMGRNCEQCKPFYFQHPERDIR	PNLCEPCTCDPAGSENGGICDGYTDFS	360						
QY	361	IAGQCRCKLHVEGERCDVCKEGFYDLSA	EDPYGCKSCACNPLGTPGGN	PCDSETGYCYC	420					
Db	361	IAGQCRCKLHVEGERCDVCKEGFYDLSA	EDPYGCKSCACNPLGTPGGN	PCDSETGYCYC	420					
QY	421	KRLVTGQRCDQCL	POHFWGLSNDLDGCRPCDCLGGALNNS	CESDSGQCSCLPHMIGRQC	480					
Db	421	KRLVTGQRCDQCL	POHFWGLSNDLDGCRPCDCLGGALNNS	CESDSGQCSCLPHMIGRQC	480					
QY	481	EVESGYFTTLDHYTYEAEANLPGVVV	VERQYIQDRIPSWTGTGFRVPEGAYLEFFI	540						
Db	481	EVESGYFTTLDHYTYEAEANLPGVVV	VERQYIQDRIPSWTGTGFRVPEGAYLEFFI	540						
QY	541	DNIPYSMEYEILIRYEPQLPDHWEKAVIT	VQRP	KGKIPASSRCNGTVPDDDNQVVS	SPGS	600				
Db	541	DNIPYSMEYEILIRYEPQLPDHWEKAVIT	VQRP	KGKIPASSRCNGTVPDDDNQVVS	SPGS	600				
QY	601	RYVVLPRPVC	FEKGMNVTYRLELPQYTASGSDVES	SPYTFIDSLVLMPYCKSLDIFT	VGGS	660				
Db	601	RYVVLPRPVC	FEKGMNVTYRLELPQYTASGSDVES	SPYTFIDSLVLMPYCKSLDIFT	VGGS	660				
QY	661	GDGEVNTSAWET	FORVRCLENSRSVVKTPMTDVC	RNIIFSI	SALIHQTGLACECDPQ	QGS	720			
Db	661	GDGEVNTSAWET	FORVRCLENSRSVVKTPMTDVC	RNIIFSI	SALIHQTGLACECDPQ	QGS	720			
QY	721	SSVCDP	NGGQCQCRPNVVGRTCNRCAPGTF	FGP	NGCKPCDCHLQGS	ASAFCAIT	QCH	780		
Db	721	SSVCDP	NGGQCQCRPNVVGRTCNRCAPGTF	FGP	NGCKPCDCHLQGS	ASAFCAIT	QCH	780		
QY	781	CFQGIYARQC	DRCLPGYWGFPSCQPCQCNGHALD	CDT	VTGEC	LS	CDYTTGHN	CER	CLAG	840
Db	781	CFQGIYARQC	DRCLPGYWGFPSCQPCQCNGHALD	CDT	VTGEC	LS	CDYTTGHN	CER	CLAG	840
QY	841	YGDPIIGSGDHCR	PCPDGPD	SGRQFARSCYQDPVTL	QLACVCDPGYIGSR	CDDC	CASG	900		
Db	841	YGDPIIGSGDHCR	PCPDGPD	SGRQFARSCYQDPVTL	QLACVCDPGYIGSR	CDDC	CASG	900		

Db	841	YYGDPIIGSGDHCR	PCPCPDGPD	SGRQFARSCYQDPVTL	QLACVCDPGYIGSR	CDDC	CASG	900
QY	901	FFGNPSDFGSGCQPCQCHNIDT	TDPEACDKOTGRCLKCLYHTEGDH	CQLCQYGYGDAL	960			
Db	901	FFGNPSDFGSGCQPCQCHNIDT	TDPEACDKOTGRCLKCLYHTEGDH	CQLCQYGYGDAL	960			
QY	961	RQDCRKVCNYLGT	VKEHCNGSDCHCDKATGCSCSLPNVIGQNC	DRCAPNTWQLASGTGC	1020			
Db	961	RQDCRKVCNYLGT	VKEHCNGSDCHCDKATGCSCSLPNVIGQNC	DRCAPNTWQLASGTGC	1020			
QY	1021	GPCNCNAHSFGPSCNEFTGQCQCMPGFGGRT	CSECQELFWGDDP	VECRACD	CDPRGIET	1080		
Db	1021	GPCNCNAHSFGPSCNEFTGQCQCMPGFGGRT	CSECQELFWGDDP	VECRACD	CDPRGIET	1080		
QY	1081	PQCDQSTGQVCVEGVEGPRCDKCTRGYSGVFPD	CTPCHQCFALWD	AIIGELTNR	THKFL	1140		
Db	1081	PQCDQSTGQVCVEGVEGPRCDKCTRGYSGVFPD	CTPCHQCFALWD	AIIGELTNR	THKFL	1140		
QY	1141	EKAKALKISGVIGPYRETVD	SVVEKKVNEIKDILAQSPAAEPLKNIGILFEEAEKLT	KDVT	1200			
Db	1141	EKAKALKISGVIGPYRETVD	SVVEKKVNEIKDILAQSPAAEPLKNIGILFEEAEKLT	KDVT	1200			
QY	1201	EKMAQVEVKLTDTASQSNSTAGELGALQAE	ESLDKTVKELAEQLEFIKNSDIQ	GALDSI	1260			
Db	1201	EKMAQVEVKLTDTASQSNSTAGELGALQAE	ESLDKTVKELAEQLEFIKNSDIQ	GALDSI	1260			
QY	1261	TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVED	LMLERESPFEKEQEEQARLLDEL	1320				
Db	1261	TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVED	LMLERESPFEKEQEEQARLLDEL	1320				
QY	1321	AGKLQSLDLSAAAQMTCTGTPPGAD	CSECECGGNCR	TDEGEKKCGGPGCGGLVTVAHSAW	1380			
Db	1321	AGKLQSLDLSAAAQMTCTGTPPGAD	CSECECGGNCR	TDEGEKKCGGPGCGGLVTVAHSAW	1380			
QY	1381	QKAMDFDRDVL	SALAEVEQLSKMVSEAKVR	ADEAKQNAQDVLLKTNATKEKVDKSNEDLR	1440			
Db	1381	QKAMDFDRDVL	SALAEVEQLSKMVSEAKVR	ADEAKQNAQDVLLKTNATKEKVDKSNEDLR	1440			
QY	1441	NLIKQIRNFL	TEDSADLDSIEAVANEVLKSGNASTPQQLQNL	TEDIR	ERVETLSQVEVIL	1500		
Db	1441	NLIKQIRNFL	TEDSADLDSIEAVANEVLKSGNASTPQQLQNL	TEDIR	ERVETLSQVEVIL	1500		
QY	1501	QQSAADI	ARAEALLLEEAKRASKSATDVKVTADMVKEALEEAEKAQVAAEKAIKQADED	IQ	1560			
Db	1501	QQSAADI	ARAEALLLEEAKRASKSATDVKVTADMVKEALEEAEKAQVAAEKAIKQADED	IQ	1560			
QY	1561	GTQNL	LTSIESETAASEETLTNASQRISKLER	NVEELKRKAAQNSGEAEYIEKVVISVKQ	1620			
Db	1561	GTQNL	LTSIESETAASEETLTNASQRISKLER	NVEELKRKAAQNSGEAEYIEKVVISVKQ	1620			
QY	1621	NADDVKKTLDGEL	DEKYYKKVESLIAQKTEESADARRKAE	LLQNEAKTLLAQANSKIQLLE	1680			
Db	1621	NADDVKKTLDGEL	DEKYYKKVESLIAQKTEESADARRKAE	LLQNEAKTLLAQANSKIQLLE	1680			
QY	1681	DLERKYEDNQKYLE	DKAQELVRLEGEVRSLLKDI	SEKVAVYSTCL	1725			
Db	1681	DLERKYEDNQKYLE	DKAQELVRLEGEVRSLLKDI	SEKVAVYSTCL	1725			

RESULT 2
AAB48451
ID AAB48451 standard; protein; 1725 AA.
XX
AC AAB48451;
XX
DT 02-MAR-2001 (first entry)
XX
DE Mouse laminin 8 polypeptide, SEQ ID NO: 20.
XX
KW Mouse; laminin 8; neuroprotective; angiogenic; osteopathic;
KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;
KW vascular tissue injury; neural injury; angiogenesis regulation.
XX

OS Mus musculus.
XX WO20006732-A2.
XX PD 09-NOV-2000.
XX 28-APR-2000; 2000WO-US011543.
XX 30-APR-1999; 99US-0131720P.
PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.
PR 11-FEB-2000; 2000US-0182012P.
XX (BIOS-) BIOSTRATUM INC.
PA Kortessmaa J, Tryggvason K;
XX WPI; 2000-687539/67.
DR N-PSDB; AAC83712.
XX Purified laminin 8 protein, useful for research and therapeutic purposes
PT including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.
XX Claim 5; Page 189-194; 245pp; English.
XX The present sequence is a laminin 8 polypeptide chain. Laminins are a
CC family of heterotrimeric glycoproteins that function via binding
CC interactions with neighbouring cell receptors and by forming laminin
CC networks. They are signalling molecules which influence cellular
CC function. Laminin 8 is useful for treating injuries to tissue of
CC mesenchymal origin, such as bone, cartilage, tendon, and ligament,
CC treating injuries to vascular tissue, promoting cell attachment and
CC migration, ex vivo cell therapy, improving the biocompatibility of
CC medical devices, and preparing improved cell culture devices and media.
CC Laminin 8 is also useful for promoting re-endothelialisation at the site
CC of vascular injuries, improving the take of grafts, improving the
CC biocompatibility of medical devices, treating neural injuries (neural
CC regeneration), regulating angiogenesis, and promoting cell attachment and
CC migration
XX Sequence 1725 AA;
Query Match 100.0%; Score 9429; DB 3; Length 1725;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 1725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EPYCIIVSHLOEDKKCFICDSRDPYHETLNPDLSHLIENVTTFAPNRLKIWQSENGVENV 60
Db 1 EPYCIIVSHLOEDKKCFICDSRDPYHETLNPDLSHLIENVTTFAPNRLKIWQSENGVENV 60
QY 61 TIQLDLEAEFFHFLIMTFKTFRPAAMLIERSDDFGKTGWVRYRYPAYDCESFPFGISTGP 120
Db 61 TIQLDLEAEFFHFLIMTFKTFRPAAMLIERSDDFGKTGWVRYRYPAYDCESFPFGISTGP 120
QY 121 MKKVDDIIICDSRYSDIPEPSTEGEVIFRALDPAPFKIEDPYSPRIONLLKITNLRKFKVLH 180
Db 121 MKKVDDIIICDSRYSDIPEPSTEGEVIFRALDPAPFKIEDPYSPRIONLLKITNLRKFKVLH 180
QY 181 TLGDNLLDSRMEIREKYVYAYVDMVVRGNCFCYGHASECAPVDGVNVEEVEGMVHGCMCR 240
Db 181 TLGDNLLDSRMEIREKYVYAYVDMVVRGNCFCYGHASECAPVDGVNVEEVEGMVHGCMCR 240
QY 241 HNTKGLNCELMDVFYHDLFWRPAEGRNSNACKKNCNEHSSSCHFDMAVFLATGNVSGV 300
Db 241 HNTKGLNCELMDVFYHDLFWRPAEGRNSNACKKNCNEHSSSCHFDMAVFLATGNVSGV 300
QY 301 CDNCQHTMGRNCEQCKPFYFQHPERDIRDNLCEPCTCDPAGSENGGICDGYTDFSVGL 360
Db 301 CDNCQHTMGRNCEQCKPFYFQHPERDIRDNLCEPCTCDPAGSENGGICDGYTDFSVGL 360
QY 361 IAGQCRCKLHVGEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGNCPCDSETGYCYC 420

Db 361 IAGQCRCKLHVGEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGNCPCDSETGYCYC 420
QY 421 KRLVTGORCDQCLPOHWGLSNDLDGCRPCDDCLGGALNNSCEDSGCCSCLPHMIGRQCN 480
Db 421 KRLVTGORCDQCLPOHWGLSNDLDGCRPCDDCLGGALNNSCEDSGCCSCLPHMIGRQCN 480
QY 481 EVESGYFTTLDHYIYEAEZANLPGVYVVERQYIQDIRIPSWTGPVVRVPEGAYLEFFI 540
Db 481 EVESGYFTTLDHYIYEAEZANLPGVYVVERQYIQDIRIPSWTGPVVRVPEGAYLEFFI 540
QY 541 DNIPYSMEYEILIRYEPOLPDHWEKAVITVORPGKIPASSRCGNTVDDDDNQVVSLSPGS 600
Db 541 DNIPYSMEYEILIRYEPOLPDHWEKAVITVORPGKIPASSRCGNTVDDDDNQVVSLSPGS 600
QY 601 RYVVLPRPVCFEKGMNYTVRLELPQYTASGSDVESPYTFIDSLVLMPCYCKSLDIFTVGG 660
Db 601 RYVVLPRPVCFEKGMNYTVRLELPQYTASGSDVESPYTFIDSLVLMPCYCKSLDIFTVGG 660
QY 661 GDGEVNTSAWETFQYRCLENSRSVVKTPMTDVCNIIIFSALIHQITGLACECDPQGS 720
Db 661 GDGEVNTSAWETFQYRCLENSRSVVKTPMTDVCNIIIFSALIHQITGLACECDPQGS 720
QY 721 SSVCDPNGGQCQCRPNVVGRTCNRCAPGTGFGPNGCKPCDCHLQGSASAFCDAITGQCH 780
Db 721 SSVCDPNGGQCQCRPNVVGRTCNRCAPGTGFGPNGCKPCDCHLQGSASAFCDAITGQCH 780
QY 781 CFQGIYARQCRCPLPGYWGFPSCQPCQCNHGHALDCDVTGECSCQDYTTGHNCRCLAG 840
Db 781 CFQGIYARQCRCPLPGYWGFPSCQPCQCNHGHALDCDVTGECSCQDYTTGHNCRCLAG 840
QY 841 YYGDPPIIGSGDHCRPCPCPDGPDGSRGRQFARSCYQDPVTLQLACVCDPGYIGSRCDCCASG 900
Db 841 YYGDPPIIGSGDHCRPCPCPDGPDGSRGRQFARSCYQDPVTLQLACVCDPGYIGSRCDCCASG 900
QY 901 FFGNPSDFGSGCQPCQCHHNIDTTDPEACDKTGRCLKLYHTEGDHCLCQYGYGDAL 960
Db 901 FFGNPSDFGSGCQPCQCHHNIDTTDPEACDKTGRCLKLYHTEGDHCLCQYGYGDAL 960
QY 961 RQDCRKVCNYLGTVKEHCNGSDCHCDKATGQCSCLPNVIGQNCDCRACNTWQLASGTGC 1020
Db 961 RQDCRKVCNYLGTVKEHCNGSDCHCDKATGQCSCLPNVIGQNCDCRACNTWQLASGTGC 1020
QY 1021 GPCNCAHSAHSGPCSCNEFTGQCQCMPGFGGRTCECQELFWGDPDVECRACDCDPRGIET 1080
Db 1021 GPCNCAHSAHSGPCSCNEFTGQCQCMPGFGGRTCECQELFWGDPDVECRACDCDPRGIET 1080
QY 1081 PQCDQSTGQCVCVEGVEGPRCDKCTRGYSGVFPDCTPCHQCFCALWDALIGELTNRTHKFL 1140
Db 1081 PQCDQSTGQCVCVEGVEGPRCDKCTRGYSGVFPDCTPCHQCFCALWDALIGELTNRTHKFL 1140
QY 1141 EKAKALKISGVIGPYRETVDVSVEKKVNEIKDILAQSPAAPLKNIGILFEEAEKLT KDVT 1200
Db 1141 EKAKALKISGVIGPYRETVDVSVEKKVNEIKDILAQSPAAPLKNIGILFEEAEKLT KDVT 1200
QY 1201 EKMAQVEVKLTDTASQSNSTAGELGALQAEAESLDKTVKELAEQLEFKNSDIQGALDSI 1260
Db 1201 EKMAQVEVKLTDTASQSNSTAGELGALQAEAESLDKTVKELAEQLEFKNSDIQGALDSI 1260
QY 1261 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRDVEDLMLERESPFKEQEEQARLLDEL 1320
Db 1261 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRDVEDLMLERESPFKEQEEQARLLDEL 1320
QY 1321 AGKLSLDLSAAQMTCGTPPGADCSSECCGPNCRDTEGEKKCGGPGCGGLVTVAHSAW 1380
Db 1321 AGKLSLDLSAAQMTCGTPPGADCSSECCGPNCRDTEGEKKCGGPGCGGLVTVAHSAW 1380
QY 1381 QKAMDFDRDVL SALAEVEQLSKMVSEAKVRADAEAKQNAQDVLLKTNATKEVKDSNEDLR 1440
Db 1381 QKAMDFDRDVL SALAEVEQLSKMVSEAKVRADAEAKQNAQDVLLKTNATKEVKDSNEDLR 1440
QY 1441 NLIKQIRNFLTSDSADLDSIEAVANEVLKSGNASTPQQLQNLNLTEDIRERVETLSQVEVIL 1500
Db 1441 NLIKQIRNFLTSDSADLDSIEAVANEVLKSGNASTPQQLQNLNLTEDIRERVETLSQVEVIL 1500

QY 1501 QQSAADIAPAEILLLEAKRASKSATDVKVTADVMVKEALEEAEKAQVAEKAQKQADEDIQ 1560
Db 1501 QQSAADIAPAEILLLEAKRASKSATDVKVTADVMVKEALEEAEKAQVAEKAQKQADEDIQ 1560
QY 1561 GTQNLLTSIESETAASEETLTNASQRISKLERNVVEELKRAAQNSGEAEYIEKVYYSVKQ 1620
Db 1561 GTQNLLTSIESETAASEETLTNASQRISKLERNVVEELKRAAQNSGEAEYIEKVYYSVKQ 1620
QY 1621 NADDVKKTLDGELDEKYYKKVESLIAQKTEESADARRKAEILLQNEAKTLLAQANSKLQILLE 1680
Db 1621 NADDVKKTLDGELDEKYYKKVESLIAQKTEESADARRKAEILLQNEAKTLLAQANSKLQILLE 1680
QY 1681 DLERKYEDNQKYLEDKAQELVRLGEVRSLLKLDISEKVAVYSTCL 1725
Db 1681 DLERKYEDNQKYLEDKAQELVRLGEVRSLLKLDISEKVAVYSTCL 1725

RESULT 3
ABB81593
ID ABB81593 standard; protein; 1725 AA.
XX
AC ABB81593;
XX
DT 19-SEP-2002 (first entry)
XX
DE Mouse laminin 10 second chain protein sequence SEQ ID NO:12.
XX
KW Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;
KW tissue repair development; laminin; healing; vascular tissue;
KW re-endothelialisation; vascular injury; cell attachment; cell stasis;
KW proliferation; migration.
XX
OS Mus musculus.
XX
PN WO200250111-A2.
XX
PD 27-JUN-2002.
XX
PF 21-DEC-2001; 2001WO-US051035.
XX
PR 21-DEC-2000; 2000US-0257449P.
PR 28-MAR-2001; 2001US-0279282P.
PR 13-NOV-2001; 2001US-00279282.
XX
PA (BIOS-) BIOSTRATUM INC.
XX
PI Tryggvason K, Doi M, Thyboll J;
XX
DR WPI; 2002-557650/59.
DR N-PSDB; ABQ72911.
XX
PT New human laminin-10 proteins, useful for accelerating the healing of
PT vascular tissue, improving the biocompatibility of grafts, or for
PT promoting re-endothelialization at the site of vascular injuries.
XX
PS Claim 9; Page 153-158; 231pp; English.
XX

The present invention describes human laminin alpha 5. Also described is an isolated laminin 10. Laminin 10 has vulnery activity. Laminins are useful in maintaining cell/tissue phenotype as well as promoting cell growth and differentiation in tissue repair development. Specifically, laminin 10 can be used for accelerating the healing injuries of vascular tissue, improving the biocompatibility of grafts useful for treating such injuries, for promoting re-endothelialisation at the site of vascular injuries, and promote cell attachment and subsequent cell stasis, proliferation, differentiation, and/or migration. The present sequence represents a second chain protein of laminin 10, from the present invention

Sequence 1725 AA;

Query Match 100.0%; Score 9429; DB 5; Length 1725;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EPYCIVSHLQEDKKCFICDSRDPYHETLNPDLSHLIENVVTFAPNRLKIWQSENGVENV 60
Db 1 EPYCIVSHLQEDKKCFICDSRDPYHETLNPDLSHLIENVVTFAPNRLKIWQSENGVENV 60
QY 61 TIQDLAEAFHFTLIMTFKTFPAAMLIERSSDFGKTGWYRYFAYDCSSFPGISGTP 120
Db 61 TIQDLAEAFHFTLIMTFKTFPAAMLIERSSDFGKTGWYRYFAYDCSSFPGISGTP 120
QY 121 MKKVDDIICDSRYSDIEPSTEGEVIFFRALDPAFKIEDPYSRIQNLKITNLRIKFVKLH 180
Db 121 MKKVDDIICDSRYSDIEPSTEGEVIFFRALDPAFKIEDPYSRIQNLKITNLRIKFVKLH 180
QY 181 TLGDNLLDSRMEIREKYYVAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCHMCR 240
Db 181 TLGDNLLDSRMEIREKYYVAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCHMCR 240
QY 241 HNTKGLNCELMDIFYHDLPRPAEGRNSNACKKNCNEHSSCHFDMAVFLATGNVSGGV 300
Db 241 HNTKGLNCELMDIFYHDLPRPAEGRNSNACKKNCNEHSSCHFDMAVFLATGNVSGGV 300
QY 301 CDNCOHNTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 360
Db 301 CDNCOHNTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 360
QY 361 IAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGPNPCDSETGYCYC 420
Db 361 IAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGPNPCDSETGYCYC 420
QY 421 KRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCDLGGALNNSCSEDSGCCSCLPHMIGRQCN 480
Db 421 KRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCDLGGALNNSCSEDSGCCSCLPHMIGRQCN 480
QY 481 EVESGYFTTLDHYIYEAEAEANLGPVWVVERQYIQDRIPSWTGPFRVPEGAYLEFFI 540
Db 481 EVESGYFTTLDHYIYEAEAEANLGPVWVVERQYIQDRIPSWTGPFRVPEGAYLEFFI 540
QY 541 DNIPYSMEYEILIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTVPDDNQVLSLSPGS 600
Db 541 DNIPYSMEYEILIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTVPDDNQVLSLSPGS 600
QY 601 RYVVLPRPVCFEKGMNYYTVRLELPQYTAGSDVESPYTFIDSLVLMYPYCKSLDIFTVGS 660
Db 601 RYVVLPRPVCFEKGMNYYTVRLELPQYTAGSDVESPYTFIDSLVLMYPYCKSLDIFTVGS 660
QY 661 GDGEVTSAWETFORYLENSRSVVKTPMTDVCNRIIFSISALIHQTGLACECDPQGS 720
Db 661 GDGEVTSAWETFORYLENSRSVVKTPMTDVCNRIIFSISALIHQTGLACECDPQGS 720
QY 721 SSVCDPNGGQCQCRPNVVGRTCNRCAPGTFFGPNCKPCDCHLQGSASAFCDAITGQCH 780
Db 721 SSVCDPNGGQCQCRPNVVGRTCNRCAPGTFFGPNCKPCDCHLQGSASAFCDAITGQCH 780
QY 781 CFQGIYARQCDRCLPGYWGFPSCQPCQCNHGDCTVTGECISCDQYTTGHNCRCLAG 840
Db 781 CFQGIYARQCDRCLPGYWGFPSCQPCQCNHGDCTVTGECISCDQYTTGHNCRCLAG 840
QY 841 YGDPPIIGSGDHCRPCPCPDGPDGSRQFARSCYQDPVTLQACVCDPQYIGSRCDDCASG 900
Db 841 YGDPPIIGSGDHCRPCPCPDGPDGSRQFARSCYQDPVTLQACVCDPQYIGSRCDDCASG 900
QY 901 FFGNPSDFGSGCQPCQCHNIDTTDPEACDKDTGRCLKCLVHTEGDHQCQLCYGYGDDAL 960
Db 901 FFGNPSDFGSGCQPCQCHNIDTTDPEACDKDTGRCLKCLVHTEGDHQCQLCYGYGDDAL 960
QY 961 RQDCRKCVCNVLGTVKEHCNCGSDCHCDKATGQCSCLPNVIGQNCRCAPNTWQLASGTGC 1020
Db 961 RQDCRKCVCNVLGTVKEHCNCGSDCHCDKATGQCSCLPNVIGQNCRCAPNTWQLASGTGC 1020
QY 1021 GPCNCNAAHSFPGSCNEFTGQCQCMFPGGRTCSCEQELFWGDDVECRACDCDPRGIET 1080

Db 1021 GPCNAAHSFGPSCNEFTGQCQMPGFGGRTSCSEQELFWGDPDVECRACDCDPRGIET 1080
Qy 1081 PQCDQSTGQCVCVEGVEGPRCDKCTRGYSGVFPDCTPCHQCQFALWDAIIGELTNRTHKFL 1140
Db 1081 PQCDQSTGQCVCVEGVEGPRCDKCTRGYSGVFPDCTPCHQCQFALWDAIIGELTNRTHKFL 1140
Qy 1141 EKAKALKISGVIQPYRETVDVSEKKVNEIKDILAQSPAAPLKNIGILFEEAEKLT KDVT 1200
Db 1141 EKAKALKISGVIQPYRETVDVSEKKVNEIKDILAQSPAAPLKNIGILFEEAEKLT KDVT 1200
Qy 1201 EKMAQVEVKLTDTASQSNSTAGELGALQAEAESLDKTVKELAEQLEFIKNSDIQGALDSI 1260
Db 1201 EKMAQVEVKLTDTASQSNSTAGELGALQAEAESLDKTVKELAEQLEFIKNSDIQGALDSI 1260
Qy 1261 TKYFQMSLEAEKRVNASITDPNSTVEQSALTRDRVEDLMLERESPFKEQEEQARLLDEL 1320
Db 1261 TKYFQMSLEAEKRVNASITDPNSTVEQSALTRDRVEDLMLERESPFKEQEEQARLLDEL 1320
Qy 1321 AKLQSLDLSAAQMTCTGPPGADCSSECGGPNCRTEGEKKCGGPGGGLVTVVAHSAW 1380
Db 1321 AKLQSLDLSAAQMTCTGPPGADCSSECGGPNCRTEGEKKCGGPGGGLVTVVAHSAW 1380
Qy 1381 QKAMDFDRDVL SALAEVEQLSKVSEAKVRADAEAKQNAQDVLLKTNATKEKVDKSNEDLR 1440
Db 1381 QKAMDFDRDVL SALAEVEQLSKVSEAKVRADAEAKQNAQDVLLKTNATKEKVDKSNEDLR 1440
Qy 1441 NLIKQIRNFLTEDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVIL 1500
Db 1441 NLIKQIRNFLTEDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVIL 1500
Qy 1501 QQSAADIARAELLLLEEAKRASKSATDVKVVTADMVKEALEEAEKAQVAEKAQKQADEDIQ 1560
Db 1501 QQSAADIARAELLLLEEAKRASKSATDVKVVTADMVKEALEEAEKAQVAEKAQKQADEDIQ 1560
Qy 1561 GTQNL LTSIESETAASEETLTNASQRISKLERNVEELKRKAAQNSGEAEYIEKVVSVKQ 1620
Db 1561 GTQNL LTSIESETAASEETLTNASQRISKLERNVEELKRKAAQNSGEAEYIEKVVSVKQ 1620
Qy 1621 NADDVKKTLTGELDEKYYKVESLIAQKTEESADARRKAELLQNEAKTL LAQANSKLQ LLE 1680
Db 1621 NADDVKKTLTGELDEKYYKVESLIAQKTEESADARRKAELLQNEAKTL LAQANSKLQ LLE 1680
Qy 1681 DLERKYEDNQYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1725
Db 1681 DLERKYEDNQYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1725
RESULT 4
AAB19799
ID AAB19799 standard; protein; 1786 AA.
XX
AC AAB19799;
XX
DT 05-MAR-2001 (first entry)
XX
DE Mouse laminin 2 beta-1 chain.
XX
KW Laminin 2; mouse; nerve regeneration; angiogenic; cell adhesion;
degenerative muscle disorder; muscular dystrophy; cell therapy.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
Peptide 1. .21
FT /label= Signal_peptide
FT Protein 22. .1786
FT /label= Mature_protein
XX
PN WO2000066730-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US011378.

XX 30-APR-1999; 99US-0131720P.
PR 15-JUN-1999; 99US-0139198P.
PR 12-JUL-1999; 99US-0143289P.
PR 24-SEP-1999; 99US-0155945P.
XX
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
PI Yurchenco P;
XX
DR WPI; 2000-687537/67.
DR N-PSDB; AAA88899.
XX
PT Purified laminin 2 protein, useful for research and therapeutic purposes
including peripheral nerve regeneration, treatment of degenerative muscle
disorders, angiogenesis regulation, and ex vivo cell therapy.
XX
PS Claim 5; Page 212-218; 305pp; English.
XX
CC The present sequence is that of the beta-1 chain of mouse laminin 2.
CC Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1
CC (100 kDa) chains. It is thought to be specifically required for
CC stabilizing myotubes during skeletal muscle development, and for
CC preventing apoptosis. Genetic defects in human laminin 2 structure or
CC expression are associated with a major type of congenital muscular
CC dystrophy. Laminin 2 is also thought to be important in Schwann
CC cell/basal lamina interactions. The invention provides laminin 2 alpha-2,
CC beta-1 and gamma-1 chain polypeptides (see AAB19791-806) and the
CC polynucleotides encoding them (see AAA88891-906), methods for making
CC recombinant laminin 2, cells that express recombinant laminin 2, and
CC methods for using purified laminin 2 for research and therapeutic
CC purposes including peripheral nerve regeneration, treatment of
CC degenerative muscle disorders, angiogenesis regulation, promoting cell
CC attachment and migration, ex vivo cell therapy, improving the take of
CC grafts, improving the biocompatibility of medical devices and preparing
CC improved culture devices and media
XX
SQ Sequence 1786 AA;
Query Match 100.0%; Score 9429; DB 3; Length 1786;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EPYCIVSHLOEDKKCFICDSRDPYHETLNPDSHLIENVVTTFAPNRLKIWWQSENGVENV 60
Db 62 EPYCIVSHLOEDKKCFICDSRDPYHETLNPDSHLIENVVTTFAPNRLKIWWQSENGVENV 121
Qy 61 TIQLDLEAEFFHFTLMTFKTRPAAMLIERSDPFGKTGWVYRYFAYDCESFPFGISTGP 120
Db 122 TIQLDLEAEFFHFTLMTFKTRPAAMLIERSDPFGKTGWVYRYFAYDCESFPFGISTGP 181
Qy 121 MKKVDDDIICDSRYSDIEPSTEGEVIFRALDPAPFKIEDPSPRIQNLLKITNLRKIFVKLH 180
Db 182 MKKVDDDIICDSRYSDIEPSTEGEVIFRALDPAPFKIEDPSPRIQNLLKITNLRKIFVKLH 241
Qy 181 TLGDNLLDSRMEIREKYYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGHCPCR 240
Db 242 TLGDNLLDSRMEIREKYYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGHCPCR 301
Qy 241 HNTKGLNCEL CMDFYHDL PWRPAEGRNSNACKKNCNEHSSSCHFDMAVFLATGNVSGGV 300
Db 302 HNTKGLNCEL CMDFYHDL PWRPAEGRNSNACKKNCNEHSSSCHFDMAVFLATGNVSGGV 361
Qy 301 CDNCQHNTMGRNCEQCKPFYFQHPERDIRDNLCEPCTCDPAGSENGGICDGYTDFSVGL 360
Db 362 CDNCQHNTMGRNCEQCKPFYFQHPERDIRDNLCEPCTCDPAGSENGGICDGYTDFSVGL 421
Qy 361 IAGQCRCKLHVEGERCDVCKEGFYDL SAEDPYGCKSCACNPLGTIPGGNPCDSETGYCYC 420
Db 422 IAGQCRCKLHVEGERCDVCKEGFYDL SAEDPYGCKSCACNPLGTIPGGNPCDSETGYCYC 481
Qy 421 KRLVTGQRCDQCLPQHGLSNDLDGCRPCDCDILGALNNSCEDSGQCSCLPHMIGRQCN 480

Db 482 KRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCDLGGALNNSCEDSGQCSCLPHMIGRCQN 541
QY 481 EVESGYFTTLDHYIYEAEANLPGVVVVERQYIQDRIPSWTGPGRVVRPEGAYLEFFI 540
Db 542 EVESGYFTTLDHYIYEAEANLPGVVVVERQYIQDRIPSWTGPGRVVRPEGAYLEFFI 601
QY 541 DNIPYSMEYBILIRYEPQLPDHWEKAVITVQRPKIPASSRRCGNTVPDDDNQVVSLSPGS 600
Db 602 DNIPYSMEYBILIRYEPQLPDHWEKAVITVQRPKIPASSRRCGNTVPDDDNQVVSLSPGS 661
QY 601 RYVVLPRPVCFEKGMNYYTVRLELPQYTAGSDVESPYTFIDSLVLMPCYCKSLDIFTVGG 660
Db 662 RYVVLPRPVCFEKGMNYYTVRLELPQYTAGSDVESPYTFIDSLVLMPCYCKSLDIFTVGG 721
QY 661 GDGEVTSAWETFORYRCLENSRSVVKTPTMTDVCNIIIFSISALIHQTLGACECDPOGSL 720
Db 722 GDGEVTSAWETFORYRCLENSRSVVKTPTMTDVCNIIIFSISALIHQTLGACECDPOGSL 781
QY 721 SSVCDPNGGQCQCRPNVVGRTCNRCAPGTFGFGPNGCKPCDCHLQGSASAFCAITGQCH 780
Db 782 SSVCDPNGGQCQCRPNVVGRTCNRCAPGTFGFGPNGCKPCDCHLQGSASAFCAITGQCH 841
QY 781 CFQGIYARQDRCLPGYWGFPSPCQPCQCNHGLDCTVTGECILSCDYTTGHNCRCLAG 840
Db 842 CFQGIYARQDRCLPGYWGFPSPCQPCQCNHGLDCTVTGECILSCDYTTGHNCRCLAG 901
QY 841 YGDPPIIGSGDHCRPCPCPDGPDGSGRQFARSCYQDPVTQLACVCDPQYIGSRCDDCASG 900
Db 902 YGDPPIIGSGDHCRPCPCPDGPDGSGRQFARSCYQDPVTQLACVCDPQYIGSRCDDCASG 961
QY 901 FFGNPSDFGSCQPCQCHHNIDTTDPEACDKDTGRCLKCLYHTEGDHCQLCQYGYGDAL 960
Db 962 FFGNPSDFGSCQPCQCHHNIDTTDPEACDKDTGRCLKCLYHTEGDHCQLCQYGYGDAL 1021
QY 961 RQDCRKVCNVLGTVKEHNCNGSDCHCDKATGQCCLPNVIGQNCDCRCAPNTWQLASGTGC 1020
Db 1022 RQDCRKVCNVLGTVKEHNCNGSDCHCDKATGQCCLPNVIGQNCDCRCAPNTWQLASGTGC 1081
QY 1021 GPCNCNAHSPGSPSCNEFTGQCQCMPFGGRTCSECQELFWGDPDVECRACDCDPRGIET 1080
Db 1082 GPCNCNAHSPGSPSCNEFTGQCQCMPFGGRTCSECQELFWGDPDVECRACDCDPRGIET 1141
QY 1081 PQCDQSTGQCVCEGVGPRCDKCTRGYSGVFPDCTPCHQCPCALWDAIIGELTNRTHKFL 1140
Db 1142 PQCDQSTGQCVCEGVGPRCDKCTRGYSGVFPDCTPCHQCPCALWDAIIGELTNRTHKFL 1201
QY 1141 EKAKALKISGIVGIPYRETVDVSEKKNVNEIKDILAQSPAAEPLKNIGILFEEAEKLTKDVT 1200
Db 1202 EKAKALKISGIVGIPYRETVDVSEKKNVNEIKDILAQSPAAEPLKNIGILFEEAEKLTKDVT 1261
QY 1201 EKMAQVEVKLTDTASQSNSTAGELGALQAEAESLDKTVKELAEQLEFIKNSDIOGALDSI 1260
Db 1262 EKMAQVEVKLTDTASQSNSTAGELGALQAEAESLDKTVKELAEQLEFIKNSDIOGALDSI 1321
QY 1261 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLESPPFKEQEEQARLDEL 1320
Db 1322 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLESPPFKEQEEQARLDEL 1381
QY 1321 AGKLOSLDLSAAQMTCTGTPPGADCSSECGGNCRCTDEGEKKCGGPGCGGLVTVAHSAW 1380
Db 1382 AGKLOSLDLSAAQMTCTGTPPGADCSSECGGNCRCTDEGEKKCGGPGCGGLVTVAHSAW 1441
QY 1381 QKAMDFDRDVLASALAEVQLSKMVSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDLR 1440
Db 1442 QKAMDFDRDVLASALAEVQLSKMVSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDLR 1501
QY 1441 NLIKQIRNFLTSDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVIL 1500
Db 1502 NLIKQIRNFLTSDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVIL 1561
QY 1501 QQSAADIARAEILLLEAKRASKSATDVKTADMVKEALEEAEKAQVAEAKAIKQADEDIQ 1560
Db 1562 QQSAADIARAEILLLEAKRASKSATDVKTADMVKEALEEAEKAQVAEAKAIKQADEDIQ 1621

QY 1561 GTQNLLTSIESETAASEETLTNASQRISKLERNVEELKRKAQNSGEAEYIEKVVYSVKQ 1620
Db 1622 GTQNLLTSIESETAASEETLTNASQRISKLERNVEELKRKAQNSGEAEYIEKVVYSVKQ 1681
QY 1621 NADDVKKILDGELDEKYYKKVESLIAQKTEESADARRKAEELLQNEAKTLLAQANSKLQLE 1680
Db 1682 NADDVKKILDGELDEKYYKKVESLIAQKTEESADARRKAEELLQNEAKTLLAQANSKLQLE 1741
QY 1681 DLERKYEDNQKYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1725
Db 1742 DLERKYEDNQKYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1786
RESULT 5
AAB48450
ID AAB48450 standard; protein; 1786 AA.
XX
AC AAB48450;
DT 02-MAR-2001 (first entry)
XX
DE Mouse laminin 8 polypeptide, SEQ ID NO: 18.
XX
KW Mouse; laminin 8; neuroprotective; angiogenic; osteopathic;
KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;
KW vascular tissue injury; neural injury; angiogenesis regulation.
XX
OS Mus musculus.
XX
PN WO200066732-A2.
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US011543.
XX
PR 30-APR-1999; 99US-0131720P.
PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.
PR 11-FEB-2000; 2000US-0182012P.
XX
PA (BIOS-) BIOSTRATUM INC.
XX
PI Kortessmaa J, Tryggvason K;
XX
DR WPI; 2000-687539/67.
XX N-PSDB; AAC83711.
PT Purified laminin 8 protein, useful for research and therapeutic purposes
PT including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.
XX
PS Claim 5; Page 176-182; 245pp; English.
XX
CC The present sequence is a laminin 8 polypeptide chain. Laminins are a
CC family of heterotrimeric glycoproteins that function via binding
CC interactions with neighbouring cell receptors and by forming laminin
CC networks. They are signalling molecules which influence cellular
CC function. Laminin 8 is useful for treating injuries to tissue of
CC mesenchymal origin, such as bone, cartilage, tendon, and ligament,
CC treating injuries to vascular tissue, promoting cell attachment and
CC migration, ex vivo cell therapy, improving the biocompatibility of
CC medical devices, and preparing improved cell culture devices and media.
CC Laminin 8 is also useful for promoting re-endothelialisation at the site
CC of vascular injuries, improving the take of grafts, improving the
CC biocompatibility of medical devices, treating neural injuries (neural
CC regeneration), regulating angiogenesis, and promoting cell attachment and
CC migration
XX
SQ Sequence 1786 AA;

Query Match 100.0%; Score 9429; DB 3; Length 1786;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1725;		Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	EPYCIIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENAVTTTAPNRLKIWMQSENGVENV	60						
Db	62	EPYCIIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENAVTTTAPNRLKIWMQSENGVENV	121						
QY	61	TIQLDLEAEFFHFLIMTFKTFRPAAMLIERSSDFGKTGWVRYFYAYDCESSFPFGISTGP	120						
Db	122	TIQLDLEAEFFHFLIMTFKTFRPAAMLIERSSDFGKTGWVRYFYAYDCESSFPFGISTGP	181						
QY	121	MKKVDDIICDSRYSDIETPSTEGEVIIFRALDPAPKIEDPYSPRIONLLKITNLRIFKFKLH	180						
Db	182	MKKVDDIICDSRYSDIETPSTEGEVIIFRALDPAPKIEDPYSPRIONLLKITNLRIFKFKLH	241						
QY	181	TLGDNLLDSRMEIREKYYIAYVDMVVRGNCFCYGHASECAPVDGVNVEEVGMVHGCMCR	240						
Db	242	TLGDNLLDSRMEIREKYYIAYVDMVVRGNCFCYGHASECAPVDGVNVEEVGMVHGCMCR	301						
QY	241	HNTKGLNCELMDYFHDLPWRPAEGRNSNACKKCNKNEHSSSCHFDMAVFLATGNVSGGV	300						
Db	302	HNTKGLNCELMDYFHDLPWRPAEGRNSNACKKCNKNEHSSSCHFDMAVFLATGNVSGGV	361						
QY	301	CNQCQHTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL	360						
Db	362	CNQCQHTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL	421						
QY	361	IAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGGNPCDSETGYCYC	420						
Db	422	IAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGGNPCDSETGYCYC	481						
QY	421	KRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCDLGGLNNSCSEDSGQCSCLPHMIGRQCN	480						
Db	482	KRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCDLGGLNNSCSEDSGQCSCLPHMIGRQCN	541						
QY	481	EVEGYYFTTLDHYIYEAEANLPGVWVVERQYIQDRIPSWTGPFGFVRVPEGAYLEFFI	540						
Db	542	EVEGYYFTTLDHYIYEAEANLPGVWVVERQYIQDRIPSWTGPFGFVRVPEGAYLEFFI	601						
QY	541	DNIPYSMEYEILIRYEPQLPHWEKAVITVORPGKIPASSRCGNTVPDDDNQVVSLSPGS	600						
Db	602	DNIPYSMEYEILIRYEPQLPHWEKAVITVORPGKIPASSRCGNTVPDDDNQVVSLSPGS	661						
QY	601	RYVLP RPVCFEKGMNVTVRLELPQYTAGSDVESPYTFIDSLVLMPYCKSLDIFTVGS	660						
Db	662	RYVLP RPVCFEKGMNVTVRLELPQYTAGSDVESPYTFIDSLVLMPYCKSLDIFTVGS	721						
QY	661	GDGEVTSANWETFORYRCLENSRSVVKTPMTDVCNRIIFSALIHQTLGACBDDPQGS	720						
Db	722	GDGEVTSANWETFORYRCLENSRSVVKTPMTDVCNRIIFSALIHQTLGACBDDPQGS	781						
QY	721	SSVCDPNGGQCQCRPNVVGRTNRCAPGTGFGPNGCKPCDCDLQGSASAFCDAITGQCH	780						
Db	782	SSVCDPNGGQCQCRPNVVGRTNRCAPGTGFGPNGCKPCDCDLQGSASAFCDAITGQCH	841						
QY	781	CFQGIYARQCDRCLPGYWGFPSCQPCQCNHGLDCTVTGECCLSCQDYTTTGHNCERCLAG	840						
Db	842	CFQGIYARQCDRCLPGYWGFPSCQPCQCNHGLDCTVTGECCLSCQDYTTTGHNCERCLAG	901						
QY	841	YYGDPPIIGSGDHCRCPCPDGPDGSGRQFARSCYQDPVTIQLACVCDPGYIGSRCDDCASG	900						
Db	902	YYGDPPIIGSGDHCRCPCPDGPDGSGRQFARSCYQDPVTIQLACVCDPGYIGSRCDDCASG	961						
QY	901	FFGNPSDFGGSCQPCQCHNIDITDPEACDKDTGRCLKCLYHTEGDHQCQLCQYGYGDAL	960						
Db	962	FFGNPSDFGGSCQPCQCHNIDITDPEACDKDTGRCLKCLYHTEGDHQCQLCQYGYGDAL	1021						
QY	961	RQDCRKVCNLYLGTVKEHNCNGSDCHCDKATGQCSCLPNVIGQNCDCRCAPNWQLASGTGC	1020						
Db	1022	RQDCRKVCNLYLGTVKEHNCNGSDCHCDKATGQCSCLPNVIGQNCDCRCAPNWQLASGTGC	1081						
QY	1021	GPCNCNAHSAHSGPSCNEFTGQCQCMFGFGGRTCSCEQLFWGDDPDVECRACDCDPRGIET	1080						
Db	1082	GPCNCNAHSAHSGPSCNEFTGQCQCMFGFGGRTCSCEQLFWGDDPDVECRACDCDPRGIET	1141						

QY	1081	POCDQSTGQCVCVEGVGPRCDKCTRGYSGVFPDCTPCHQCFCALWDAIGELTNRTHKFL	1140
Db	1142	POCDQSTGQCVCVEGVGPRCDKCTRGYSGVFPDCTPCHQCFCALWDAIGELTNRTHKFL	1201
QY	1141	EKAKALKISGVIGPYRETVDSEKKNVNEIKDILAQSPAAEPLKNIGILFEEAEKLTQDVT	1200
Db	1202	EKAKALKISGVIGPYRETVDSEKKNVNEIKDILAQSPAAEPLKNIGILFEEAEKLTQDVT	1261
QY	1201	EKVAQVEVKLTDTASQSNSTAGELGALQAEAESLDKTVKELAEQLEFIKNSDIQCALDSI	1260
Db	1262	EKVAQVEVKLTDTASQSNSTAGELGALQAEAESLDKTVKELAEQLEFIKNSDIQCALDSI	1321
QY	1261	TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLERESPFKEQEEQARLLDEL	1320
Db	1322	TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLERESPFKEQEEQARLLDEL	1381
QY	1321	AGKLQSLDLSAAAQMTCTGTPPGADCSESECCGGPNCPTDEGEKKCGGPGCGGLVTVASAW	1380
Db	1382	AGKLQSLDLSAAAQMTCTGTPPGADCSESECCGGPNCPTDEGEKKCGGPGCGGLVTVASAW	1441
QY	1381	QKAMDFDRDVL SALAEVEQLSKMVSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDLR	1440
Db	1442	QKAMDFDRDVL SALAEVEQLSKMVSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDLR	1501
QY	1441	NLIKQIRNFLTSDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVIL	1500
Db	1502	NLIKQIRNFLTSDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVIL	1561
QY	1501	QQAADIARAELLLLEAEKRAKSKSATDVKVTDAMVKEALEEAEAKAQAQADEDDIQ	1560
Db	1562	QQAADIARAELLLLEAEKRAKSKSATDVKVTDAMVKEALEEAEAKAQAQADEDDIQ	1621
QY	1561	GTQNLTSIESETAASEETLTNASQRIKSLERNVEELKRAAQAQNSGEAEYIEKVVSVKQ	1620
Db	1622	GTQNLTSIESETAASEETLTNASQRIKSLERNVEELKRAAQAQNSGEAEYIEKVVSVKQ	1681
QY	1621	NADDVKTKLDGELDEKYKVESLIAQKTESADARRKAEELLQNEAKTLLAQANSKLQJLE	1680
Db	1682	NADDVKTKLDGELDEKYKVESLIAQKTESADARRKAEELLQNEAKTLLAQANSKLQJLE	1741
QY	1681	DLERKYEDNQKYLEDKAQELVRLGEVRSLLKQISEKVAVYSTCL	1725
Db	1742	DLERKYEDNQKYLEDKAQELVRLGEVRSLLKQISEKVAVYSTCL	1786

RESULT 6

ABB81592
ID ABB81592 standard; protein; 1786 AA.

XX ABB81592;

DT 19-SEP-2002 (first entry)

XX Mouse laminin 10 second chain protein sequence SEQ ID NO:10.

XX Laminin alpha 5; laminin 10; vulneryary; cell growth; differentiation;
KW tissue repair development; laminin; healing; vascular tissue;
KW re-endothelialisation; vascular injury; cell attachment; cell stasis;
KW proliferation; migration.

OS Mus musculus.

XX Key Location/Qualifiers
FH Peptide 1..21

FT /label= signal

FT Protein 22..1786

FT /label= laminin_10_second_chain

XX WO200250111-A2.

XX 27-JUN-2002.

XX

21-DEC-2001; 2001WO-US051035.
21-DEC-2000; 2000US-0257449P.
28-MAR-2001; 2001US-0279282P.
13-NOV-2001; 2001US-00279282.
XX
PA (BIOS-) BIOSTRATUM INC.
XX
XX Tryggvason K, Doi M, Thyboll J;
PI
XX WPI; 2002-557650/59.
DR N-PSDB; ABQ72910.
XX
PT New human laminin-10 proteins, useful for accelerating the healing of
PT vascular tissue, improving the biocompatibility of grafts, or for
PT promoting re-endothelialization at the site of vascular injuries.
XX
PS Claim 9; Page 140-145; 231pp; English.
XX
CC The present invention describes human laminin alpha 5. Also described is
CC an isolated laminin 10. Laminin 10 has vulnerary activity. Laminins are
CC useful in maintaining cell/tissue phenotype as well as promoting cell
CC growth and differentiation in tissue repair development. Specifically,
CC laminin 10 can be used for accelerating the healing injuries of vascular
CC tissue, improving the biocompatibility of grafts useful for treating such
CC injuries, for promoting re-endothelialisation at the site of vascular
CC injuries, and promote cell attachment and subsequent cell stasis,
CC proliferation, differentiation, and/or migration. The present sequence
CC encodes a second chain protein of laminin 10, from the present invention
XX
SQ Sequence 1786 AA;
Query Match 100.0%; Score 9429; DB 5; Length 1786;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EPYCIYVSHLQEDKKCFICDSRDPYHETLNPDSGLIENVVTFAPNRLKIWQSENGV 60
DB 62 EPYCIYVSHLQEDKKCFICDSRDPYHETLNPDSGLIENVVTFAPNRLKIWQSENGV 121
QY 61 TIQDLEAEFHTLIMTFKTRPAAMLIERSSDFGKTGWYRYPAYDCESSFPGISGTP 120
DB 122 TIQDLEAEFHTLIMTFKTRPAAMLIERSSDFGKTGWYRYPAYDCESSFPGISGTP 181
QY 121 MKKYDDIICDSRYSDIEPSTEGEVIFRALDPAPKIEDPYSPRIQNLKITNRIKFVKLH 180
DB 182 MKKYDDIICDSRYSDIEPSTEGEVIFRALDPAPKIEDPYSPRIQNLKITNRIKFVKLH 241
QY 181 TLGDNLLDSRMEIREKYIYAYVDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGMCR 240
DB 242 TLGDNLLDSRMEIREKYIYAYVDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGMCR 301
QY 241 HNTKGLNCELMDYFHDLPWRPAEGRNSNACKKNCNEHSSSCHFDMAVFLATGNVSGV 300
DB 302 HNTKGLNCELMDYFHDLPWRPAEGRNSNACKKNCNEHSSSCHFDMAVFLATGNVSGV 361
QY 301 CDNCQHTMGRNCEQCKPFYFQHPERDIRDNLCEPCTCDPAGSENGGICDGYTDFSVGL 360
DB 362 CDNCQHTMGRNCEQCKPFYFQHPERDIRDNLCEPCTCDPAGSENGGICDGYTDFSVGL 421
QY 361 IAGCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGGNPCDSETGYCYC 420
DB 422 IAGCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGGNPCDSETGYCYC 481
QY 421 KRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCLGGALNNSCEDSGQCSCLPHMIGRCN 480
DB 482 KRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCLGGALNNSCEDSGQCSCLPHMIGRCN 541
QY 481 EVESGYFTTLDHYIYEAEANLPGVVVVERQYIQDRIPSWTGPVVRPEGAYLEFFI 540
DB 542 EVESGYFTTLDHYIYEAEANLPGVVVVERQYIQDRIPSWTGPVVRPEGAYLEFFI 601
QY 541 DNIPYSMEYEILIRYEPQPDHWEKAVITVQRPKIPASSRCGNTVPDDDNQVVSLSPGS 600

DB 602 DNIPYSMEYEILIRYEPQPDHWEKAVITVQRPKIPASSRCGNTVPDDDNQVVSLSPGS 661
QY 601 RYVLPVPVCFEKGMYTVRLELPQYTASGSDVESPYTFIDSLVLMPYCKSLDIFTVGG 660
DB 662 RYVLPVPVCFEKGMYTVRLELPQYTASGSDVESPYTFIDSLVLMPYCKSLDIFTVGG 721
QY 661 GDGEVTSAWETFORYRCLENSRSVVKTPTMTDVCRNIIFSISALIHQTLGACEDPQ 720
DB 722 GDGEVTSAWETFORYRCLENSRSVVKTPTMTDVCRNIIFSISALIHQTLGACEDPQ 781
QY 721 SSVCDPNGGQCCQCRPNVVGRTNRCAPGTGFGPNGCKPCDCHLQGSASAFCDAITG 780
DB 782 SSVCDPNGGQCCQCRPNVVGRTNRCAPGTGFGPNGCKPCDCHLQGSASAFCDAITG 841
QY 781 CFQGIYARQCDRCLPLGYWGFSPCQPCQCNHGDCTVTGECCLSCQDYTTTGHNCER 840
DB 842 CFQGIYARQCDRCLPLGYWGFSPCQPCQCNHGDCTVTGECCLSCQDYTTTGHNCER 901
QY 841 YGDPPIIGSGDHCRCPCPCPDGSDSGRQFARSCYQDPVTLQACVCDPVGIGSRCD 900
DB 902 YGDPPIIGSGDHCRCPCPCPDGSDSGRQFARSCYQDPVTLQACVCDPVGIGSRCD 961
QY 901 FFGNPSDFGSGCQPCQCHNIDTTPDPEACDKDTGRCLKCLYHTEGDHCLCQYGYGD 960
DB 962 FFGNPSDFGSGCQPCQCHNIDTTPDPEACDKDTGRCLKCLYHTEGDHCLCQYGYGD 1021
QY 961 RQDCRKVCNYLGTIVKEHNGSDCHCDKATGQCSCLPNVIGONCDRCAPNTWQLASGT 1020
DB 1022 RQDCRKVCNYLGTIVKEHNGSDCHCDKATGQCSCLPNVIGONCDRCAPNTWQLASGT 1081
QY 1021 GPCNCAHSAHSGPSCNEFTGQCQCMFPGGRTSECEQELFWGDPDVECRACDDPRGI 1080
DB 1082 GPCNCAHSAHSGPSCNEFTGQCQCMFPGGRTSECEQELFWGDPDVECRACDDPRGI 1141
QY 1081 PQDQSTGQCVCEGVEGPRCDKCTRGYSVGFDPCTPCHQCFALWDALIGELTNRTHK 1140
DB 1142 PQDQSTGQCVCEGVEGPRCDKCTRGYSVGFDPCTPCHQCFALWDALIGELTNRTHK 1201
QY 1141 EKAKALKISGIVGIPYRETVDSVEKKVNEIKDILAQSPAAEPLKKNIGILFEEAEK 1200
DB 1202 EKAKALKISGIVGIPYRETVDSVEKKVNEIKDILAQSPAAEPLKKNIGILFEEAEK 1261
QY 1201 EKMAQVEVKLTDTASQSNSTAGELGALQAEASLDKTVKELAEQLEFIKNSDIOGAL 1260
DB 1262 EKMAQVEVKLTDTASQSNSTAGELGALQAEASLDKTVKELAEQLEFIKNSDIOGAL 1321
QY 1261 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRVEDLMLERESPFEQEEQARLLDEL 1320
DB 1322 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRVEDLMLERESPFEQEEQARLLDEL 1381
QY 1321 AGKQSLDLSAAQMTCTGTPPGADCSSECEGCGNCRDTEGEKKCGGPGCGGLTVVAH 1380
DB 1382 AGKQSLDLSAAQMTCTGTPPGADCSSECEGCGNCRDTEGEKKCGGPGCGGLTVVAH 1441
QY 1381 OKAMDFDRDVLALAEVEQLSKMVSEAKVRADEAKQNAQDVLKTNATKVKVDSNED 1440
DB 1442 OKAMDFDRDVLALAEVEQLSKMVSEAKVRADEAKQNAQDVLKTNATKVKVDSNED 1501
QY 1441 NLIKQIRNFLTSDSADLDSIEAVANEVLKSGNASTPQOLQNLTEDIRERVETLSQVE 1500
DB 1502 NLIKQIRNFLTSDSADLDSIEAVANEVLKSGNASTPQOLQNLTEDIRERVETLSQVE 1561
QY 1501 QQSAADIAEAELLLLEAEKASKSATDVKTADVMKEALEAEAKQAAEKAKIQADEDI 1560
DB 1562 QQSAADIAEAELLLLEAEKASKSATDVKTADVMKEALEAEAKQAAEKAKIQADEDI 1621
QY 1561 GTQNLITLTSIESETAASEETLTNASQRIKSLERNVEELKRAAQNNGEAEYIEKVVS 1620
DB 1622 GTQNLITLTSIESETAASEETLTNASQRIKSLERNVEELKRAAQNNGEAEYIEKVVS 1681
QY 1621 NADDVKTKTLDGELDEKVKVESLIAOKTEESADARRKAEKLLQNEAKTLAQANSKL 1680

Db 1682 NADDVKKTLDELDEKYYKVESLIAQKTESADARRKAELLQNEAKTLAQAANSKLQLE 1741
Qy 1681 DLERKYEDNQYLEDKAQELVRLGEVRSLLKDISEKVAVYSTCL 1725
Db 1742 DLERKYEDNQYLEDKAQELVRLGEVRSLLKDISEKVAVYSTCL 1786

RESULT 7
AAW50894
ID AAW50894 standard; protein; 1776 AA.
XX
AC AAW50894;

XX 07-DEC-1998 (first entry)
XX Mouse laminin B1 chain.
XX Laminin; mouse; beta-amyloid; amyloidosis; Alzheimer's disease;
KW Down's syndrome; hereditary cerebral haemorrhage; inflammation;
KW malignancy; Familial Mediterranean Fever; multiple myeloma;
KW type II diabetes; prion disease; Creutzfeldt-Jacob disease; CJD;
KW Gertsmann-Straussler syndrome; kuru; scrapie; haemodialysis;
KW carpal tunnel syndrome; senile cardiac amyloid polyneuropathy;
KW Familial Amyloidotic Polyneuropathy; thyroid carcinoma; diagnosis;
KW therapy.

XX Mus sp.
XX WO9815179-A1.
XX 16-APR-1998.
XX 08-OCT-1997; 97WO-US018145.
XX 08-OCT-1996; 96US-0027981P.

PA (UNIW) UNIV WASHINGTON.
XX Castillo G, Snow AD;
XX WPI; 1998-240534/21.
XX

PT Use of laminin and fragments - for developing products for use in the
PT diagnosis and treatment of amyloid disease, e.g. Alzheimer's disease or
PT CJD.

PS Claim 15; Page 90-93; 132pp; English.

XX This is the amino acid sequence of the mouse laminin B1 chain. The
CC primary object of the invention is to use laminin, laminin-derived
CC protein fragments and/or laminin-derived polypeptides as potent
CC inhibitors of amyloid formation, deposition, accumulation and/or
CC persistence in Alzheimer's disease and other amyloidoses. The laminin
CC products (see AAW5088-98) may include mouse or human laminin A or A1
CC chain, laminin B1 or B2 chain, laminin A2 chain (merosin), laminin G1
CC chain, the globular repeats of the laminin A1 chain and the beta-amyloid
CC binding domain of the laminin A chain. A claimed method for treating an
CC amyloid disease comprises administering a polypeptide having a
CC conformational similarity to a fragment of a laminin protein. A method
CC for diagnosing an amyloid disease involves determining levels of laminin
CC in a sample. Production of laminin or its fourth globular repeat in vivo
CC provides a method for in vivo inhibition of beta-amyloid amyloidosis. The
CC products and methods can be used for the diagnosis, prognosis, monitoring
CC and treatment of amyloidoses such as Alzheimer's disease, Down's syndrome
CC and hereditary cerebral haemorrhage with amyloidosis of the Dutch type
CC (where the specific amyloid is the beta-amyloid protein), the amyloidosis
CC associated with chronic inflammation, various forms of malignancy and
CC Familial Mediterranean Fever (AA amyloid or inflammation-association
CC amyloidosis), the amyloidosis associated with multiple myeloma and other
CC B-cell abnormalities (AL amyloid), the amyloidosis associated with type
CC II diabetes (amylin or islet amyloid), the amyloidosis associated with
CC prion diseases including Creutzfeldt-Jacob disease, Gertsmann-Straussler
CC syndrome, kuru and animal scrapie (PrP amyloid), the amyloidosis

CC associated with long-term haemodialysis and carpal tunnel syndrome (beta
CC 2-microglobulin amyloid), the amyloidosis associated with senile cardiac
CC amyloid and Familial Amyloidotic Polyneuropathy (prealbumin or
CC transthyretin amyloid), and the amyloidosis associated with endocrine
CC tumours such as medullary carcinoma of the thyroid (variant of
CC procalcitonin)
XX
SQ Sequence 1776 AA;

Query Match 99.3%; Score 9363; DB 2; Length 1776;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1715; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 EPYCIVSHLQEDKKCFICDSRDPYHETLNPDHSHLIENVTTFAPNRLKIWWQSENGVENV 60
Db 62 EPYCIVSHLQEDKKCFICDSRDPYHETLNPDHSHLIENVTTFAPNRLKIWWQSENGVENV 121
Qy 61 TIQLDLEAEFFHFTLIMTEKTFRPAAMLIERSSDFGKTGWVYRYFAYDCSSFPFGISTGP 120
Db 122 TIQLDLEAEFFHFTLIMTEKTFRPAAMLIERSSDFGKTGWVYRYFAYDCSSFPFGISTGP 181
Qy 121 MKKVDDIICDSRYSYDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLLKITNLRKFVKLH 180
Db 182 MKKVDDIICDSRYSYDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLLKITNLRKFVKLH 241
Qy 181 TLGDNLLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGVNEEVEGVHGHCMCR 240
Db 242 TLGDNLLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGVNEEVEGVHGHCMCR 301
Qy 241 HNTKGLNCELMDFFYHDLFWRPAEGRNSNACKKNCNEHSSSCHFDMAVFLATGNVSGGV 300
Db 302 HNTKGLNCELMDFFYHDLFWRPAEGRNSNACKKNCNEHSSSCHFDMAVFLATGNVSGGV 361
Qy 301 CDNCQHNTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 360
Db 362 CDNCQHNTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 421
Qy 361 IAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGGNPCDSETGYCYC 420
Db 422 IAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGGNPCDSETGYCYC 481
Qy 421 KRLVTGQRCDQCLPQHWSLNDLDGCRPCDCDLGGALNNSCEDSGQCSCLPHMIGRQCN 480
Db 482 KRLVTGQRCDQCLPQHWSLNDLDGCRPCDCDLGGALNNSCEDSGQCSCLPHMIGRQCN 541
Qy 481 EVESGYFTTLDHYIYEAEANLGPVGVVVERQYIQRIPSWTGPFGFVRVPEGAYLEFFI 540
Db 542 EVESGYFTTLDHYIYEAEANLGPVGVVVERQYIQRIPSWTGPFGFVRVPEGAYLEFFI 601
Qy 541 DNIPYSMEYEILIRYEPQLDHEKAVITVQRPKIPASSRRCGNTVPDDDNQVVSLSPGS 600
Db 602 DNIPYSMEYEILIRYEPQLDHEKAVITVQRPKIPASSRRCGNTVPDDDNQVVSLSPGS 661
Qy 601 RYVVLPRPVCFEKGMNVTVRLELPQYTAGSDVESPYTFIDSLVLMPYCKSLDIFTVGS 660
Db 662 RYVVLPRPVCFEKGMNVTVRLELPQYTAGSDVESPYTFIDSLVLMPYCKSLDIFTVGS 721
Qy 661 GDGEVTSNASETQRYRCLNSRSVVKTPMTDVCNIIIFSISALIHQTGLACECDPOGSL 720
Db 722 GDGEVTSNASETQRYRCLNSRSVVKTPMTDVCNIIIFSISALIHQTGLACECDPOGSL 781
Qy 721 SSVCDPNGGQCQCRPNVVGRTNRCAPGTFGFGPNCKPCDCHLQGSASAFCDAITGOCH 780
Db 782 SSVCDPNGGQCQCRPNVVGRTNRCAPGTFGFGPNCKPCDCHLQGSASAFCDAITGOCH 841
Qy 781 CFQGIYARQCDCRCLPGYWGFPSCQPCQCNHGLDCTVTGECCLSCQDYTTGHNCERCLAG 840
Db 842 CFQGIYARQCDCRCLPGYWGFPSCQPCQCNHGLDCTVTGECCLSCQDYTTGHNCERCLAG 901
Qy 841 YYGDPPIIGSGDHCRCPCPDGPDGSGRQFARSCYQDPVTLQACVCDPFGYIGSRCDDCAGS 900
Db 902 YYGDPPIIGSGDHCRCPCPDGPDGSGRQFARSCYQDPVTLQACVCDPFGYIGSRCDDCAGS 961

QY 901 FFGNPSDFGSCQPCQCHNIDTTDPEACDKDTGRCLKCLYHTEGHCQLCOVGYGDAL 960
Db 962 FFGNPSDFGSCQPCQCHNIDTTDPEACDKDTGRCLKCLYHTEGHCQLCOVGYGDAL 1021
QY 961 RQDCRCVCNLTGTVKEHCHGSDCHCDKATGQCSCLPNVIGQNCDCRCAPNTWQLASGTGC 1020
Db 1022 RQDCRCVCNLTGTVKEHCHGSDCHCDKATGQCSCLPNVIGQNCDCRCAPNTWQLASGTGC 1081
QY 1021 GPCNCNAHSGFSPSCNEFTGQCQCMFPGFGRGTCSECBELFWGDDVECRACDCDPRGIET 1080
Db 1082 GPCNCNAHSGFSPSCNEFTGQCQCMFPGFGRGTCSECBELFWGDDVECRACDCDPRGIET 1141
QY 1081 PQCDQSTGQVCVCEGVEGPRCDKCTRGYSYGVFPDCTPCHQCFALWDALIGELTNRTHKFL 1140
Db 1142 PQCDQSTGQVCVCEGVEGPRCDKCTRGYSYGVFPDCTPCHQCFALWDALIGELTNRTHKFL 1201
QY 1141 EKAKALKISGVIPIGYRETVDSEKKNVNEIKDILAQSPAAEPLKNIGILFEEAEKLTQDVT 1200
Db 1202 EKAKALKISGVIPIGYRETVDSEKKNVNEIKDILAQSPAAEPLKNIGILFEEAEKLTQDVT 1261
QY 1201 EKMAQVEVLTDTASQSNSTAGELGALQAEASLDKTVKELAEQLEFIKNSDIQGALDSI 1260
Db 1262 EKMAQVEVLTDTASQSNSTAGELGALQAEASLDKTVKELAEQLEFIKNSDIQGALDSI 1321
QY 1261 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLERESPFEQEEQARLLDEL 1320
Db 1322 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLERESPFEQEEQARLLDEL 1381
QY 1321 AGKLSLDSAAQMTCTGPPGADCSSECGGNCRNDEGEKCGGPGGGLVTVASAW 1380
Db 1382 AGKLSLDSAAQMTCTGPPGADCSSECGGNCRNDEGEKCGGPGGGLVTVASAW 1441
QY 1381 QKAMDFDRDVLALAEVEQLSKMSEAKVRADEAKQNAQDVLLKTNAKEKVDKSNEDLR 1440
Db 1442 QKAMDFDRDVLALAEVEQLSKMSEAKVRADEAKQNAQDVLLKTNAKEKVDKSNEDLR 1501
QY 1441 NLIKQIRNLTEDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVIL 1500
Db 1502 NLIKQIRNLTEDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVIL 1561
QY 1501 QQSAADIAFAELLLEAEKRAKASATDVKTADVMVKEALEEAEKAQVAEKAQKQADEDIQ 1560
Db 1562 QQSAADIAFAELLLEAEKRAKASATDVKTADVMVKEALEEAEKAQVAEKAQKQADEDIQ 1621
QY 1561 GTQNLTSIESETAASEETLTNASQRISKLRNVEBELKRAAQNSEGEABYIEKVVSVKQ 1620
Db 1622 GTQNLTSIESETAASEETLTNASQRISKLRNVEBELKRAAQNSEGEABYIEKVVSVK- 1680
QY 1621 NADDVKTLDGELDEKVKVESLIAQKTESADARRKAEALLQNEAKTLAQANSKLQLE 1680
Db 1681 ---DVKTLDGELDEKVKVESLIAQKTESADARRKAEALLQNEAKTLAQANSKLQLE 1737
QY 1681 DLERKYEDNQKYLEDKAQELVRLEGEVRSLLKDISEKVA 1719
Db 1738 DLERKYEDNQKYLEDKAQELVRLEGEVRSLLKDISEKVA 1776

RESULT 8
AAP91672
ID AAP91672 standard; protein; 1764 AA.
XX
AC AAP91672;
XX
DT 25-MAR-2003 (revised)
DT 31-OCT-2002 (revised)
DT 29-JUN-1990 (first entry)
XX
DE Primary amino acid sequence of B1 chain of laminin.
XX
KW Laminin B1 chain fragment; heparin; prosthetic devices;
KW cell culture substrates; cell adhesion promoter; nerve regeneration;
KW wound healing; implant acceptance; cell attachment; metastasis inhibitor.
XX

OS Mus musculus.
OS Synthetic.
FH Key
FT Peptide
FT Peptide
FT Peptide
FT Peptide
XX WO8901493-A.
XX 23-FEB-1989.
XX 19-AUG-1987; 87US-00087157.
XX 19-AUG-1987; 87US-00087157.
XX (MINU) MINNESOTA UNIVERSITY.
XX Charonis A, Furcht LT;
XX WPI; 1989-068855/09.
XX New laminin B1 chain polypeptide(s) - for promoting heparin binding and cell adhesion.
XX Disclosure; Page ?; 42pp; English.
XX The new polypeptides have an amino acid sequence corresp. to a laminin B1 chain fragment having specific binding capacity for heparin. Specifically mentioned are the two polypeptides F9 and F13 (see FT). The polypeptides may be used to promote binding of heparin to synthetic substrates and promote cell adhesion, eg endothelial, melanoma, fibrosarcoma, glioma and pheochromocytoma cells. They may be useful for assisting nerve regeneration, promoting wound healing, implant acceptance, cell attachment to culture substrates and inhibiting metastasis of malignant cells. They may be prepd. by conventional Merrifield solid-phase synthesis. Also claimed are prosthetic devices and cell culture substrates coated with the new polypeptides. (Updated on 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PR field.)
XX Sequence 1764 AA;
SQ

Query Match 98.7%; Score 9307.5; DB 1; Length 1764;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1707; Conservative 4; Mismatches 13; Indels 1; Gaps 1;
QY 1 EPYCIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENV 60
Db 41 EPYCIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENV 100
QY 61 TIQDLAEAFHFTHLIMTFKTRPAAMLIERSDFGKTGWVRYRYPAYDCESFPFGISTGP 120
Db 101 TIQDLAEAFHFTHLIMTFKTRPAAMLIERSDFGKTGWVRYRYPAYDCESFPFGISTGP 160
QY 121 MKKVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLKLTNLRKIFVKLH 180
Db 161 MKGVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLKLTNLRKIFVKLH 220
QY 181 TLGDNLLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGHCRCR 240
Db 221 TLGDNLLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGHCRCR 280
QY 241 HNTKGLNCELMDYFHDLPWRPAEGRNSNACKKNCNEHSSSCHFDMAVFLATGNVSGGV 300
Db 281 HNTKGLNCELMDYFHDLPWRPAEGRNSNACKKNCNEHSSSCHFDMAVFLATGNVSGGV 340
QY 301 CDNCQHTMGRNCEQCKPFYFQHPERDIRDPNLCBPCTCDPAGSENGGICDGYTDFSVGL 360
Db 341 CDNCQHTMGRNCEQCKPFYFQHPERDIRDPNLCBPCTCDPAGSENGGICDGYTDFSVGL 400
QY 361 IAGQCRCKLHVEGERCDVCKEGFYDLSEADPYGCKSCACNPLGTIPGGNCPDSEYCYC 420

Db 401 IAGQCRCKLHVGERCDVCKEGFTDLAEDPYGCKSCACNPLGLTTPGNGPCDSETGYCYC 460
QY 421 KRLVTGQRCDQCLPQHGLNSNDLDGCRPCDCDLGGALNNSCEDSGQCSCLPHMIGROCN 480
Db 461 KRLVTGQRCDQCLPQHGLNSNDLDGCRPCDCDLGGALNNSCEDSGQCSCLPHMIGROCN 520
QY 481 EVESGYFTTLDHYIYBAAEANLPGVVVVERQYIQDRIPSWTGPGRVVRPEGAYLEFFI 540
Db 521 EVESGYFTTLDHYIYBAAEANLPGVVVVERQYIQDRIPSWTGPGRVVRPEGAYLEFFI 580
QY 541 DNIPYSMEYEILIRYEPQPDHWEKAVITVQRPKIPASSRCGNTVPDDNQVVSLSPGS 600
Db 581 DNIPYSMEYEILIRYEPQPDHWEKAVITVQRPKIPASSRCGNTVPDDNQVVSLSPGS 640
QY 601 RYVVLPRPVCFEKGMNVTVRLELPOYTASGSDVESPYTFIDSLVLMPCYCKSLDIFTVGS 660
Db 641 RYVVLPRPVCFEKGMNVTVRLELPOYTASGSDVESPYTFIDSLVLMPCYCKSLDIFTVGS 700
QY 661 GDGEVNTSAWETFQYRCLNRSRVVKTPTMTDVCNIIIFSISALIHQTLGACECDPQGS 720
Db 701 GDGEVNTSAWETFQYRCLNRSRVVKTPTMTDVCNIIIFSISALIHQTLGACECDPQGS 760
QY 721 SSVCDPNGGCQCRPNVVGRTNRCAPGTFGFGPNCKPCDCHLQGSASAFCDAITGQCH 780
Db 761 SSVCDPNGGCQCRPNVVGRTNRCAPGTFGFGPNCKPCDCHLQGSASAFCDAITGQCH 820
QY 781 CFQGIYARQCDRCLPGYWGFPSCQPCQCNHGDCTVTGECCLSCQDYTTGNHCERCLAG 840
Db 821 CFQGIYARQCDRCLPGYWGFPSCQPCQCNHGDCTVTGECCLSCQDYTTGNHCERCLAG 880
QY 841 YYGDPFIIGSDHCRPCPCPDGSDGRQFARSCYQDPVTLQLACVCDPGYIGSRCDDCASG 900
Db 881 YYGDPFIIGSDHCRPCPCPDGSDGRQFARSCYQDPVTLQLACVCDPGYIGSRCDDCASG 940
QY 901 FFGNPSDFGSGCQPCQCHNIDTDPACDKDTGRCLKCLYHTEGDHQCQLCOGYGXDAL 960
Db 941 FFGNPSDFGSGCQPCQCHNIDTDPACDKDTGRCLKCLYHTEGDHQCQLCOGYGXDAL 1000
QY 961 RQDCRKVCNVLGTVKEHNGSDCHCDKATGQCSCLPNVIGQNCDCRCAPNTWQLASGTGC 1020
Db 1001 RQDCRKVCNVLGTVKEHNGSDCHCDKATGQCSCLPNVIGQNCDCRCAPNTWQLASGTGC 1060
QY 1021 GPCNCNAAHSFGPSCNEFTGQCQCMPGFGGRTCECQELFWGDPDVECRACDCDPRGIET 1080
Db 1061 GPCNCNAAHSFGPSCNEFTGQCQCMPGFGGRTCECQELFWGDPDVECRACDCDPRGIET 1120
QY 1081 PQCDQSTGQCVCEGVEGPRCDKCTRGYSGVFPDCTPCHOCFALWDAIIGELTNRTHKFL 1140
Db 1121 PQCDQSTGQCVCEGVEGPRCDKCTRGYSGVFPDCTPCEQCFALWDAIIGELTNRTHKFL 1180
QY 1141 EKAKALKISGVIGPYRETVDSEKKNKIDILAQSPAAEPLKNIGILFEEAEKLTKDVT 1200
Db 1181 EKAKALKISGVIGTRETVDSEKKNKIDILAQIPAAEPLKNIGILFEEAEELTKDVT 1240
QY 1201 EKMAQVEVKLTDTASQSNSTAGELGALQAEAESLDKTVKELAEQLEFIKNSDIOGALDSI 1260
Db 1241 EKMAQVEVKLTDTASQSNHAGELGALQAGAESLDKTVKELAEQLEFIKNSDIOGALDSI 1300
QY 1261 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDMLERESPFEQEEQEARLLDEL 1320
Db 1301 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDMLERESPFEQEEQEARLLDEL 1360
QY 1321 AGKLQSLDLSAAAQMTCTGTPPGADCESECGPNCRCTDEGEKKCGGPGCGGLVTVHAWSAW 1380
Db 1361 AGKLQSLDLSAAAQMTCTGTPPGADCESECGPNCRCTDEGEKKCGGPGCGGLVTVHAWSAW 1420
QY 1381 QKAMDFDRDVLASALAEVEQLSKMWSEAKVRADEAKQNAQDVLKTNATKEKVDKSNEDLR 1440
Db 1421 QKAMDFDRDVLASALAEVEQLSKMWSEAKVRADEAKQNAQDVLKTNATKEKVDKSNEDLR 1480
QY 1441 NLIKQIRNFLTDSADLDSIEAVANEVLKSGNASTPQQLQNLFTEDIRERVETLSQVEVIL 1500
Db 1481 NLIKQIRNFLTDSADLDSIEAVANEVLKSGNASTPQQLQNLFTEDIRERVETLSQVEVIL 1540

QY 1501 QQSAADIARAELLLEBAKRASKSATDVKVTADMVKEALEEAEKAQVAAEKAIKQADEDIQ 1560
Db 1541 QQSAADIARAELLLEBAKRASKSATDVKVTADMVKEALEEAEKAQVAAEKAIKQADEDIQ 1600
QY 1561 GTQNLITSIESETAASEETLTNASQRIKSLERNVEELKRKAAQNSGEAEYIEKVYYSVKQ 1620
Db 1601 GTQNLITSIESETAASEETLTNASQRIKSLERNVEELKRKAAQNSGEAEYIEKVYYSVKQ 1660
QY 1621 NADDVKKTLTGELDEKYYKVESLIAQKTEESADARRKAELLQNEAKTLLAQANSKIQLLE 1680
Db 1661 NADDVKKTLTGELD-KYKVESLIAQKTEESADARRKAELLQNEAKTLLAQANSKIQLLE 1719
QY 1681 DLERKYEDNQYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1725
Db 1720 DLERKYEDNQYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1764

RESULT 9
AAB19798
ID AAB19798 standard; protein; 1765 AA.
XX
AC AAB19798;
XX
DT 05-MAR-2001 (first entry)
XX
DE Human laminin 2 mature beta-1 chain.
XX
KW Laminin 2; human; nerve regeneration; angiogenic; cell adhesion;
KW degenerative muscle disorder; muscular dystrophy; cell therapy.
XX
OS Homo sapiens.
XX
PN WO2000066730-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US011378.
XX
PR 30-APR-1999; 99US-0131720P.
PR 15-JUN-1999; 99US-0139198P.
PR 12-JUL-1999; 99US-0143289P.
PR 24-SEP-1999; 99US-0155945P.
XX
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
PI Yurchenco P;
XX
DR WPI; 2000-687537/67.
DR N-PSDB; AAA88898.
XX
PT Purified laminin 2 protein, useful for research and therapeutic purposes
PT including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.
XX
PS Claim 5; Page 199-204; 305pp; English.
XX
CC The present sequence is that of the human laminin 2 beta-1 chain mature
CC protein. Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and
CC gamma-1 (100 kDa) chains. It is thought to be specifically required for
CC stabilizing myotubes during skeletal muscle development, and for
CC preventing apoptosis. Genetic defects in its structure or expression are
CC associated with a major type of congenital muscular dystrophy. Laminin 2
CC is also thought to be important in Schwann cell/basal lamina
CC interactions. The invention provides laminin 2 alpha-2, beta-1 and gamma-
CC 1 chain polypeptides (see AAB19791-806) and the polynucleotides encoding
CC them (see AAA88891-906), methods for making recombinant laminin 2, cells
CC that express recombinant laminin 2, and methods for using purified
CC laminin 2 for research and therapeutic purposes including peripheral
CC nerve regeneration, treatment of degenerative muscle disorders,
CC angiogenesis regulation, promoting cell attachment and migration, ex vivo
CC cell therapy, improving the take of grafts, improving the
CC biocompatibility of medical devices and preparing improved culture

XX 30-APR-1999; 99US-0131720P.
PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.
PR 11-FEB-2000; 2000US-0182012P.
XX
PA (BIOS-) BIOSTRATUM INC.
XX
XX Kortessmaa J, Tryggvason K;
PI
XX
DR WPI; 2000-687539/67.
DR N-PSDB; AAC83710.
XX
XX Purified laminin 8 protein, useful for research and therapeutic purposes
PT including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.
XX
XX Claim 5; Page 163-168; 245pp; English.
XX
XX The present sequence is a laminin 8 polypeptide chain. Laminins are a
CC family of heterotrimeric glycoproteins that function via binding
CC interactions with neighbouring cell receptors and by forming laminin
CC networks. They are signalling molecules which influence cellular
CC function. Laminin 8 is useful for treating injuries to tissue of
CC mesenchymal origin, such as bone, cartilage, tendon, and ligament,
CC treating injuries to vascular tissue, promoting cell attachment and
CC migration, ex vivo cell therapy, improving the biocompatibility of
CC medical devices, and preparing improved cell culture devices and media.
CC Laminin 8 is also useful for promoting re-endothelialisation at the site
CC of vascular injuries, improving the take of grafts, improving the
CC biocompatibility of medical devices, treating neural injuries (neural
CC regeneration), regulating angiogenesis, and promoting cell attachment and
CC migration
XX
SQ Sequence 1765 AA;
Query Match 94.1%; Score 8873; DB 3; Length 1765;
Best Local Similarity 92.9%; Pred. No. 0;
Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;
QY 1 EPYCIYVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENV 60
DB 41 EPYCIYVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENV 100
QY 61 TIQLDLAEAFHFTLIMTFKTRPAAMLIERSSDFGTWGVYRYFAYDCSESPGISTGP 120
DB 101 TIQLDLAEAFHFTLIMTFKTRPAAMLIERSSDFGTWGVYRYFAYDCSESPGISTGP 160
QY 121 MKKVDDIICDSRYSIDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLLKITNLRKFVKLH 180
DB 161 MKKVDDIICDSRYSIDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLLKITNLRKFVKLH 220
QY 181 TLGDNLLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMCR 240
DB 221 TLGDNLLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMCR 280
QY 241 HNTKGLNCELAMDYHDLPLWRPAEGRNSNACKKNCNCHSSCHFDMAVFLATGNVSGGV 300
DB 281 HNTKGLNCELAMDYHDLPLWRPAEGRNSNACKKNCNCHSSCHFDMAVFLATGNVSGGV 340
QY 301 CDNCQHNMTGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 360
DB 341 CDNCQHNMTGRNCEQCKPFYFQHPERDIRDPNFCERCICDPAGSQNEGICDSYTDFTSTGL 400
QY 361 IAGQCRKLVHEGERCDVCKEGFYDLSEAEDPYGCKSCACNPLGTIPGGNPCDSETHCYC 420
DB 401 IAGQCRKLVHEGERCDVCKEGFYDLSSSEDPFGCKSCACNPLGTIPGGNPCDSETHCYC 460
QY 421 KRLVTGQRCDQCLPQHGLNSDLDCRPPCDCLGGALNNSCSEDSGQCSCLPHMIGRQCN 480
DB 461 KRLVTGQRCDQCLPQHGLNSDLDCRPPCDCLGGALNNSCFAESGQCSCLPHMIGRQCN 520
QY 481 EVESGYFTTLDHYIYEAEEANLGPVVVVERQYIQDRIPSWTGPVVRPEGAYLEFFI 540

DB 521 EVEPGYFATLDHYLYEAEEANLPGVSIQVERQYIQDRIPSWTGAQFVRPEGAYLEFFI 580
QY 541 DNIPYSMEYEILIRYEPQIPDHWEKAVITVQRPKIPASSRCGNTVPDDDNQVVSLSPGS 600
DB 581 DNIPYSMEYDILIRYEPQIPDHWEKAVITVQRPGRIPSTSSRCGNTIPDDDNQVVSLSPGS 640
QY 601 RYVVLPRPVCFEKGMNVTYVLELPOYTASGSDVESPYTFIDSLVMPYCKSLDIFTVGG 660
DB 641 RYVVLPRPVCFEKGMNVTYVLELPOYTSSDSDVESPYTFIDSLVMPYCKSLDIFTVGG 700
QY 661 GDGEVNTSAWETFQRYRCLENSRSVVKTPMTDVCNRIIFSISALIHQTLGACEDPQGS 720
DB 701 GDGEVNTSAWETFQRYRCLENSRSVVKTPMTDVCNRIIFSISALLHQTGLACEDPQGS 760
QY 721 SSVCDPNGGQCCQCRPNVVGRTCNRCAPGTGFGFGNGCKPCDCHLQGSASAFCAITGQCH 780
DB 761 SSVCDPNGGQCCQCRPNVVGRTCNRCAPGTGFGFGSGCKPCDCHLQGSVNAFCNPVTGQCH 820
QY 781 CFQGIYARQCDRCLPLGYWGPSPCQPCQCNHGLDCTVTGECCLSCQDYYTGHNCERCLAG 840
DB 821 CFQGIYARQCDRCLPLGYWGPSPCQPCQCNHGLDCTVTGECCLSCQDYYTGHNCERCLAG 880
QY 841 YYGDPFIIGSGDHCRPCPCPDGSDGRQFARSYQDPVTIQLACVCDPFGYIGSRCDDCASG 900
DB 881 YYGDPFIIGSGDHCRPCPCPDGSDGRQFARSYQDPVTIQLACVCDPFGYIGSRCDDCASG 940
QY 901 FFGNPSDFGGSCQPCQCHHNIIDTTPDPAACDKDTGRCLKCLYHTEGDHQCQCYGYGDAL 960
DB 941 YFGNPSDFGGSCQPCQCHHNIIDTTPDPAACDKDTGRCLKCLYHTEGDHQCQCYGYGDAL 1000
QY 961 RQDCRKVCNYLGTVKEHCNCSGDCHDKATGQCSCLNENNVIGQNCDCRCAPTWQLASGTGC 1020
DB 1001 RQDCRKVCNYLGTVKEHCNCSGDCHDKATGQCSCLNENNVIGQNCDCRCAPTWQLASGTGC 1060
QY 1021 GPCNCNAAHSFGPSCNEFTGQCCMPGFGGRTCSCEQLFWGDDPVECRACDCDPRGIET 1080
DB 1061 DPCNCNAAHSFGPSCNEFTGQCCMPGFGGRTCSCEQLFWGDDPVECRACDCDPRGIET 1120
QY 1081 PQCDQSTGQCVCEGVEGPRCDKCTRGYSVGFPCDTPCHQCFALWDAIIGELTNRTHKFL 1140
DB 1121 PQCDQSTGQCVCEGVEGPRCDKCTRGYSVGFPCDTPCHQCFALWDAIIGELTNRTHKFL 1180
QY 1141 EKAKALKISGVIQPYRETVDSEKVKVNEIKDILAQSPAEPKLNIGILFEEAEKLPKDV 1200
DB 1181 EKAKALKISGVIQPYRETVDSEKVKVNEIKDILAQSPAEPKLNIGILFEEAEKLPKDV 1240
QY 1201 EKMAQVEVKTDTASQSNSTAGELGALQAEESLDKTVKELAEQLEFIKNSDIQGLDSI 1260
DB 1241 EMMAQVEVKTDTASQSNSTAGELGALQAEESLDKTVKELAEQLEFIKNSDIQGLDSI 1300
QY 1261 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRDRVEDLMLERESPFKEQEEQARLLDEL 1320
DB 1301 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRDRVEDLMLERESPFKEQEEQARLLDEL 1360
QY 1321 AGKQLSLDLASAAQMTCTGTPPGADCSSECECGPNCRTDEGEKCKGPGCGGLVTVAHSAW 1380
DB 1361 AGKQLSLDLASAAQMTCTGTPPGADCSSECECGPNCRTDEGEKCKGPGCGGLVTVAHSAW 1420
QY 1381 QKAMDFDRDVLASALAEVEQLSKMVSEAKVRADEAKQNAQDVLKTNATKEKVDKSNEDLR 1440
DB 1421 QKAMDFDRDVLASALAEVEQLSKMVSEAKVRADEAKQNAQDVLKTNATKEKVDKSNEDLR 1480
QY 1441 NLIKQIRNFLTQDSADLSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVIL 1500
DB 1481 NLIKQIRNFLTQDSADLSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVIL 1540
QY 1501 QQSAADIARAELLLLEAKRASKATDVKVVTADMVKEALEEAEKAAQVAAEKAIKQADEDIQ 1560
DB 1541 QHSAADIARAELLLLEAKRASKATDVKVVTADMVKEALEEAEKAAQVAAEKAIKQADEDIQ 1600
QY 1561 GTQNLLTSIESETAASEETLTNASQRIKSLERNVEELKRAAQNQSGEAEYIEKVVSVKQ 1620

Db 1601 GTQNLTSIESETAASEETLNFASORISELERNVEELKRAAQNSEAEYIEKVYTVKQ 1660
QY 1621 NADDVKKTLDELDEKYYKVESLIAQKTESADARRKAEALLQNEAKTLQAQNSKLQLE 1680
Db 1661 SAEDVKKTLDELDEKYYKVENLIAKTESADARRKAEMLQNEAKTLQAQNSKLQLLK 1720
QY 1681 DLERKYEDNQYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1725
Db 1721 DLERKYEDNQYLEDKAQELARLEGEVRSLLKDISQKAVYSTCL 1765

RESULT 11

ABB81591
ID ABB81591 standard; protein; 1765 AA.
XX
AC ABB81591;
XX
DT 19-SEP-2002 (first entry)
XX
DE Human laminin 10 second chain protein sequence SEQ ID NO:8.
XX
KW Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;
KW tissue repair development; laminin; healing; vascular tissue;
KW re-endothelialisation; vascular injury; cell attachment; cell stasis;
KW proliferation; migration.
XX
OS Homo sapiens.
XX
PN WO200250111-A2.
XX
PD 27-JUN-2002.
XX
PF 21-DEC-2001; 2001WO-US051035.
XX
PR 21-DEC-2000; 2000US-0257449P.
PR 28-MAR-2001; 2001US-0279282P.
PR 13-NOV-2001; 2001US-00279282.
XX
PA (BIOS-) BIOSTRATUM INC.
XX

PI Tryggvason K, Doi M, Thyboll J;
XX
XX WPI; 2002-557650/59.
DR N-PSDB; ABQ72909.
XX
PT New human laminin-10 proteins, useful for accelerating the healing of
PT vascular tissue, improving the biocompatibility of grafts, or for
PT promoting re-endothelialization at the site of vascular injuries.
XX
PS Claim 9; Page 126-132; 231pp; English.
XX

CC The present invention describes human laminin alpha 5. Also described is
CC an isolated laminin 10. Laminin 10 has vulnery activity. Laminins are
CC useful in maintaining cell/tissue phenotype as well as promoting cell
CC growth and differentiation in tissue repair development. Specifically,
CC laminin 10 can be used for accelerating the healing injuries of vascular
CC tissue, improving the biocompatibility of grafts useful for treating such
CC injuries, for promoting re-endothelialisation at the site of vascular
CC injuries, and promote cell attachment and subsequent cell stasis,
CC proliferation, differentiation, and/or migration. The present sequence
CC represents a second chain protein of laminin 10, from the present
XX invention

SQ Sequence 1765 AA;

Query Match 94.1%; Score 8873; DB 5; Length 1765;
Best Local Similarity 92.9%; Pred. No. 0;
Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

QY 1 EPYCVSHLQEDKXCFICSDSDPYHETLNPDSHLIENVVTTTFAPNRLKIWQSENGVENV 60
Db 41 EPYCVSHLQEDKXCFICNSQDPYHETLNPDSHLIENVVTTTFAPNRLKIWQSENGVENV 100

QY 61 TIQLDLAEAFHFTLIMTFTFRPAAMLIERSDFGKTGWYRYFAYDCESSFPGISGTP 120
Db 101 TIQLDLAEAFHFTLIMTFTFRPAAMLIERSDFGKTGWYRYFAYDCEASFPGISGTP 160
QY 121 MKKVDDIIICDSRYSDIEPSTEGEVIFFALDPAFKIEDPYSPIQNLKITNLRIKFKVLH 180
Db 161 MKKVDDIIICDSRYSDIEPSTEGEVIFFALDPAFKIEDPYSPIQNLKITNLRIKFKVLH 220
QY 181 TLGDNLLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHCHMCR 240
Db 221 TLGDNLLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHCHMCR 280
QY 241 HNTKGLNCELNDYHDLWPRPAEGRNSNACKKNCNEHSSSCHFDMAVFLATGNVSGGV 300
Db 281 HNTKGLNCELNDYHDLWPRPAEGRNSNACKKNCNEHSSSCHFDMAVFLATGNVSGGV 340
QY 301 CDNCOHNTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 360
Db 341 CDDCOHNTMGRNCEQCKPFYFQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTGL 400
QY 361 IAGQCRCKLHVEGERCDVCKEGFYDLSEADPYGCKSCACNPLGTIPGGNPCDSETGYCYC 420
Db 401 IAGQCRCKLHVEGERCDVCKEGFYDLSEADPYGCKSCACNPLGTIPGGNPCDSETGYCYC 460
QY 421 KRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCLGGALNNSCSEDSGQCSCLPHMIGRCQN 480
Db 461 KRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCLGGALNNSCSEDSGQCSCLPHMIGRCQN 520
QY 481 EVESGYFTTLDHYIYEAEEANLGGVVRVVERQYIQDRIPSWTGGFVRVPEGAYLEFFI 540
Db 521 EPEGYFPATLDHYLYEAEEANLGGVVRVVERQYIQDRIPSWTGGFVRVPEGAYLEFFI 580
QY 541 DNIPYSMEYELIRYEPQLPDHWEKAVITVORPGKIIPASSRCGNTVPPDDNQQVVSLSPGS 600
Db 581 DNIPYSMEYELIRYEPQLPDHWEKAVITVORPGKIIPASSRCGNTVPPDDNQQVVSLSPGS 640
QY 601 RYVVLPRPVCFEKGMNTYTVRLELDQYTAGSDVESPYTFIDSLVLMPCYCKSLDIFTVGS 660
Db 641 RYVVLPRPVCFEKGMNTYTVRLELDQYTAGSDVESPYTFIDSLVLMPCYCKSLDIFTVGS 700
QY 661 GDGEVTSNASETFORRYRCLENSRSVVKTPMTDVCNIIIFISALIHOTGLACECDPQGS 720
Db 701 GDGEVTSNASETFORRYRCLENSRSVVKTPMTDVCNIIIFISALIHOTGLACECDPQGS 760
QY 721 SSVCDPENGGOCCRPNVVGRTCNRCAPGTGFGPNCXPCDCHLQGSASAFCDAITGQCH 780
Db 761 SSVCDPENGGOCCRPNVVGRTCNRCAPGTGFGPNCXPCDCHLQGSASAFCDAITGQCH 820
QY 781 CFQGIYARQCDRLPGYWGFPSPCQCNGHALDCDVTGECCLSCDQYTTGHCNRCCLAG 840
Db 821 CFQGIYARQCDRLPGYWGFPSPCQCNGHALDCDVTGECCLSCDQYTTGHCNRCCLAG 880
QY 841 YGDPPIIGSGDHCRPCPCPDGSDGRQFARSCYQDPVTLQACVCDPGYIGSRCDCCASG 900
Db 881 YGDPPIIGSGDHCRPCPCPDGSDGRQFARSCYQDPVTLQACVCDPGYIGSRCDCCASG 940
QY 901 FFGNPSDFGSGCQPCQCHENITDTPDPEACDKDTGRCLKLYHTEGDHCOLCQYGYGDAL 960
Db 941 YFGNPSDFGSGCQPCQCHENITDTPDPEACDKDTGRCLKLYHTEGDHCOLCQYGYGDAL 1000
QY 961 RODCRKVCNLYLGTVKEHNCNSDCHCDKATGQCSCLPNVIGONCDRCAPNTWQLASGTGC 1020
Db 1001 RODCRKVCNLYLGTVKEHNCNSDCHCDKATGQCSCLPNVIGONCDRCAPNTWQLASGTGC 1060
QY 1021 GPCNCNAAHSFGPSCNEFTGQCCQMPGFGGRTCSCEQLFWGDPDVECRACDDPRGIET 1080
Db 1061 DPCNCNAAHSFGPSCNEFTGQCCQMPGFGGRTCSCEQLFWGDPDVECRACDDPRGIET 1120
QY 1081 PQCDQSTGQCVCEGVEGPRCDKTRGYSGVFPDCTPCHQCFALWDAIIGELTNRTHKFL 1140
Db 1121 PQCDQSTGQCVCEGVEGPRCDKTRGYSGVFPDCTPCHQCFALWDAIIGELTNRTHKFL 1180
QY 1141 EKAKALKISGVIPIRETVDVSVEKKVNEIKDILAQSPAAPLKNIGILFEEAEKLTQDVT 1200

Db 1181 EKAKALKISGVIGPYRETVDVSVERKVSEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDV 1240
Qy 1201 EKMAQVEVKLTDTASQSNSTAGELQAQAEASLDKTVKELAEQLEFIKNSDIQALDSI 1260
Db 1241 EMMAQVEVKLSDBTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSI 1300
Qy 1261 TKYFQMSLEAEKRVNASTTDPNSTVEQSLTRDRVEDLMLERESPFKEQEEQARLLDEL 1320
Db 1301 TKYFQMSLEAEERVNASTTEPNSTVEQSLMRDRVEDVMMERESQFKEQEEQARLLDEL 1360
Qy 1321 AGKLQSLDLSAAQMTCTGTPPGADCSSECGGPNCRDTDEGEKKCGGPGCGGLVTVAHSAW 1380
Db 1361 AGKLQSLDLSAAAEVMTCTGTPPGASCSETECGGPNCRDTDEGERKCGGPGCGGLVTVAHNAW 1420
Qy 1381 QKAMDFDRDVLASALAEVEQLSKMVSEAKVRADEAKONAQDVLLKTNATKEKVDKSNEDLR 1440
Db 1421 QKAMDLDQDVLASALAEVEQLSKMVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNEDLR 1480
Qy 1441 NLIKQIRNFLTQDSADLDSIEAVANEVLKSGNASTPQQLQNLTDIERVETLSQVEVIL 1500
Db 1481 NLIKQIRNFLTQDSADLDSIEAVANEVLKSGNASTPQQLQNLTDIERVESLSQVEVIL 1540
Qy 1501 QQSAADIARAELLLEBAKRAKRSATDVKVVTADVMVKEALEEAEKAAQVAAEKAIKQADEDIQ 1560
Db 1541 QHSAADIARAEMLLLEBAKRAKRSATDVKVVTADVMVKEALEEAEKAAQVAAEKAIKQADEDIQ 1600
Qy 1561 GTQNLLTSIESETAASEETLTNASQRIKSLERNVEELKRKAQNSGAEYIEKVVSVKQ 1620
Db 1601 GTQNLLTSIESETAASEETLTNASQRISELERNVEELKRKAQNSGAEYIEKVVSVKQ 1660
Qy 1621 NADDVKKTLTGELDEKVKVYVESLIAQKTEESADARRKAELLQNEAKTLLAQANSKLQLLK 1680
Db 1661 SAEDVKKTLTGELDEKVKVYVESLIAQKTEESADARRKAEMLQNEAKTLLAQANSKLQLLK 1720
Qy 1681 DLERKYEDNQYLEDKAQLVRLEGEVRSLLKDISEKVAVYSTCL 1725
Db 1721 DLERKYEDNQYLEDKAQLARLEGEVRSLLKDISQKAVAVYSTCL 1765

RESULT 12
AAW50893
ID AAW50893 standard; protein; 1786 AA.
XX
AC AAW50893;
XX
DT 07-DEC-1998 (first entry)
XX
DE Human laminin B1 chain.
XX
KW Laminin; human; beta-amyloid; amyloidosis; Alzheimer's disease;
KW Down's syndrome; hereditary cerebral haemorrhage; inflammation;
KW malignancy; Familial Mediterranean Fever; multiple myeloma;
KW type II diabetes; prion disease; Creutzfeldt-Jacob disease; CJD;
KW Gertsmann-Straussler syndrome; kuru; scrapie; haemodialysis;
KW carpal tunnel syndrome; senile cardiac amyloid polyneuropathy;
KW Familial Amyloidotic Polyneuropathy; thyroid carcinoma; diagnosis;
KW therapy.
XX
OS Homo sapiens.
XX
PN WO9815179-A1.
XX
PD 16-APR-1998.
XX
PF 08-OCT-1997; 97WO-US018145.
XX
PR 08-OCT-1996; 96US-0027981P.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Castillo G, Snow AD;
XX

WPI; 1998-240534/21.
Use of laminin and fragments - for developing products for use in the diagnosis and treatment of amyloid disease, e.g. Alzheimer's disease or CJD.
Claim 15; Page 86-89; 132pp; English.
This is the amino acid sequence of the human laminin B1 chain. The primary object of the invention is to use laminin, laminin-derived protein fragments and/or laminin-derived polypeptides as potent inhibitors of amyloid formation, deposition, accumulation and/or persistence in Alzheimer's disease and other amyloidoses. The laminin products (see AAW50888-98) may include mouse or human laminin A or A1 chain, laminin B1 or B2 chain, laminin A2 chain (merosin), laminin G1 chain, the globular repeats of the laminin A1 chain and the beta-amyloid binding domain of the laminin A chain. A claimed method for treating an amyloid disease comprises administering a polypeptide having a conformational similarity to a fragment of a laminin protein. A method for diagnosing an amyloid disease involves determining levels of laminin in a sample. Production of laminin or its fourth globular repeat in vivo provides a method for in vivo inhibition of beta-amyloid amyloidosis. The products and methods can be used for the diagnosis, prognosis, monitoring and treatment of amyloidoses such as Alzheimer's disease, Down's syndrome and hereditary cerebral haemorrhage with amyloidosis of the Dutch type (where the specific amyloid is the beta-amyloid protein), the amyloidosis associated with chronic inflammation, various forms of malignancy and Familial Mediterranean Fever (AA amyloid or inflammation-association amyloidosis), the amyloidosis associated with multiple myeloma and other B-cell abnormalities (AL amyloid), the amyloidosis associated with type II diabetes (amylin or islet amyloid), the amyloidosis associated with prion diseases including Creutzfeldt-Jacob disease, Gertsmann-Straussler syndrome, kuru and animal scrapie (PrP amyloid), the amyloidosis associated with long-term haemodialysis and carpal tunnel syndrome (beta 2-microglobulin amyloid), the amyloidosis associated with senile cardiac amyloid and Familial Amyloidotic Polyneuropathy (prealbumin or transthyretin amyloid), and the amyloidosis associated with endocrine tumours such as medullary carcinoma of the thyroid (variant of procalcitonin)

Query Match 94.1%; Score 8873; DB 2; Length 1786;
Best Local Similarity 92.9%; Pred. No. 0;
Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;
Sequence 1786 AA;
Qy 1 EPYCIIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENV 60
Db 62 EPYCIIVSHLQEDKKCFICDSQDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENV 121
Qy 61 TIQLDLEAEFHFTHLIMTFKTRPAAMLIERSDFGKTGWVYRYFAYDCESFPGISTGP 120
Db 122 TIQLDLEAEFHFTHLIMTFKTRPAAMLIERSDFGKTGWVYRYFAYDCESFPGISTGP 181
Qy 121 MKKVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPIQNLLKITNLRKFVKLH 180
Db 182 MKKVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPIQNLLKITNLRKFVKLH 241
Qy 181 TLGDNLLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMCR 240
Db 242 TLGDNLLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMCR 301
Qy 241 HNTKGLNCELMDFFYHDLFWPRAEGRNSNACKKNCNEHSSSCHFDMAVFLATGNVSGGV 300
Db 302 HNTKGLNCELMDFFYHDLFWPRAEGRNSNACKKNCNEHSSSCHFDMAVFLATGNVSGGV 361
Qy 301 CDNCQHNMTGRNCEQCKPFYQHPERDIRDPNLCBPCTCDPAGSENGGICDGYTDFSVGL 360
Db 362 CDDCQHNMTGRNCEQCKPFYQHPERDIRDPNLCBPCTCDPAGSENGGICDGYTDFSVGL 421
Qy 361 IAGQCRCKLHVEGERCDVCKEGFYDLSEADPYGCKSKACNPLGTIPGGNPNCDSETGYCYC 420
Db 422 IAGQCRCKLHVEGERCDVCKEGFYDLSEADPYGCKSKACNPLGTIPGGNPNCDSETGYCYC 481

QY 421 KRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCDLGGLNNSCSEDSGQCSCPLHMIQRQCN 480
Db 482 KRLVTGQHCDQCLPQHWGLSNDLDGCRPCDCDLGGLNNSCFAESGQCSCRPHMIGRQCN 541
QY 481 EVESGYFTTLDHYIYEAEEANLPGVWVVERQYIQRIPSWTGPGRVVRPEGAYLEFFI 540
Db 542 EVERGYFATLDHYLYEAEEANLPGVSIIVERQYIQRIPSWTGPGRVVRPEGAYLEFFI 601
QY 541 DNIPIYSMEYEILIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTVPDDDNQVVSLSPGS 600
Db 602 DNIPIYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPFSSRCGNTIPDDDNQVVSLSPGS 661
QY 601 RYVVLPRPVCFEKGMNVTVRLELPOYTASGSDVESPYTFIDSLVLMPYCKSLDIFTVGS 660
Db 662 RYVVLPRPVCFEKGTNYTVRLELPOYTSSDSDVESPYTLIDSLVLMPYCKSLDIFTVGS 721
QY 661 GDGEVINSAWETFORYRCLNSRSVVKTPTMTDVCNIIIFSALIHQTGLACECDPQGS 720
Db 722 GDGVVINSAWETFORYRCLNSRSVVKTPTMTDVCNIIIFSISALLHQTGLACECDPQGS 781
QY 721 SSVCDPNNGQCQCRPNVVGRTCNRCAPGTFGFGPGNGCKPCDCHLQGSASAFCDAITGQCH 780
Db 782 SSVCDPNNGQCQCRPNVVGRTCNRCAPGTFGFGPGSGCKPCECHLQGSVNAFCNPTVGTQCH 841
QY 781 CFQGIYARQCDRCLPGYWGFPSCQPCQCNHGLDCTVTGECCLSCQDYTTGHNCERCLAG 840
Db 842 CFQGVYARQCDRCLPGHWGFPSCQPCQCNHGLDCTVTECLNQCQDYTMGHNCERCLAG 901
QY 841 YYGDPPIIGSDHCRPCPCPDGPDGSRGFARSCYQDPVTQLACVCDPGYIGSRCDDCASG 900
Db 902 YYGDPPIIGSDHCRPCPCPDGPDGSRGFARSCYQDPVTQLACVCDPGYIGSRCDDCASG 961
QY 901 FFGNPSDFGSCQPCQCHNIDTTDPEACDKDTGRCLKCLYHTEGDHCQLCQYGYGDAL 960
Db 962 YFGNPSDFGSCQPCQCHNIDTTDPEACDKETGRCLKCLYHTEGEHCQCFRFGYGDAL 1021
QY 961 RQDRKCKVCNVLGTVKEHNGSDCHCDKATGQCSCCLPNVIGQNCDCRCPNTWQLASGTGC 1020
Db 1022 RQDRKCKVCNVLGTVOEHNGSDCQCDKATGQCCLPNVIGQNCDCRCPNTWQLASGTGC 1081
QY 1021 GPCNCNAHSFGPSCNEFTGQCQCMFGFGGRTCECQELFWGDDPDVECRACDCDPERGIET 1080
Db 1082 DPCNCNAHSFGPSCNEFTGQCQCMFGFGGRTCECQELFWGDDPDVECRACDCDPERGIET 1141
QY 1081 PQCDQSTGQCVCVEGVEGPRCDKCTRGYSGVFPDCTPCHQCFALWDAAIGELTNRTHKFL 1140
Db 1142 PQCDQSTGQCVCVEGVEGPRCDKCTRGYSGVFPDCTPCHQCFALWDVIIAELTNRTHRFL 1201
QY 1141 EKAKALKISGIVGYPYRETVDVSVEKKVNEIKDILAQSPAAEPLKNIGILFEEAEKLTQDVT 1200
Db 1202 EKAKALKISGIVGYPYRETVDVSVERKVSEIKDILAQSPAAEPLKNIGILFEEAEKLTQDVT 1261
QY 1201 EKMAQVEVKLTDTASQSNSTAGELGALQAEASLDKTVKELAQLEFIKNSDIOGALDSI 1260
Db 1262 EMMAQVEVKLSDBTTSQSNSTAKELDSLQTEAESLDNTVKELAQLEFIKNSDIRGALDSI 1321
QY 1261 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLERESPFKEQQEEQARLLDEL 1320
Db 1322 TKYFQMSLEAEKRVNASTTEPNSTVEQSALMRDRVEDVMMERESQFKEKQEEQARLLDEL 1381
QY 1321 AGKLQSLDLSAAQMTCTGTPPGADCSSEBGGPNCRCTDEGEKKCGGPGCGGLVTVAHSAW 1380
Db 1382 AGKLQSLDLSAAAEMTCTGTPPGASCSETECGGPNCRCTDEGERKCGGPGCGGLVTVAHNAW 1441
QY 1381 QKAMDFDRDVLGALAEVEQLSKMVSEAKVRADEAKQNAQDVLLKTNATKEKVKDSNEDLR 1440
Db 1442 QKAMDLQDVLGALAEVEQLSKMVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNEDLR 1501
QY 1441 NLIKQIRNFLTDSADLDSIEAVANEVLKSGNASTPQQLQNLNLTEDIRERVETLSQVEVIL 1500
Db 1502 NLIKQIRNFLTQDSADLDSIEAVANEVLKMEMPSTPQQLQNLNLTEDIRERVESLSQVEVIL 1561

QY 1501 QQSAADIARAELLLEAKRASKSATDVKVTADMVKEALEEAEKAQVAAEKAIKQADEDIQ 1560
Db 1562 QHSAADIARAEMLLLEAKRASKSATDVKVTADMVKEALEEAEKAQVAAEKAIKQADEDIQ 1621
QY 1561 GTQNLLTSISETAASEETLTNASQRI SKLERNVEELKRKAAQNSGEAEYIEKVYISVKQ 1620
Db 1622 GTQNLLTSISETAASEETLTNASQRI SE LERNVEELKRKAAQNSGEAEYIEKVYITVKQ 1681
QY 1621 NADDVKKTLDGELDEKYYKKVESLTAQKTEESADARRKAE LLQNEAKTLLAQANSKLQLE 1680
Db 1682 SAEDVKKTLDGELDEKYYKKVENLIAK KTEESADARRKAEMLQNEAKTLLAQANSKLQLLK 1741
QY 1681 DLERKYEDNQKYLEDKAQELVRLGEVRSLLKDI SEKVAVYSTCL 1725
Db 1742 DLERKYEDNQRYLEDKAQELARLEGEVRSLLKDISQKVAVYSTCL 1786
RESULT 13
AAB16522
ID AAB16522 standard; protein; 1786 AA.
XX AAB16522;
AC AAB16522;
DT 27-OCT-2000 (first entry)
XX Human laminin protein sequence.
DE Angiogenesis-inhibiting protein receptor; angiogenesis; angiostatin;
XX endostatin; plasminogen; laminin; treatment; wound healing; solid tumour;
KW psoriasis; scleroderma; myocardial angiogenesis; Crohn's disease;
KW cerebral collateral; arteriovenous malformation; rubeosis; cancer;
KW diabetic retinopathy; arthritis; wound healing; peptic ulcer;
KW Helicobacter related disease; fracture; cat scratch fever.
XX Homo sapiens.
OS WO200032631-A2.
PN 08-JUN-2000.
XX 06-DEC-1999; 99WO-US028897.
PF 04-DEC-1998; 98US-00206059.
XX (ENTR-) ENTREMED INC.
PA Macdonald NJ, Sim KL;
XX WPI; 2000-412290/35.
XX New angiogenesis-inhibiting protein receptors, useful in methods for
PT treating diseases and processes that are mediated by angiogenesis, such
PT as solid tumors, psoriasis, scleroderma and myocardial angiogenesis.
XX Claim 1; Fig 6A; 100pp; English.
XX This invention relates to angiogenesis-inhibiting protein receptors, and
CC the DNA sequences encoding them. Angiogenesis is the generation of new
CC blood vessels into a tissue, and normally occurs in wound healing, foetal
CC and embryonal development and the formation of the corpus luteum,
CC endometrium and placenta. Angiostatin is a protein (see AAB16450 and
CC AAA68202) involved in angiogenesis, and has an amino acid sequence
CC similar to that of a plasminogen fragment (see murine plasminogen
CC AAB16490). Angiostatin has the ability to inhibit angiogenesis.
CC Endostatin is also an angiogenesis inhibiting protein (see AAB16451 and
CC AAA68203). Sequences AAA68242 and AAB16522 represent coding and protein
CC sequences of human laminin. Laminin is an angiostatin binding regions of
CC and some of the peptides of the invention share homology with regions of
CC laminin. Peptides AAB16452-B16521 (excluding AAB16490) are the
CC angiogenesis-inhibiting protein receptor fragments of the invention. The
CC peptides bind either angiostatin or endostatin and can be used in methods
CC for treating diseases and processes that are mediated by angiogenesis,
CC such as solid tumours, psoriasis, scleroderma, myocardial angiogenesis,

CC	Crohn's disease, cerebral collaterals, arteriovenous malformations,									
CC	rubeosis, diabetic retinopathy, arthritis, wound healing, peptic ulcers,									
CC	Helicobacter related diseases, fractures, placentation and cat scratch									
CC	fever. They are useful for the detection and prognosis of cancer. DNA									
CC	sequences A628204-A628241 encode the peptides of the invention									
XX										
SQ	Sequence 1786 AA;									
	Query Match 94.1%; Score 8873; DB 3; Length 1786;									
	Best Local Similarity 92.9%; Pred. No. 0;									
	Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0									
QY	1	EPYCIYVSHLQEDKKCFICSDRDPYHETLNPDSHLIENVVTTFAPNRLKIWQSENGVENV	60							
Db	62	EPYCIYVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVVTTFAPNRLKIWQSENGVENV	121							
QY	61	TIQLDLEAEFHFTHLIMTFKTPRPAAMLIERSSDFGTWGVYRYFAYDCESPFGISTGP	120							
Db	122	TIQLDLEAEFHFTHLIMTFKTPRPAAMLIERSSDFGTWGVYRYFAYDCEASFPFGISTGP	181							
QY	121	MKKYVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLLKITNLRIKFVKLH	180							
Db	182	MKKYVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLLKITNLRIKFVKLH	241							
QY	181	TLGDNLLDSRMEIREKYVYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGVHGHCMCR	240							
Db	242	TLGDNLLDSRMEIREKYVYAVYDMVVRGNCFCYGHASECAPVDGFNEEVEGVHGHCMCR	301							
QY	241	HNTKGLNCELAMDYHDLPRPAEGRNSNACKKNCNNEHSSCHFDMAVFLATGNVSGGV	300							
Db	302	HNTKGLNCELAMDYHDLPRPAEGRNSNACKKNCNNEHSSCHFDMAVYLATGNVSGGV	361							
QY	301	CDNCQHTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL	360							
Db	362	CDDCQHTMGRNCEQCKPFYFQHPERDIRDPNFCERCCTCDPAGSQNEGICDSYDFSTGL	421							
QY	361	IAGQCRCKLVHEGERCDVCKEGFYDLSEAEDPYGCKSKACNPLGTIPGGNPCDSETGYCYC	420							
Db	422	IAGQCRCKLVNVEGEHCDVCKEGFYDLSSDDPFYGCKSKACNPLGTIPGGNPCDSETGHYCYC	481							
QY	421	KRLVTGORCDQCLPOHWGLSNDLDCRPRCDCLGGALNNSCEDSGQCSCLPHMIGRCQN	480							
Db	482	KRLVTGOHCDQCLPEHWGLSNDLDCRPRCDCLGGALNNSCFAESGQCSRPHMIGRCQN	541							
QY	481	EVESGYFTTLDHYIYEAEANLPGVVVVERQYIQDRIPSWTGPVVRVPEGAYLEFFI	540							
Db	542	EVPEGYFATLDHYLYEAEANLPGVSVIVERQYIQDRIPSWTGPVVRVPEGAYLEFFI	601							
QY	541	DNIPYSMEYEILIRYEPQLPDHWEKAVITVORPGKIPASSRCGNTVPDDDNQVVSLSPGS	600							
Db	602	DNIPYSMEYDILIRYEPQLPDHWEKAVITVORPGRIPTSSRCGNTIPDDDNQVVSLSPGS	661							
QY	601	RYVVLPRPVCFEKGMNYYTVRLELPOYTASGSDVESPYTFIDSLVLMPYCKSLDIFTVGS	660							
Db	662	RYVVLPRPVCFEKGNTYTVRLELPOYTSSDSDVESPYTLIDSLVLMPYCKSLDIFTVGS	721							
QY	661	GDGEVTSNAWETFORYRCLENSRSVVKTPTMTDVCNRIIFSISALIHQTGLACECDPQGS	720							
Db	722	GDGVVTSNAWETFORYRCLENSRSVVKTPTMTDVCNRIIFSISALLHQTGLACECDPQGS	781							
QY	721	SSVCDPNGQCCQCRPNVVGRTCNRCAPGTFFGPGNGCKPCDCHLQGSASAFCDAITGQCH	780							
Db	782	SSVCDPNGQCCQCRPNVVGRTCNRCAPGTFFGPGSGCKPCDCHLQGSVNAFCNPVTGQCH	841							
QY	781	CFQGIYARQCDRCLPGYWGFPSCQPCQNGHALDCTVTGSECLSCQDYTTGHNCRCLAG	840							
Db	842	CFQGVYARQCDRCLPGHWGFPSCQPCQNGHADDDCPVTGSECLNCQDYTMGHNCRCLAG	901							
QY	841	YGGDPIIGSDHCRPCPCPDGPDGSRQFARSCYQDPVTLQACVCDPGYIGSRCDDCASG	900							
Db	902	YGGDPIIGSDHCRPCPCPDGPDGSRQFARSCYQDPVTLQACVCDPGYIGSRCDDCASG	961							
QY	901	FFGNPSDFGSCQPCQCHNIDTTDPEACDKDTGRCLKCLYHTEGDHCOLCQYGYGDAL	960							

Db	962	YFGNPFSEVGGSCQPCQCHNIDTTDPEACDKETGRCLKCLYHTEGEHCQCFRFGYGDAL	1021							
QY	961	RQCRKVCVNYLGTVKEHNGSDCHCDKATGQCSCLPNVIGONCDRCAPNTWQLASGTGC	1020							
Db	1022	RQCRKVCVNYLGTVQEHNGSDCQCDKATGQCLCLPNVIGONCDRCAPNTWQLASGTGC	1081							
QY	1021	GPCNCAAHSFPGPSCNEFTGQCQCMPPGFGGRTCSCEQLFWGDDPDVECRACDCDPRGIET	1080							
Db	1082	DPCNCAAHSFPGPSCNEFTGQCQCMPPGFGGRTCSCEQLFWGDDPDVECRACDCDPRGIET	1141							
QY	1081	PQCDQSTGQCVCEGVEGPRCDKCTRGYSGVFPDCTPCHQCFALWDALIGELTNRTHKFL	1140							
Db	1142	PQCDQSTGQCVCEGVEGPRCDKCTRGYSGVFPDCTPCHQCFALWDVILIAELTNRTHKFL	1201							
QY	1141	EKAKALKISGVIGPYRETVDSEKVKVNEIKDILAQSPAAEPLKNIGILFEEAEKLIKDYT	1200							
Db	1202	EKAKALKISGVIGPYRETVDSEKVKVSEIKDILAQSPAAEPLKNIGILFEEAEKLIKDYT	1261							
QY	1201	EKMAQVEVKLTDTASQSNSTAGELGALQAAESLDTVKELAEQLFINKNSDIQGALDSI	1260							
Db	1262	EMMAQVEVKLSDTTSQSNSTAKELDSLQTEAESLDTVKELAEQLFINKNSDIRGALDSI	1321							
QY	1261	TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLERESPFEKQEQEEQARLLDEL	1320							
Db	1322	TKYFQMSLEAEERNVASTTPEPSTVEQSALMRDRVEDVMMERESQFKEKQEQEARLLDEL	1381							
QY	1321	AGKLSLDLSAAAQMTCTGTPPGADCSSECGGPNCRDTDEGEKKCGGPGGLVTVAHSAW	1380							
Db	1382	AGKLSLDLSAAAEMTCGTPPGASCSETGCGGPNCRDTDEGERKCGGPGGLVTVAHNAW	1441							
QY	1381	OKAMDFDRDVLALAEVEQLSKMVSEAKVRADEAKQNAQDVLKTNATKEKVKDSNEDLR	1440							
Db	1442	OKAMDLDDQVLSALAEVEQLSKMVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNEELR	1501							
QY	1441	NLIKQIRNFLTEDSADLDSIEAVANEVLKSGNASTPQQQLQNLTEDIRERVETLSQVEVIL	1500							
Db	1502	NLIKQIRNFLTQDSADLDSIEAVANEVLKMEPSTPQQQLQNLTEDIRERVESLSQVEVIL	1561							
QY	1501	QSSAADIAEAELLLLEAKRASKSATDVKVTADMVKEALEEAEKAQVAAEKAIKQADEDIQ	1560							
Db	1562	QSSAADIAEAELLLLEAKRASKSATDVKVTADMVKEALEEAEKAQVAAEKAIKQADEDIQ	1621							
QY	1561	GTQNLTSIESETAASEETLTNASQRIKSLERNVEELKRAAQNSGEAEYIEKVVSVKQ	1620							
Db	1622	GTQNLTSIESETAASEETLTNASQRISELERNVEELKRAAQNSGEAEYIEKVVSVKQ	1681							
QY	1621	NADDVKITLDGELDEKYKKVESLIAQKTEESADARRKAEILLQNEAKTLAQANSKLQLE	1680							
Db	1682	SAEDVKITLDGELDEKYKKVENLIAKTEESADARRKAEMLQNEAKTLAQANSKLQLLK	1741							
QY	1681	DLERKYEDNQKYLEDKAQELVRLGEVRSLLKDISKQVAVYSTCL	1725							
Db	1742	DLERKYEDNQRYLEDKAQELARLEGEVRSLLKDISQKQVAVYSTCL	1786							

RESULT 14

AAB19797
ID AAB19797 standard; protein; 1786 AA.

XX AAB19797;

XX 05-MAR-2001 (first entry)

XX Human laminin 2 beta-1 chain.

XX Laminin 2; human; nerve regeneration; angiogenic; cell adhesion;
KW degenerative muscle disorder; muscular dystrophy; cell therapy.

XX Homo sapiens.

XX Key Location/Qualifiers
FH Peptide 1. .21

FT	Protein	/label= Signal_peptide
FT		22. .1786
FT		/label= Mature_protein
XX	WO200066730-A2.	
XX		
PD	09-NOV-2000.	
XX		
PF	28-APR-2000; 2000WO-US011378.	
XX		
PR	30-APR-1999; 99US-0131720P.	
PR	15-JUN-1999; 99US-0139198P.	
PR	12-JUL-1999; 99US-0143289P.	
PR	24-SEP-1999; 99US-0155945P.	
XX		
PA	(UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.	
XX		
PI	Yurchenco P;	
XX		
DR	WPI; 2000-687537/67.	
XX	N-PSDB; AAA88897.	
PT	Purified laminin 2 protein, useful for research and therapeutic purposes	
PT	including peripheral nerve regeneration, treatment of degenerative muscle	
PT	disorders, angiogenesis regulation, and ex vivo cell therapy.	
XX		
PS	Claim 5; Page 186-191; 305pp; English.	
XX		
CC	The present sequence is that of the beta-1 chain of human laminin 2.	
CC	Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1	
CC	(100 kDa) chains. It is thought to be specifically required for	
CC	stabilizing myotubes during skeletal muscle development, and for	
CC	preventing apoptosis. Genetic defects in its structure or expression are	
CC	associated with a major type of congenital muscular dystrophy. Laminin 2	
CC	is also thought to be important in Schwann cell/basal lamina	
CC	interactions. The invention provides laminin 2 alpha-2, beta-1 and gamma-	
CC	1 chain polypeptides (see AAB19791-806) and the polynucleotides encoding	
CC	them (see AAA88891-906), methods for making recombinant laminin 2, cells	
CC	that express recombinant laminin 2, and methods for using purified	
CC	laminin 2 for research and therapeutic purposes including peripheral	
CC	nerve regeneration, treatment of degenerative muscle disorders,	
CC	angiogenesis regulation, promoting cell attachment and migration, ex vivo	
CC	cell therapy, improving the take of grafts, improving the	
CC	biocompatibility of medical devices and preparing improved culture	
XX	devices and media	
SQ	Sequence 1786 AA;	
	Query Match 94.1%; Score 8873; DB 3; Length 1786;	
	Best Local Similarity 92.9%; Pred. No. 0;	
	Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;	
QY	1 EPYCIVSHLQEDKCFICNSQDPYHETLNPDShLIENVTTFPAPNRLKIWQSENGVENV 60	
DB	62 EPYCIVSHLQEDKCFICNSQDPYHETLNPDShLIENVTTFPAPNRLKIWQSENGVENV 121	
QY	61 TIQLDLEAEFHFTHLIMTFKTRPAAMLIERSSDFGKTGWVRYFPAYDCESSFPGISGCP 120	
DB	122 TIQLDLEAEFHFTHLIMTFKTRPAAMLIERSSDFGKTGWVRYFPAYDCEASFPGISGCP 181	
QY	121 MKKVDDIICDSRYSIDIEPSTEGEVI FRALDPAFKIEDPYSPIQNLLKITNLRKIFVKLH 180	
DB	182 MKKVDDIICDSRYSIDIEPSTEGEVI FRALDPAFKIEDPYSPIQNLLKITNLRKIFVKLH 241	
QY	181 TLGDNLLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGHCRCR 240	
DB	242 TLGDNLLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGHCRCR 301	
QY	241 HNTKGLNCEL CMD FVHDL PWRPAEGRNSNACKNCNEHSSSCHFDMAVFLATGNVSGGV 300	
DB	302 HNTKGLNCEL CMD FVHDL PWRPAEGRNSNACKNCNEHSSSCHFDMAVFLATGNVSGGV 361	
QY	301 CDNCQHNTMGRNCEQCKPFYQHPERDIRDPNLCPEPCTCDPAGSENGGICDGYTDFSVGL 360	

Db	362 CDDCQHNTMGRNCEQCKPFYQHPERDIRDPNLCPEPCTCDPAGSQNEGICDSYDFSTGL 421	
QY	361 IAGQCRCKLHVEGERCDVCKEGFYDLSEAEDPYGCKSCACNPLGTIPGGNCPDSETGYCYC 420	
DB	422 IAGQCRCKLHVEGERCDVCKEGFYDLSSDPFGCKSCACNPLGTIPGGNCPDSETGHCYC 481	
QY	421 KRLVTGQRCDQCLPQHWSLNDLDGCRPCDCDLGGALNNSCSEDSGQCSCLPHMIGRQCN 480	
DB	482 KRLVTGQRCDQCLPQHWSLNDLDGCRPCDCDLGGALNNSCFAESGQCSCLPHMIGRQCN 541	
QY	481 EVESGYFTTLDHYIYEAEEANLPGVVVVERQYIQDRIPSWTGPFRVPEGAYLEFFI 540	
DB	542 EVERGYFATLDHYLYEAEEANLPGVSIIVERQYIQDRIPSWTGPFRVPEGAYLEFFI 601	
QY	541 DNIPYSMEYEILIRYEPQLPDHWEKAVITVQRPKIPASSRRCGNTVPDDDNQVVSLSPGS 600	
DB	602 DNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPTSRRCGNTIPDDDNQVVSLSPGS 661	
QY	601 RYVVLPRPVCFEKGMNVTVRLELPQYTAGSGSDVESPYTFIDSLVLMPCYKSLDIFTVGS 660	
DB	662 RYVVLPRPVCFEKGMNVTVRLELPQYTAGSGSDVESPYTFIDSLVLMPCYKSLDIFTVGS 721	
QY	661 GDGEVNTNSAWETFORYRCLENSRSVVKTPMTDVCNRIIPFISALIHQTGLACECDPQSG 720	
DB	722 GDGVNTNSAWETFORYRCLENSRSVVKTPMTDVCNRIIPFISALLHQTGLACECDPQSG 781	
QY	721 SSVCDPNGGQCCQCRPNVGRTRCNRCAPGTGFGGPGNGKPCDCDLQGSASAFCAITGQCH 780	
DB	782 SSVCDPNGGQCCQCRPNVGRTRCNRCAPGTGFGGPGNGKPCDCDLQGSVNAFCNPVTGQCH 841	
QY	781 CFQGIYARQCDRCLPGYWGFPSPQPCQCNHGDCTVTGECCLSCQDYTTGHNCERCLAG 840	
DB	842 CFQGVYARQCDRCLPGYWGFPSPQPCQCNHGDCTVTGECCLSCQDYTTGHNCERCLAG 901	
QY	841 YYGDPPIIGSGDHCRCPCPDGDSGRQFARSQYQDPVTLQACVCDPQYIGSRCDDCASG 900	
DB	902 YYGDPPIIGSGDHCRCPCPDGDSGRQFARSQYQDPVTLQACVCDPQYIGSRCDDCASG 961	
QY	901 FFGNPSDFGSGCQPCQCHNIDITTDPEACDKDTGRCLKCLYHTEGDHCLCQYGYGDAL 960	
DB	962 YFGNPSDFGSGCQPCQCHNIDITTDPEACDKDTGRCLKCLYHTEGDHCLCQYGYGDAL 1021	
QY	961 RODCRKVCNVLGTIVKEHNGSDCHCDKATGQCSCLPNVIGQNCRCAPNTWQLASGTGC 1020	
DB	1022 RODCRKVCNVLGTIVKEHNGSDCHCDKATGQCSCLPNVIGQNCRCAPNTWQLASGTGC 1081	
QY	1021 GPCNCAHSGFPGSCNEFTGQCCQMPFGGRTCEQELFWGDDVECRACDCDPRGIET 1080	
DB	1082 DPCNCAHSGFPGSCNEFTGQCCQMPFGGRTCEQELFWGDDVECRACDCDPRGIET 1141	
QY	1081 PQCDQSTGQCVVEGVGPRCDKCTRGYSGVFPDCTPCHQCFALWDIAIGELTNRTHKFL 1140	
DB	1142 PQCDQSTGQCVVEGVGPRCDKCTRGYSGVFPDCTPCHQCFALWDIAIGELTNRTHRFL 1201	
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QY	1201 EKMAQVEVKLTDTASQSNSTAGELGALQAEAESLDKTVKELAEQLEFIKNSDIQGALDSI 1260	
DB	1262 EMMAQVEVKLSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSI 1321	
QY	1261 TKYFQMSLEAEKRYNASTTDPNSTVEQSALTDRVEDLMLERESPFKEQEEQARLLDEL 1320	
DB	1322 TKYFQMSLEAEERVNASTTDPNSTVEQSALTDRVEDLMLERESPFKEQEEQARLLDEL 1381	
QY	1321 AGKLQSLDLSAAAQMTCTGTPPGADCSESECGGPNCRDTEGEKKCGGCGGLVTVHAWSA 1380	
DB	1382 AGKLQSLDLSAAAEMTCTGTPPGASCSETECGGPNCRDTEGERKCGGCGGGLVTVHAWSA 1441	
QY	1381 QKAMDPRDRLVLSALAEVEQLSKMVSEAKVRADEAKQNAQDVLTKTNATKEKVDKSNEDLR 1440	

Db	962	YFGNPSEVGGSCQPCQCHNNIDTTDPEACDKETGRCLKCLYHTEGEHCQFCRFGYYGDAL	1021
QY	961	RODCRKVCNYLGTVKEHCNGSDCHCDKATGQCSCLPNVIGONCDRCAPNTWQLASGTGC	1020
Db	1022	RODCRKVCNYLGTVQEHCHNGSDCQCCKATGQCLCLPNVIGONCDRCAPNTWQLASGTGC	1081
QY	1021	GPCNCNAHSFGPSCNEFTGQCQCMPGFGGRTCSQCQLFWGDPDVECRACDCDPRGIET	1080
Db	1082	DFCNCNAHSFGPSCNEFTGQCQCMPGFGGRTCSQCQLFWGDPDVECRACDCDPRGIET	1141
QY	1081	PQCDQSTGQCVCEGVEGPRCDKCTRGYSGVFPDCTPCHQCFALWDIAIGELTNRTHKFL	1140
Db	1142	PQCDQSTGQCVCEGVEGPRCDKCTRGYSGVFPDCTPCHQCFALWDVIAELTNRTHREF	1201
QY	1141	EKAKALKISGVIOPYRETVDSEKKNVEIKDILAQSPAAPLKNIGILFEEAEKLTQDVT	1200
Db	1202	EKAKALKISGVIOPYRETVDSEKKNVEIKDILAQSPAAPLKNIGILFEEAEKLTQDVT	1261
QY	1201	EKMAQVEVKLTDTASQSNSTAGELGALQAEASLDKTVKELAEQLEFIKNSDIOGALDSI	1260
Db	1262	ENMAQVEVKLSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSI	1321
QY	1261	TKYFQMSLEAEKRVNASTDPNSTVEQSALTRDRVEDLMLERESPFFKEQEEQEARLLDEL	1320
Db	1322	TKYFQMSLEAEERNVASTTEPNSTVEQSALMRDRVEDVMMERESQFKEQEEQEARLLDEL	1381
QY	1321	AGKLSLDLSAAAQMTCTGTPPGADCSSECGGNPCRTDEGEKKCGGPGCGGLVTVAHSAW	1380
Db	1382	AGKLSLDLSAAAEMTCGTPPGASCSETECGGNPCRTDEGERKCGGPGCGGLVTVAHNAW	1441
QY	1381	QKAMDPRDVLALAEVEQISKNVSEAKVRADEAKQNAQDVLKTNATKEKVDKSNEDLR	1440
Db	1442	QKAMDLDQDVLALAEVEQISKNVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNEELR	1501
QY	1441	NLIKQIRNFLTSDSADLDSIEAVANEVLKSGNASTPOOLQNLTEDIRERVEVLSQVEVIL	1500
Db	1502	NLIKQIRNFLTQDSADLDSIEAVANEVLKMEMPTPOOLQNLTEDIRERVEVLSQVEVIL	1561
QY	1501	QQSAADTARAELLLEAAKRAKSATDVKVTDVMVKEALEEAEAKAQVAAEKAIKQADEDIQ	1560
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Db	1622	GTQNLTSIESETAASEETLFNASQRISELERNVEELKRAAQNSGEAEYTEKVVYTVKQ	1681
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Db	1682	SAEDVKKTLDGELDEKYKKVENLIAKTEESADARRKAEMLQNEAKTLLAQANSKLQLLK	1741
QY	1681	DLERKYEDNQKYLEDKAQELVRLEGEVRSLLKDISQKAVYSTCL	1725
Db	1742	DLERKYEDNQRYLEDKAQELARLEGEVRSLLKDISQKAVYSTCL	1786

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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:30:58 ; Search time 13.0493 Seconds
(without alignments)
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Perfect score: 9429
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	9429	100.0	1725	4	US-09-561-818A-20
3	9429	100.0	1786	4	US-09-562-702A-18
4	9429	100.0	1786	4	US-09-561-818A-18
5	8873	94.1	1765	4	US-09-562-702A-16
6	8873	94.1	1765	4	US-09-561-818A-16
7	8873	94.1	1786	4	US-09-562-702A-14
8	8873	94.1	1786	4	US-09-561-818A-14
9	8873	94.1	1786	4	US-09-561-709B-9
10	5489	58.2	1196	1	US-08-144-121-4
11	5489	58.2	1196	2	US-08-735-893-4
12	4914	52.1	1799	4	US-09-845-583A-6
13	4783	50.7	1798	4	US-09-561-709B-11
14	4778	50.7	1798	4	US-09-845-583A-8
15	3712.5	39.4	1761	4	US-09-561-709B-1
16	2967.5	31.5	1101	4	US-09-561-709B-5
17	2808	29.8	1342	4	US-09-561-709B-13
18	1637.5	17.4	1572	4	US-09-562-702A-32
19	1637.5	17.4	1572	4	US-09-561-818A-28
20	1637.5	17.4	1605	4	US-09-562-702A-30
21	1637.5	17.4	1605	4	US-09-561-818A-26
22	1622.5	17.2	1576	4	US-09-562-702A-24
23	1622.5	17.2	1576	4	US-09-561-818A-24
24	1622.5	17.2	1584	4	US-09-562-702A-28
25	1622.5	17.2	1609	4	US-09-562-702A-22
26	1622.5	17.2	1609	4	US-09-561-818A-22
27	1622.5	17.2	1617	4	US-09-562-702A-26

28	1619	17.2	271	1	US-08-152-019A-28	Sequence 28, Appl
29	1584	16.8	3635	4	US-09-845-583A-2	Sequence 2, Appl
30	1548	16.4	279	1	US-08-152-019A-29	Sequence 29, Appl
31	1542	16.4	278	2	US-08-460-309-13	Sequence 13, Appl
32	1542	16.4	278	2	US-08-125-077-13	Sequence 13, Appl
33	1534	16.3	3075	2	US-08-460-309-5	Sequence 5, Appl
34	1534	16.3	3075	2	US-08-125-077-5	Sequence 5, Appl
35	1533	16.3	3111	2	US-08-460-309-4	Sequence 4, Appl
36	1533	16.3	3111	2	US-08-125-077-4	Sequence 4, Appl
37	1527.5	16.2	3088	4	US-09-562-702A-8	Sequence 8, Appl
38	1527.5	16.2	3089	4	US-09-562-702A-4	Sequence 4, Appl
39	1527.5	16.2	3110	4	US-09-562-702A-2	Sequence 2, Appl
40	1527.5	16.2	3110	4	US-09-562-702A-6	Sequence 6, Appl
41	1527.5	16.2	3110	4	US-09-561-709B-7	Sequence 7, Appl
42	1497.5	15.9	3084	4	US-09-562-702A-12	Sequence 12, Appl
43	1497.5	15.9	3106	4	US-09-562-702A-10	Sequence 10, Appl
44	1484	15.7	1587	4	US-09-845-583A-10	Sequence 10, Appl
45	1484	15.7	1587	4	US-09-561-709B-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-09-562-702A-20
; Sequence 20, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 1725
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-562-702A-20

Query Match	100.0%	Score 9429;	DB 4;	Length 1725;
Best Local Similarity	100.0%;	Pred. No. 0;		
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361 Db IAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGGNPCDSETGYCYC 420
421 QY KRLVTGQRCDQCLPQHGLSNDLDGCRPCDCLGALNNSCSEDSQCSCCLPHMIGROCN 480
421 Db KRLVTGQRCDQCLPQHGLSNDLDGCRPCDCLGALNNSCSEDSQCSCCLPHMIGROCN 480
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481 Db EVESGYFTTLDHYIYEAEEANLPGVAVVERQYIQDRIPSWTGTGFRVPEGAYLEFFI 540
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1141 Db EKAKALKISGVIPIRETVDVSVEKKVNEIKDILAQSPAAEPLKNIGILFEEAEKLTQDVT 1200
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1201 Db EKMAQVEVKLTDTASQSNSTAGELGALQAEASLDKTVKELAQLEFIKNSDIOGALDSI 1260
1261 QY TKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRVEDLMLRESPPFKEQEEQARLLDEL 1320
1261 Db TKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRVEDLMLRESPPFKEQEEQARLLDEL 1320
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1621 Db NADDVKKTLDGELDEKYEKKVESLIAQKTEESADARRKAEELLQNEAKTLLAQANSKLQLE 1680
1681 QY DLERKYEDNQKYLEDKAQLVLRLEGEVRSLLKDISEKVAVYSTCL 1725
1681 Db DLERKYEDNQKYLEDKAQLVLRLEGEVRSLLKDISEKVAVYSTCL 1725

RESULT 2

US-09-561-818A-20
; Sequence 20, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortessmaa, Jarrko
; APPLICANT: Tytgvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 20
; LENGTH: 1725
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-561-818A-20

Query Match 100.0%; Score 9429; DB 4; Length 1725;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPYCIIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENV 60
Db 1 EPYCIIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENV 60
QY 61 TIQDLLEAEFHFTLIMTFKTRPAAMLIERSDDFGKTGWVRYRYPAYDCESSFPGISTGP 120
Db 61 TIQDLLEAEFHFTLIMTFKTRPAAMLIERSDDFGKTGWVRYRYPAYDCESSFPGISTGP 120
QY 121 MKKVDDIICDSRYSDIEPSTEGEVIFRALDPAPKIEDPYSPRIONLLKITNLRKFKVLH 180
Db 121 MKKVDDIICDSRYSDIEPSTEGEVIFRALDPAPKIEDPYSPRIONLLKITNLRKFKVLH 180
QY 181 TLGNLLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNVEEGVHGHCMCR 240
Db 181 TLGNLLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNVEEGVHGHCMCR 240
QY 241 HNTKGLNCELAMDYFHDLPWRPAEGRNSNACKKNCNEHSSSCHFDMAVFLATGNVSGV 300
Db 241 HNTKGLNCELAMDYFHDLPWRPAEGRNSNACKKNCNEHSSSCHFDMAVFLATGNVSGV 300
QY 301 CDNCQNTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 360
Db 301 CDNCQNTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 360
QY 361 IAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGGNPCDSETGYCYC 420

Db 361 IAGQCRCKLHVEGERCDVCKEGFYDLAEDPYGCKSCACNPLGTIPGGNPCDSETGYCYC 420

QY 421 KRLVTGQRCDQCLPQHGLSNDLDGCRPCDCDLGGALNNSCEDSGQCSCLPHMIGRQCN 480

Db 421 KRLVTGQRCDQCLPQHGLSNDLDGCRPCDCDLGGALNNSCEDSGQCSCLPHMIGRQCN 480

QY 481 EVESGYFTTLDHYIYEAEANLPGVWVVERQYIQDIRIPSWTGPGRVPEGAYLEFFI 540

Db 481 EVESGYFTTLDHYIYEAEANLPGVWVVERQYIQDIRIPSWTGPGRVPEGAYLEFFI 540

QY 541 DNIPYSMEYEILIRYEPQLPDHWEKAVITVORPGKIPASSRCGNTVPDDNQVVSLSPGS 600

Db 541 DNIPYSMEYEILIRYEPQLPDHWEKAVITVORPGKIPASSRCGNTVPDDNQVVSLSPGS 600

QY 601 RYVVLPRPVCFEKGMNYYTVLELPOYTASGSDVESPYTFIDSLVLMPYCKSLDIFTVGS 660

Db 601 RYVVLPRPVCFEKGMNYYTVLELPOYTASGSDVESPYTFIDSLVLMPYCKSLDIFTVGS 660

QY 661 GDGEVNTSAWETFQRYRCLENSRSVVKTPMTDVCRNIIPISALIHQTLGACECDPQGS 720

Db 661 GDGEVNTSAWETFQRYRCLENSRSVVKTPMTDVCRNIIPISALIHQTLGACECDPQGS 720

QY 721 SSVCDPENGQCCQCRPNVVGRTNRCAPGTGFGPNCGKPCDCHLQGSASAFCDAITGOCH 780

Db 721 SSVCDPENGQCCQCRPNVVGRTNRCAPGTGFGPNCGKPCDCHLQGSASAFCDAITGOCH 780

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Db 781 CFQGIYARQCDRLPGYWGFPSCQPCQCNHGLDCTVTGECLSCQDYTTGHNCERCLAG 840

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Db 841 YYGDPPIGSGDHRPCPCPDGPDGSRQFARSCYQDPVTQLACVCDPQYIGSRCDDCASG 900

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Db 901 FFGNPSDFGSCQPCQCHNIDTTDPEACDKOTGRCLKCLYHTEGDHCQLCQYGYGDAL 960

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Db 961 RQDCRKVCNVLGTVKEHCNGSDCHCDKATGCSCLPNVIGQNCDCRCAPNTWQLASGTGC 1020

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Db 1021 GPCNCNAAHSFGPSCNEFTQCOCMPGFGGRTCECQELFWGDPDVECRACDCDPRGIET 1080

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Db 1081 PQCDQSTGQCVCEGVEGPRCDKCTRGYSGVFPDCTPCHQCFALWDAAIIGELTNRTHKFL 1140

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Db 1141 EKAKALKISGVIQPYRETVDVSEKKNVEIKDILAQSPAAPLKNIGILFEEAEKLTKDVT 1200

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Db 1201 EKMAQVEVKLTDTASQSNSTAGELGALQAEAESLDKTVKELAEQLEFIKNSDIOGALDSI 1260

QY 1261 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLESPPFKEQEEQARLLDEL 1320

Db 1261 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLESPPFKEQEEQARLLDEL 1320

QY 1321 AGKLOSLDLASAAQMTCTPPGADCESECGPNCRDTDEGEKKCGGPGGLVTVHAWSAW 1380

Db 1321 AGKLOSLDLASAAQMTCTPPGADCESECGPNCRDTDEGEKKCGGPGGLVTVHAWSAW 1380

QY 1381 QKAMDFDRDVLASALAEVEQLSKMVEAKVRADEAKQNAQDVLLKTNATKEKVKDKSNEDLR 1440

Db 1381 QKAMDFDRDVLASALAEVEQLSKMVEAKVRADEAKQNAQDVLLKTNATKEKVKDKSNEDLR 1440

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Db 1441 NLIKQIRNFELTDSADLDSIEAVANEVLKSGNASTPQQLQNLITEDIRERVETLSQVEVIL 1500

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Db 1501 QQSAADIARAELLLEEAERASKSATDVKVTDVMVKEALEEAQAAEKAIKQADEDIQ 1560

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Db 1561 GTQNLITSIESETAASEETLTNASQRIKSLERNVEELKRKAAQNSGEAEYIEKVVSVKQ 1620

QY 1621 NADDVKKTLDGELDEKYYKKVESLIAQKTEESADARRKAEILLQNEAKTLLAQANSKLQLE 1680

Db 1621 NADDVKKTLDGELDEKYYKKVESLIAQKTEESADARRKAEILLQNEAKTLLAQANSKLQLE 1680

QY 1681 DLERKYEDNQKYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1725

Db 1681 DLERKYEDNQKYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1725

RESULT 3

US-09-562-702A-18

; Sequence 18, Application US/09562702A

; Patent No. 6632790

; GENERAL INFORMATION:

; APPLICANT: Yurchenco, Peter

; TITLE OF INVENTION: Laminin 2 and Methods for Its Use

; FILE REFERENCE: 99-274-B

; CURRENT APPLICATION NUMBER: US/09/562,702A

; CURRENT FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: 60/155,945

; PRIOR FILING DATE: 1999-09-24

; PRIOR APPLICATION NUMBER: 60/143,289

; PRIOR FILING DATE: 1999-07-12

; PRIOR APPLICATION NUMBER: 60/139,198

; PRIOR FILING DATE: 1999-06-15

; PRIOR APPLICATION NUMBER: 60/131,720

; PRIOR FILING DATE: 1999-04-30

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 18

; LENGTH: 1786

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-562-702A-18

Query Match 100.0%; Score 9429; DB 4; Length 1786;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPYCIIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVTTFAPNRLKIWWQSENGVENV 60

Db 62 EPYCIIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVTTFAPNRLKIWWQSENGVENV 121

QY 61 TIQLDLEAEFHTHLIMTFTKFRPAAMLIERSDFGKTGWVRYFAYDCSSFPGISTGP 120

Db 122 TIQLDLEAEFHTHLIMTFTKFRPAAMLIERSDFGKTGWVRYFAYDCSSFPGISTGP 181

QY 121 MKKVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPIQNLLKITNLRKIFVKLH 180

Db 182 MKKVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPIQNLLKITNLRKIFVKLH 241

QY 181 TLGDNLLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGHCMCR 240

Db 242 TLGDNLLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGHCMCR 301

QY 241 HNTKGLNCELQCMDFYHDLPRWPAEGRNSNACKKNCNEHSSCHFDMAVFLATGNVSGGV 300

Db 302 HNTKGLNCELQCMDFYHDLPRWPAEGRNSNACKKNCNEHSSCHFDMAVFLATGNVSGGV 361

QY 301 CDNCQHNTMGRNCEQCKPFYFQHBERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 360

Db 362 CDNCQHNTMGRNCEQCKPFYFQHBERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 421

QY 361 IAGQCRCKLHVEGERCDVCKEGFYDLAEDPYGCKSCACNPLGTIPGGNPCDSETGYCYC 420

Db 422 IAGQCRCKLHVEGERCDVCKEGFYDLAEDPYGCKSCACNPLGTIPGGNFCDSYCYC 481
QY 421 KRLVTGQRCDQCLPQHGLSNDLDGCRPCDCLGGALNNSCEDSGQCSCLPHMIGRQCN 480
Db 482 KRLVTGQRCDQCLPQHGLSNDLDGCRPCDCLGGALNNSCEDSGQCSCLPHMIGRQCN 541
QY 481 EVESGYFTTLDHYIYEABEANLPGVVVVERQYIQDRIPSWTGPGRVPEGAYLEFFI 540
Db 542 EVESGYFTTLDHYIYEABEANLPGVVVVERQYIQDRIPSWTGPGRVPEGAYLEFFI 601
QY 541 DNIPYSMEYEILIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTVPDDNQVVSLSPGS 600
Db 602 DNIPYSMEYEILIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTVPDDNQVVSLSPGS 661
QY 601 RYVVLPRPVCFEKGMNYYTVRLQLPYTASGSDVESPYTFIDSLVLMPYCKSLDIFTVGS 660
Db 662 RYVVLPRPVCFEKGMNYYTVRLQLPYTASGSDVESPYTFIDSLVLMPYCKSLDIFTVGS 721
QY 661 GDGEVTSAWETFORYRCLNSRSVVKTPMTDVCRNIIFISALIHQTLGACECDPQGS 720
Db 722 GDGEVTSAWETFORYRCLNSRSVVKTPMTDVCRNIIFISALIHQTLGACECDPQGS 781
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Db 782 SSVCDPNGGQCQCRPNVVGRTCNRCAPGTGFGPNCGKPCDCHLQGSASAFCDAITGQCH 841
QY 781 CFQGIYARQCDRCLPGYWGFPSCQPCQCNHGDCTVTGECCLSCQDYTTGHNCRCLAG 840
Db 842 CFQGIYARQCDRCLPGYWGFPSCQPCQCNHGDCTVTGECCLSCQDYTTGHNCRCLAG 901
QY 841 YYGDPRIIGSGDHCRPCPCPDGSDGRQFARSQYQDPVTQLACVCDPGYIGSRCDDCASG 900
Db 902 YYGDPRIIGSGDHCRPCPCPDGSDGRQFARSQYQDPVTQLACVCDPGYIGSRCDDCASG 961
QY 901 FFGNPSDFGSGSQPCQCHNIDITDTPACDKDTGRCLKCLYHTEGDHCQLCOQYGYGDAL 960
Db 962 FFGNPSDFGSGSQPCQCHNIDITDTPACDKDTGRCLKCLYHTEGDHCQLCOQYGYGDAL 1021
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Db 1022 RQDCRKVCNLYLGTVKEHNGSDCHCDKATGQCSCLPNVIGQNCDCRCAPIWOLASGTGC 1081
QY 1021 GPCNCNAAHSFGPSCNEFTGQCQCMFGGRTCECQELFWGDPDVECRACDCDPRGIET 1080
Db 1082 GPCNCNAAHSFGPSCNEFTGQCQCMFGGRTCECQELFWGDPDVECRACDCDPRGIET 1141
QY 1081 PQCDQSTGQCVCVEGVGPRCDKCTRGYSGVFPDCTPCHQCQFALWDAAIIGELTNRTHKFL 1140
Db 1142 PQCDQSTGQCVCVEGVGPRCDKCTRGYSGVFPDCTPCHQCQFALWDAAIIGELTNRTHKFL 1201
QY 1141 EKAKALKISGVIGPYRETVDVSVEKKVNEIKDILAQSPAABEPLKNIGILFEEAEKLTQDVT 1200
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QY 1201 EKMAQVEVKLTDTASQSNSTAGELGALQAEAESLDTVKELAEQLEFIKNSDIOGALDSI 1260
Db 1262 EKMAQVEVKLTDTASQSNSTAGELGALQAEAESLDTVKELAEQLEFIKNSDIOGALDSI 1321
QY 1261 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLESPPFKEQEEQARLLDEL 1320
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QY 1321 AGKLQSLDLASAAQMTGCTPPGADCSSECGPNCRCTDEGEKKCGGPGCGGLVTVAHSAW 1380
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QY 1381 QKAMDFDRDVLASALAEVEQLSKWVSEAKVRADEAKQNAQDVLLKTNATKEKVKDSNEDLR 1440
Db 1442 QKAMDFDRDVLASALAEVEQLSKWVSEAKVRADEAKQNAQDVLLKTNATKEKVKDSNEDLR 1501
QY 1441 NLIKQIRNFLTEDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVIL 1500

Db 1502 NLIKQIRNFLTEDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVIL 1561
QY 1501 QQSAADIAEAELLEEAKRASKSATDVKVVTADMVKEALEEAEKAQVAAEKAIKQADEDIQ 1560
Db 1562 QQSAADIAEAELLEEAKRASKSATDVKVVTADMVKEALEEAEKAQVAAEKAIKQADEDIQ 1621
QY 1561 GTONLLTSIESETAASEETLTNASQRISKLERNVVEELKRKAAQNSGEAEYIEKVYYSVKQ 1620
Db 1622 GTONLLTSIESETAASEETLTNASQRISKLERNVVEELKRKAAQNSGEAEYIEKVYYSVKQ 1681
QY 1621 NADDVKKTLDGELDEKYKVESLIAQKTEESADARRKAEELLQNEAKTLLAQANSKLQLE 1680
Db 1682 NADDVKKTLDGELDEKYKVESLIAQKTEESADARRKAEELLQNEAKTLLAQANSKLQLE 1741
QY 1681 DLERKYEDNQKYLEDKAQELVRLEGEVRSLLKDISBKVAVYSTCL 1725
Db 1742 DLERKYEDNQKYLEDKAQELVRLEGEVRSLLKDISBKVAVYSTCL 1786

RESULT 4

US-09-561-818A-18
; Sequence 18, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortessmaa, Jarrko
; APPLICANT: Tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-561-818A-18

Query Match 100.0%; Score 9429; DB 4; Length 1786;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPYCIVSHLQEDKKCFICDSRDPYHETLNPDShLIENVVTFAPNRLKIWWQSENGVENV 60
Db 62 EPYCIVSHLQEDKKCFICDSRDPYHETLNPDShLIENVVTFAPNRLKIWWQSENGVENV 121
QY 61 TIQLDLBAEFHFTHLIMTFKTRPAAMLIERSDDFGKTVGYRYFAYDCESSFPGISTGP 120
Db 122 TIQLDLBAEFHFTHLIMTFKTRPAAMLIERSDDFGKTVGYRYFAYDCESSFPGISTGP 181
QY 121 MKKVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLKITNLRIKFVKLH 180
Db 182 MKKVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLKITNLRIKFVKLH 241
QY 181 TLGDNLLDSRMEIREKYYAVYDMVVRGNCFYGHASECAPVDGVNEEVEGMVHGHCRCR 240
Db 242 TLGDNLLDSRMEIREKYYAVYDMVVRGNCFYGHASECAPVDGVNEEVEGMVHGHCRCR 301
QY 241 HNTKGLNCELMDFYHDLWPWPAPAEGRNSNACKKCNCHSSSCHFDMAVFLATGNVSGGV 300
Db 302 HNTKGLNCELMDFYHDLWPWPAPAEGRNSNACKKCNCHSSSCHFDMAVFLATGNVSGGV 361
QY 301 CDNCQHNTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 360
Db 362 CDNCQHNTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 421
QY 361 IAGQCRCRKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGGNPCDSETGYCYC 420
Db 422 IAGQCRCRKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGGNPCDSETGYCYC 481
QY 421 KRLVTGQRCDQCLPQHGLSNDLDGCRPCDCLGGALNNSCEDSGQCSCLPHMIGRQCN 480
Db 482 KRLVTGQRCDQCLPQHGLSNDLDGCRPCDCLGGALNNSCEDSGQCSCLPHMIGRQCN 541

QY 481 EVESGYFTTLDHYIYEAEEANLPGVWVVERQYIQDRIPSWTGPGFVRVPEGAYLEFFI 540
Db 542 EVESGYFTTLDHYIYEAEEANLPGVWVVERQYIQDRIPSWTGPGFVRVPEGAYLEFFI 601
QY 541 DNIPIYSMEYEILIRYEPQLPDHWEKAVITVORPGKIPASSRCGNTVPDDNQVWSLSPGS 600
Db 602 DNIPIYSMEYEILIRYEPQLPDHWEKAVITVORPGKIPASSRCGNTVPDDNQVWSLSPGS 661
QY 601 RYVVLPRPVCFEKGMNYYVRLLELPQYTAGSDVESPYTFIDSLVLMPCYCKSLDIFTVGGS 660
Db 662 RYVVLPRPVCFEKGMNYYVRLLELPQYTAGSDVESPYTFIDSLVLMPCYCKSLDIFTVGGS 721
QY 661 GDGEVNTSAWETFQRYRCLNSRSVVKTPMTDVCNIIIPISALIHQITGLACECDPQGS 720
Db 722 GDGEVNTSAWETFQRYRCLNSRSVVKTPMTDVCNIIIPISALIHQITGLACECDPQGS 781
QY 721 SSVCDPNGGQCQCRPNVVGRTCNRCAPGTFGFGNGCKPCDCHLQGSASAFCDAITGOCH 780
Db 782 SSVCDPNGGQCQCRPNVVGRTCNRCAPGTFGFGNGCKPCDCHLQGSASAFCDAITGOCH 841
QY 781 CFQGIYARQCDRLPGYWGFPSCQPCQCNHGDCTVTGECCLSCQDYTTGHNCRCLAG 840
Db 842 CFQGIYARQCDRLPGYWGFPSCQPCQCNHGDCTVTGECCLSCQDYTTGHNCRCLAG 901
QY 841 YYGDPPIIGSDHCRPCPCPDGSDSGRQFARSCYQDPVTQLACVCDPBGYIGSRCDDCASG 900
Db 902 YYGDPPIIGSDHCRPCPCPDGSDSGRQFARSCYQDPVTQLACVCDPBGYIGSRCDDCASG 961
QY 901 FFGNPSDFGGSCQPCQCHNIDTTDPEACDKDTGRCLKCLYHTEGDHCQLCOGYGGDAL 960
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Db 1442 QKAMDFDRDVL SALAEVEQLSKMVSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDLR 1501
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Db 1622 GTQNLLTSIESETAASEETLTNASQRISKLERNVEELKRKAAQNSGEAEYIEKVYSVKQ 1681
QY 1621 NADDVKKTLTGELDEKVKVESLIAQKTEESADARRKAEALLQNEAKTLLAQANSKLQLE 1680
Db 1682 NADDVKKTLTGELDEKVKVESLIAQKTEESADARRKAEALLQNEAKTLLAQANSKLQLE 1741
QY 1681 DLERKYEDNQKYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1725
Db 1742 DLERKYEDNQKYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1786

RESULT 5
US-09-562-702A-16
; Sequence 16, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 1765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-16

Query Match 94.1%; Score 8873; DB 4; Length 1765;
Best Local Similarity 92.9%; Pred. No. 0;
Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

QY 1 EPYCIIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVVTTFAPNRLKIWWQSENGVENV 60
Db 41 EPYCIIVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVVTTFAPNRLKIWWQSENGVENV 100
QY 61 TIQLDLAEAFHFTHLIMTFTFRPAAMLIERSSDFGKTGWVYRYFAYDCESFPFGISTGP 120
Db 101 TIQLDLAEAFHFTHLIMTFTFRPAAMLIERSSDFGKTGWVYRYFAYDCESFPFGISTGP 160
QY 121 MKKVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPPRIQNLLKITNLRKIFVKLH 180
Db 161 MKKVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPPRIQNLLKITNLRKIFVKLH 220
QY 181 TLGDNLLDSRMEIREKYYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMCR 240
Db 221 TLGDNLLDSRMEIREKYYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMCR 280
QY 241 HNTKGLNCEL CMDFYHDL PWRPAEGRNSNACKKNCNBSHSSCHFDMVFLATGNVSGGV 300
Db 281 HNTKGLNCEL CMDFYHDL PWRPAEGRNSNACKKNCNBSHSSCHFDMVFLATGNVSGGV 340
QY 301 CDNCQHNMTGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSGL 360
Db 341 CDDCQHNMTGRNCEQCKPFYFQHPERDIRDPNFCERCCTCDPAGSQNEGICDSTDFSTGL 400
QY 361 IAGQCRCCKLHVGERCDVCKEGFYDLSEAEDPYGCKSCACNPLGTIPGGNPCDSETGYCYC 420
Db 401 IAGQCRCCKLHVGERCDVCKEGFYDLSSDPFGCKSCACNPLGTIPGGNPCDSETGYCYC 460
QY 421 KRLVTGQCDQCLPQHGLSNDLDGCRPCDCDLGGALNNSCEDSGQCSCLPHMIGSQCN 480

QY 541 DNIPYSMEYEILIRYEPQLPDHWEKAVITVORPGKIPASSRCGNTVPDDNQVWLSPGS 600
Db 581 DNIPYSMEYDILIRYEPQLPDHWEKAVITVORPGRIPTSSRCGNTIPDDNQVWLSPGS 640
QY 601 RYVVLPRPVCFEKGMNVTVRLELPQYTAGSDVESPYTFIDSLVLMPYCKSLDIFTVGGS 660
Db 641 RYVVLPRPVCFEKGMNVTVRLELPQYTAGSDVESPYTFIDSLVLMPYCKSLDIFTVGGS 700
QY 661 GDGEVNTSAWETFORXCLNSRSVVKTPMTDVCNIIIFSISALIHQTLGACEDPQGS 720
Db 701 GDGVNTSAWETFORXCLNSRSVVKTPMTDVCNIIIFSISALIHQTLGACEDPQGS 760
QY 721 SSVCDPNGGQCQCRPNVGRTCNRCAPGTFEGFPGCKPCDCHLQGSASAFCDAITGQCH 780
Db 761 SSVCDPNGGQCQCRPNVGRTCNRCAPGTFEGFPGCKPCDCHLQGSVNAFCNPVTGQCH 820
QY 781 CFQGIYARQCDCRCLPGYWGFPSPCQPCQCNHGDHDCDVTGECCLSCQDVTGHNCCERCLAG 840
Db 821 CFQGIYARQCDCRCLPGYWGFPSPCQPCQCNHGDHDCDVTGECCLSCQDVTGHNCCERCLAG 880
QY 841 YGDPPIIGSGDHCRPCPDGPDGSDGROFARSCYQDPVTLQACVCDPGYIGSRCDDCASG 900
Db 881 YGDPPIIGSGDHCRPCPDGPDGSDGROFARSCYQDPVTLQACVCDPGYIGSRCDDCASG 940
QY 901 FFGNPSDFGSGCQPCQCHNIDITDPEACDKTGRCLKCLYHTEGDHCLCQYGYGDAL 960
Db 941 YFGNPSDFGSGCQPCQCHNIDITDPEACDKTGRCLKCLYHTEGDHCLCQYGYGDAL 1000
QY 961 RQDCRKVCVNYLGTVEHCNGSDCHCDKATGQSCSLPNVIGONCDRCAPNTWQLASGTGC 1020
Db 1001 RQDCRKVCVNYLGTVEHCNGSDCHCDKATGQSCSLPNVIGONCDRCAPNTWQLASGTGC 1060
QY 1021 GPCNCNAAHSFGPSNCFEFTGQCQCMGPGFGGRTSECEQLFWGDDPVECRACDCDPRGIET 1080
Db 1061 GPCNCNAAHSFGPSNCFEFTGQCQCMGPGFGGRTSECEQLFWGDDPVECRACDCDPRGIET 1120
QY 1081 PQCDQSTGQCVVEGVEGRCDKCTRGYSGVFPDCTPCHQCFALWDALIGELTNRTHKFL 1140
Db 1121 PQCDQSTGQCVVEGVEGRCDKCTRGYSGVFPDCTPCHQCFALWDALIGELTNRTHKFL 1180
QY 1141 EKAKALKISGVIQYRETVDSVEKKVNEIKDILAQSPAAEPLKNIIGLEAEKLTKDVT 1200
Db 1181 EKAKALKISGVIQYRETVDSVEKKVNEIKDILAQSPAAEPLKNIIGLEAEKLTKDVT 1240
QY 1201 EKMAQVEVKLTDTASQSNSTAGELGALQAEESLDKTVKELAEQLEFIKNSDIQALDSI 1260
Db 1241 EKMAQVEVKLTDTASQSNSTAGELGALQAEESLDKTVKELAEQLEFIKNSDIQALDSI 1300
QY 1261 TKYFQMSLEAEKRVNASTDPNSTVEQSALTRDRVEDLMLESFPKEQOEQARLLDEL 1320
Db 1301 TKYFQMSLEAEKRVNASTDPNSTVEQSALTRDRVEDLMLESFPKEQOEQARLLDEL 1360
QY 1321 AGKLQSLDLSAAQMTCTGTPPGACDSECEGPNCRDTEGEKCGGPGCGGLVTVAHSAW 1380
Db 1361 AGKLQSLDLSAAQMTCTGTPPGACDSECEGPNCRDTEGEKCGGPGCGGLVTVAHSAW 1420
QY 1381 QKAMDFFDRDVLALAEVEQLSKMVSEAKVRADEAKQNAQDVLKTNATKEKVDKSNEDLR 1440
Db 1421 QKAMDFFDRDVLALAEVEQLSKMVSEAKVRADEAKQNAQDVLKTNATKEKVDKSNEDLR 1480
QY 1441 NLIKQIRNFLTSDADLSTIEAVANEVLKSGNASTPQQLQNLTEDIRERVELTSQVEVIL 1500
Db 1481 NLIKQIRNFLTSDADLSTIEAVANEVLKSGNASTPQQLQNLTEDIRERVELTSQVEVIL 1540
QY 1501 QQSAADIAEAELLLLEAKRASKSATDVKVTADVMKEALEEAEKAAQVAAEKAKQADEDIQ 1560
Db 1541 QQSAADIAEAELLLLEAKRASKSATDVKVTADVMKEALEEAEKAAQVAAEKAKQADEDIQ 1600
QY 1561 GTQNLTSIESETAASEETLTNASQRISEKLERVVEELKRAAQNNGEAEYIEKVYVSKQ 1620
Db 1601 GTQNLTSIESETAASEETLTNASQRISEKLERVVEELKRAAQNNGEAEYIEKVYVSKQ 1660
QY 1621 NADDVKKTLGDGELDEKYYKKVESLIAQKTESADARRKAELLQNEAKTLLAQANSKLQLE 1680

Db 1661 SAEDVKKTLGDGELDEKYYKKVESLIAQKTESADARRKAELLQNEAKTLLAQANSKLQLLK 1720
QY 1681 DLERKYEDNQKYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1725
Db 1721 DLERKYEDNQKYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1765
RESULT 7
US-09-562-702A-14
; Sequence 14, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 14
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-14
Query Match 94.1%; Score 8873; DB 4; Length 1786;
Best Local Similarity 92.9%; Pred. No. 0;
Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;
QY 1 EPIYIVSHLOEDKKCFICDSRDPYHETLNPDShLIENVVTTFAPNRLKIWWQSENGVENV 60
Db 62 EPIYIVSHLOEDKKCFICDSRDPYHETLNPDShLIENVVTTFAPNRLKIWWQSENGVENV 121
QY 61 TIQLDLEAEFFHFTLIMTFKTRPAAMLIERSDDFGKWTGVYRYFAYDCSESSFFGISTGP 120
Db 122 TIQLDLEAEFFHFTLIMTFKTRPAAMLIERSDDFGKWTGVYRYFAYDCSESSFFGISTGP 181
QY 121 MKKVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLKITNLRIKFKVLH 180
Db 182 MKKVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLKITNLRIKFKVLH 241
QY 181 TLGNLLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGHCNCR 240
Db 242 TLGNLLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGHCNCR 301
QY 241 HNTKGLNCELMDFFYHDLPRPAEGRNSNACKKCNNEHSSCHFDMAVFLATGNVSGGV 300
Db 302 HNTKGLNCELMDFFYHDLPRPAEGRNSNACKKCNNEHSSCHFDMAVFLATGNVSGGV 361
QY 301 CDNCOHNTMGRNCEQCKPFYQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 360
Db 362 CDDCOHNTMGRNCEQCKPFYQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 421
QY 361 IAGQCRCKLHVEGERCDVCKEGFYDLSEAEDPYGCKSCACNPLGTIPGGNPCDSETGYCYC 420
Db 422 IAGQCRCKLHVEGERCDVCKEGFYDLSEAEDPYGCKSCACNPLGTIPGGNPCDSETGYCYC 481
QY 421 KRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCLGGALNNSCSESDGQCSCLPHMIGRQCN 480
Db 482 KRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCLGGALNNSCSESDGQCSCLPHMIGRQCN 541
QY 481 EVESGYFTTLDHYIYEAEANLPGVWVVERQYIQDRIPSWTGPVVRVPEGAYLEFFI 540
Db 542 EPEPGYFATLDHYIYEAEANLPGVWVVERQYIQDRIPSWTGPVVRVPEGAYLEFFI 601

QY 541 DNIPYSMEYEILIRYEPQLPDHWEKAVITVORPGKIPASSRCNGTVPDDNQVVSLSPGS 600
Db 602 DNIPYSMEYDILIRYEPQLPDHWEKAVITVORPGRIPTSSRCNGTIPDDNQVVSLSPGS 661
QY 601 RYVVLPRPVCFEKGMNYYTVRLELPQYTAGSDVESPTFIDSLVLMYPYCKSLDIFTVGS 660
Db 662 RYVVLPRPVCFEKGMNYYTVRLELPQYTAGSDVESPTFIDSLVLMYPYCKSLDIFTVGS 721
QY 661 GDGEVNTSAWETFORYRCLENSRSVVKTPMTDVCNRIIFISISALIHQTLGLACECDPQGS 720
Db 722 GDGVVNTSAWETFORYRCLENSRSVVKTPMTDVCNRIIFISISALIHQTLGLACECDPQGS 781
QY 721 SSVCDPNGGQCCQCRPNVVGRTNRCAPGTFGFGPNCGKPCDCHLQGSASAFCDAITGQCH 780
Db 782 SSVCDPNGGQCCQCRPNVVGRTNRCAPGTFGFGPNCGKPCDCHLQGSVNAFCNPTGQCH 841
QY 781 CFQGIYARQCDRCCLPGYWGFPSPQPCQCNHGALDCTVTGECCLSCQDYTTGHCNCRCLAG 840
Db 842 CFQGVYARQCDRCCLPGHWGFPSPQPCQCNHGADDDCDPVTGECCLNCQDYTMGHCNCRCLAG 901
QY 841 YYGDPHIGSGDHCRPCPCPDGSDGROFARSCYQDPVTQLACVCDPFGVIGSRCDDCASG 900
Db 902 YYGDPHIGSGDHCRPCPCPDGSDGROFARSCYQDPVTQLACVCDPFGVIGSRCDDCASG 961
QY 901 FFGNPSDFGSGCQPCQCHHNIDTTPDPAACDKTGRCLKCLYHTEGDHCLCQYGYGDAL 960
Db 962 YFGNPSDFGSGCQPCQCHHNIDTTPDPAACDKTGRCLKCLYHTEGDHCLCQYGYGDAL 1021
QY 961 RQDCRKVCNLYLGTVEHCNCGSDCHCDKATGQCCLPNVIGONCDRCAPNTWOLASGTGC 1020
Db 1022 RQDCRKVCNLYLGTVEHCNCGSDCHCDKATGQCCLPNVIGONCDRCAPNTWOLASGTGC 1081
QY 1021 GPCNCNAAHSFGPSCNEFTGQCQCMPPGFGGRTCSQCQLFWGDPDVECRACDCDPRGIET 1080
Db 1082 DPCNCNAAHSFGPSCNEFTGQCQCMPPGFGGRTCSQCQLFWGDPDVECRACDCDPRGIET 1141
QY 1081 PQCDQSTGQCVCEGVEGPRCDKCTRGYSVGFDPCTPCHQCQFALWDALIGELTNRTHKFL 1140
Db 1142 PQCDQSTGQCVCEGVEGPRCDKCTRGYSVGFDPCTPCHQCQFALWDALIGELTNRTHKFL 1201
QY 1141 EKAKALKISGVIGPYRETVDVSVEKKVNEIKDILAQSPAAEPLKNIGILFEEAEKLTKDVT 1200
Db 1202 EKAKALKISGVIGPYRETVDVSVEKKVNEIKDILAQSPAAEPLKNIGILFEEAEKLTKDVT 1261
QY 1201 EKMAQVEVKLTDTASQSNSTAGELGALQAEAESIDKTVKELAEQLEFKNDSIOGALDSI 1260
Db 1262 EMMAQVEVKLTDTASQSNSTAKELDSIQTEAESIDKTVKELAEQLEFKNDSIRGALDSI 1321
QY 1261 TKYFQMSLEAEKRVNASITDPNSTVEQSAITDRVEDLMLERESPKEQEQEQAARLDEL 1320
Db 1322 TKYFQMSLEAEKRVNASITDPNSTVEQSAITDRVEDLMLERESPKEQEQEQAARLDEL 1381
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QY 1381 QKAMDFFRDVLSALAEVEQLSKWVSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDLR 1440
Db 1442 QKAMDLDQDVLSALAEVEQLSKWVSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDLR 1501
QY 1441 NLTKQIRNFLETSDADLDSIEAVANEVLKSNASTPQOLQNTLTERIRERVETLSQVEVIL 1500
Db 1502 NLTKQIRNFLETSDADLDSIEAVANEVLKSNASTPQOLQNTLTERIRERVETLSQVEVIL 1561
QY 1501 QQSAADIAEAELLLLEAKRASKSATDVKTADVMVKEALEEAQVAAEKAIKQADEDIQ 1560
Db 1562 QHGAADIAEAELLLLEAKRASKSATDVKTADVMVKEALEEAQVAAEKAIKQADEDIQ 1621
QY 1561 GTQNLTSIESETAASEETLTNASQRIKLEARNVEELKRKAQNSGEAEYIEKVYVSVKQ 1620
Db 1622 GTQNLTSIESETAASEETLTNASQRIKLEARNVEELKRKAQNSGEAEYIEKVYVSVKQ 1681

QY 1621 NADDVKKTLGDELDEKYYKVESLIAQKTEESADARRKAEALLQNEAKTLLAQANSKLQLE 1680
Db 1682 SAEDVKKTLGDELDEKYYKVENLIAKTEESADARRKAEMLQNEAKTLLAQANSKLQLLK 1741
QY 1681 DLERKYEDNQYLEDKAQELVRLEGEVRSLLKDISQKAVVYSTCL 1725
Db 1742 DLERKYEDNQYLEDKAQELARLEGEVRSLLKDISQKAVVYSTCL 1786

RESULT 8

US-09-561-818A-14
; Sequence 14, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortessmaa, Jariiko
; APPLICANT: Tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-818A-14

Query Match 94.1%; Score 8873; DB 4; Length 1786;
Best Local Similarity 92.9%; Pred. No. 0;
Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

QY 1 EYCIIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVVTTFAPNRLKIWQSENGVENV 60
Db 62 EYCIIVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVVTTFAPNRLKIWQSENGVENV 121
QY 61 TIQLDLAEAFHFTLIMTFTFRPAAMLIERSSDFGKTGWVRYFYAYDCSSFPFGISTGP 120
Db 122 TIQLDLAEAFHFTLIMTFTFRPAAMLIERSSDFGKTGWVRYFYAYDCSSFPFGISTGP 181
QY 121 MKKVDDIICDSRYSDIEPSTEGBEVIIFRALDPAFKIEDPPSPRIQNLKILNRIKFKVLH 180
Db 182 MKKVDDIICDSRYSDIEPSTEGBEVIIFRALDPAFKIEDPPSPRIQNLKILNRIKFKVLH 241
QY 181 TLGDNLLDSRMEIREKYVYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMCR 240
Db 242 TLGDNLLDSRMEIREKYVYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMCR 301
QY 241 HNTKGLNCELMDFYHDLPRWPAEGRNSNACKKCNCSCHSDFMAVELATGNVSGV 300
Db 302 HNTKGLNCELMDFYHDLPRWPAEGRNSNACKKCNCSCHSDFMAVELATGNVSGV 361
QY 301 CDNCQHTMGRNCEQCKPFYQHPERDIRDPNLCBPCTCDPAGSENGGICDGYTDFSVGL 360
Db 362 CDNCQHTMGRNCEQCKPFYQHPERDIRDPNLCBPCTCDPAGSENGGICDGYTDFSVGL 421
QY 361 IAGQCRCKLHVEGERCDVCKEGFYDLSEADPYGCKSCACNPLGTIPGKNPCDSETGYCYC 420
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QY 421 KRLVTGORCDQCLPQHGLSNDLDGCRPCDCLGGALNNSCEDSGQCSCLPHMIGRQCN 480
Db 482 KRLVTGORCDQCLPQHGLSNDLDGCRPCDCLGGALNNSCEDSGQCSCLPHMIGRQCN 541
QY 481 EVESGYFTTLDHYIYEAEANLPGVVRVVERQYIQDRIPSWTGPFGFVRVEGAYLEFFI 540
Db 542 EVESGYFTTLDHYIYEAEANLPGVVRVVERQYIQDRIPSWTGPFGFVRVEGAYLEFFI 601
QY 541 DNIPYSMEYEILIRYEPQLPDHWEKAVITVORPGKIPASSRCNGTVPDDNQVVSLSPGS 600
Db 602 DNIPYSMEYDILIRYEPQLPDHWEKAVITVORPGRIPTSSRCNGTIPDDNQVVSLSPGS 661
QY 601 RYVVLPRPVCFEKGMNYYTVRLELPQYTAGSDVESPTFIDSLVLMYPYCKSLDIFTVGS 660

Db 662 RYVVLPRPVCFEKGTNYTVRLELPQYTSSDSVESPYTLIDSLVLMPICKSLDIFTVGGS 721
QY 661 GDGEVNTSAWETFORYRCLENSRSVVKTPMTDVCNRIIFSISALIHOTGLACECDPQGS 720
Db 722 GDGVVNTSAWETFORYRCLENSRSVVKTPMTDVCNRIIFSISALLHOTGLACECDPQGS 781
QY 721 SSVCDPNGGQCQCRPNVVGRTNRCAPGTFGFGNGCKPCDCHLQGSASAFCDAITGQCH 780
Db 782 SSVCDPNGGQCQCRPNVVGRTNRCAPGTFGFGSGCKPCCECHLQGSVNAFCNPVTGQCH 841
QY 781 CFQGIYARQCDRCLPGYWGFPSPQPCQCNGHALDCDVTGECCLSCDYTTGHNCECCLAG 840
Db 842 CFQGVYARQCDRCLPGHWGFPSPQPCQCNGHADDCDVTGECCLNCQDYTMGHNCECCLAG 901
QY 841 YYGDPPIIGSGDHCRPCPCPDGPDGSDGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCASG 900
Db 902 YYGDPPIIGSGDHCRPCPCPDGPDGSDGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCASG 961
QY 901 FFGNPSDFGSGCQPCQCHNIDTTDPEACDKDTGRCLKCLYHTEGDHCQLCYGYGDAL 960
Db 962 YFGNPSEVGSGCQPCQCHNIDTTDPEACDKETGRCLKCLYHTEGEHCQCFRFGYGDAL 1021
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QY 1021 GPCNCAHSAHSGFPCSCNEFTGCQCQCMPPGFGGRTCSQCLFWDGPDVVECRACDCDPRGIET 1080
Db 1082 DPCNCAHSAHSGFPCSCNEFTGCQCQCMPPGFGGRTCSQCLFWDGPDVVECRACDCDPRGIET 1141
QY 1081 PQCDQSTGCVCVEGVEGRCDKCTRGYSVGFDPCTPCHQCQFALWDALIELTNRTHKFL 1140
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Db 1442 QXAMDLDDQVLSALAEVEQLSKMVSEAKLRADAKQSAEDILLKTNATKERMDKSNEELR 1501
QY 1441 NLIKQIRNFLTSDSADLDSIEAVANEVLKSGNASTPQOLQNLTEDIRERVFETLSQVEVIL 1500
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Db 1562 QHSAADIARAEMLLLEAKRASKSATDVKVTDVMVKEALEEAEAKQAAEKAIAKQADEDIQ 1621
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QY 1621 NADDVKKTLDGELDEKYYKKVESILIAQKTEESADARRKAELLQNEAKTLLAQANSKIQLLLE 1680
Db 1682 SAEDVKKTLDGELDEKYYKKVENLIAKTEESADARRKAEMLQNEAKTLLAQANSKIQLLK 1741
QY 1681 DLERKYEDNQYLEDKAQELVRLEGEVRSLLKDISQKAVYSTCL 1725

Db 1742 DLERKYEDNQYLEDKAQELARLEGEVRSLLKDISQKAVYSTCL 1786
RESULT 9
US-09-561-709B-9
; Sequence 9, Application US/09561709B
; Patent No. 6682911
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Champliand, Marie-France
; APPLICANT: Olson, Pamela
; APPLICANT: Koch, Manuel
; APPLICANT: Brunken, William
; TITLE OF INVENTION: LAMININS AND USES THEREOF
; FILE REFERENCE: 10287-060001
; CURRENT APPLICATION NUMBER: US/09/561,709B
; CURRENT FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 09/168,949
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: US 60/061,609
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-709B-9
Query Match 94.1%; Score 8873; DB 4; Length 1786;
Best Local Similarity 92.9%; Pred. No. 0;
Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;
QY 1 EPYCTIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVVTTFAPNRLKIWQSENGVENV 60
Db 62 EPYCTIVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVVTTFAPNRLKIWQSENGVENV 121
QY 61 TIQLDLEAEFFHFTLIMTFKTPAAMLIERSSDFGTWGVYRYFAYDCESFPGISGTP 120
Db 122 TIQLDLEAEFFHFTLIMTFKTPAAMLIERSSDFGTWGVYRYFAYDCESFPGISGTP 181
QY 121 MKKVDDIICDSRYSIDIEPSTEGEVIFRALDPAFKIEDPYSRIONLLKITNLRIKFKVLH 180
Db 182 MKKVDDIICDSRYSIDIEPSTEGEVIFRALDPAFKIEDPYSRIONLLKITNLRIKFKVLH 241
QY 181 TLGNDLLDSRMEIREKYYIYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMCR 240
Db 242 TLGNDLLDSRMEIREKYYIYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMCR 301
QY 241 HNTKGLNCEL CMDFYHDL PWRPABGRNSNACKKCNNEHSSCHFDMAVFLATGNVSGGV 300
Db 302 HNTKGLNCEL CMDFYHDL PWRPABGRNSNACKKCNNEHSSCHFDMAVFLATGNVSGGV 361
QY 301 CDNCQHTMGRNCEQCKPFYQHPERDIRDPNLCPECTCDPAGSENGGICDGYTDFSVGL 360
Db 362 CDDCQHTMGRNCEQCKPFYQHPERDIRDPNLCPECTCDPAGSQNEGICDGYTDFSVGL 421
QY 361 IAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGGNPCDSETGYCYC 420
Db 422 IAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGGNPCDSETGYCYC 481
QY 421 KRLVTGQRCDQCLPQHWSGLNDLDGCRPCDCDLGGALNNSCSEDSGQCSCLPHMIGRQCN 480
Db 482 KRLVTGQRCDQCLPQHWSGLNDLDGCRPCDCDLGGALNNSCFAESGQCSCLPHMIGRQCN 541
QY 481 EVESGYFTTLDHYIYEAEEANLPGVWVVERQYIQRIPSWTGPGRVPEGAYLEFFI 540
Db 542 EVERGYFFATLDHYLYEAEEANLPGVSVIVERQYIQRIPSWTGPGRVPEGAYLEFFI 601
QY 541 DNIPYSMEYEILIRYEPQLPDHWEKAVITVQRPKTI PASSRCGNTVPDDDNQVVSLSPGS 600
Db 602 DNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPTRSSRCGNTIPDDDNQVVSLSPGS 661

QY 601 RYVVLPRPVCFEKGMNVTYRLLELPQYTAGSDVSPYTFIDSLVLMFYCKSLDIFTVGS 660
Db 662 RYVVLPRPVCFEKGMNVTYRLLELPQYTAGSDVSPYTFIDSLVLMFYCKSLDIFTVGS 721
QY 661 GDGEVNSAWETFORVRCLENSRSVVKTPMTDVCNRIIFISALIHOTGLACECDPQGS 720
Db 722 GDGVVNSAWETFORVRCLENSRSVVKTPMTDVCNRIIFISALIHOTGLACECDPQGS 781
QY 721 SSVCDPNGGQCQCRPNVVGRTCNRCAPGTGFGPNGKPCDCHLQSSASAFCAITGQCH 780
Db 782 SSVCDPNGGQCQCRPNVVGRTCNRCAPGTGFGPNGKPCDCHLQSSASAFCAITGQCH 841
QY 781 CFQGIYARQCDRCCLPGYWGFPSCQPCQCNHGDCTVTGECCLSCQDYTTGHNCRCLAG 840
Db 842 CFQGIYARQCDRCCLPGYWGFPSCQPCQCNHGDCTVTGECCLSCQDYTTGHNCRCLAG 901
QY 841 YGDPPIIGSGDHCRPCPDGPDGSDGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCASG 900
Db 902 YGDPPIIGSGDHCRPCPDGPDGSDGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCASG 961
QY 901 FFGNPSDFGGSCQPCQCHNIDTTPDPAEADKDTGRCLKCLYHTEGHCQLCQYGYGDAL 960
Db 962 YFGNPSDFGGSCQPCQCHNIDTTPDPAEADKDTGRCLKCLYHTEGHCQLCQYGYGDAL 1021
QY 961 RQDCKKVCNLYGTVEHCNGSDCHCDKATGQSCCLPNVIGQNCRCAPNTWQLASGTGC 1020
Db 1022 RQDCKKVCNLYGTVEHCNGSDCHCDKATGQSCCLPNVIGQNCRCAPNTWQLASGTGC 1081
QY 1021 GPCNNAHSGFGRSCNFTGQCQCMFGGRTSCQELFWGDPDVECRACDCDPRGIET 1080
Db 1082 GPCNNAHSGFGRSCNFTGQCQCMFGGRTSCQELFWGDPDVECRACDCDPRGIET 1141
QY 1081 PQDQSTGQCVCVEGPRCDKCTRGYSVGPDPCTPCHQCFALWDVIAELTNTRHFL 1140
Db 1142 PQDQSTGQCVCVEGPRCDKCTRGYSVGPDPCTPCHQCFALWDVIAELTNTRHFL 1201
QY 1141 EKAKALKISGVIQPYRETVDSEKKNVNEIKDILAQSPAAEPLKNGILFEEAEKLTQDVT 1200
Db 1202 EKAKALKISGVIQPYRETVDSEKKNVNEIKDILAQSPAAEPLKNGILFEEAEKLTQDVT 1261
QY 1201 EKMAQVEVKLTDTASQSNSTAGELGALQAEBSLDKTVKELAEQLEFIKNSDIOGALDSI 1260
Db 1262 EKMAQVEVKLTDTASQSNSTAGELGALQAEBSLDKTVKELAEQLEFIKNSDIOGALDSI 1321
QY 1261 TKYFQMSLEAEKRVNASTDPNSTVEQSALTRDRVEDLMLESPPFKEQEEQARLDLDEL 1320
Db 1322 TKYFQMSLEAEKRVNASTDPNSTVEQSALTRDRVEDLMLESPPFKEQEEQARLDLDEL 1381
QY 1321 AGKLQSLDLSAAQMTGTPPGADCSSECGPNCRCTDEGEKKGCGGPGGLVTVHAWSAW 1380
Db 1382 AGKLQSLDLSAAQMTGTPPGADCSSECGPNCRCTDEGEKKGCGGPGGLVTVHAWSAW 1441
QY 1381 QKAMDQDVLALAEVQSLKMWSEAKVRADEAKQNAQDVLKTNATKEKVKDSNEDLR 1440
Db 1442 QKAMDQDVLALAEVQSLKMWSEAKVRADEAKQNAQDVLKTNATKEKVKDSNEDLR 1501
QY 1441 NLIKQIRNFTLQDSADLDSIEAVANEVLKSGNASTPQOLQNLTPEDIRERVETLSQVEVIL 1500
Db 1502 NLIKQIRNFTLQDSADLDSIEAVANEVLKSGNASTPQOLQNLTPEDIRERVETLSQVEVIL 1561
QY 1501 QQSAADIARAELLLLEAKRASKSATDVKTADVMVKEALEEAEKQVAAEKAIKQADEDIQ 1560
Db 1562 QQSAADIARAELLLLEAKRASKSATDVKTADVMVKEALEEAEKQVAAEKAIKQADEDIQ 1621
QY 1561 GTQNLTSIESETAASEETLTNASQRIKSLERNVEELKRKAQNSGEAEYIEKVYVSVKQ 1620
Db 1622 GTQNLTSIESETAASEETLTNASQRIKSLERNVEELKRKAQNSGEAEYIEKVYVSVKQ 1681
QY 1621 NADDVKTLDGELDEKYKKVESLIAQKTEESADARRKAEQLQNEAKTLAQANSKLQLE 1680
Db 1682 SAEDVKTLDGELDEKYKKVESLIAQKTEESADARRKAEQLQNEAKTLAQANSKLQLE 1741
QY 1681 DLERKYEDNQYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1725

Db 1742 DLERKYEDNQYLEDKAQELARLEGEVRSLLKDISEKVAVYSTCL 1785
RESULT 10
US-08-144-121-4
; Sequence 4, Application US/08144121
; Patent No. 5610031
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert E.
; APPLICANT: Wagman, David W.
; TITLE OF INVENTION: BLK CHAIN OF LAMININ AND METHODS OF USE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: United States
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/144,121
; FILING DATE: 27-OCT-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: (MGH-0780.0) MGP-021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1196 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 1..250
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 251..437
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 438..807
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 808..840
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 841..1196
US-08-144-121-4

Query Match 58.2%; Score 5489; DB 1; Length 1196;
Best Local Similarity 62.4%; Pred. No. 3.6e-316;
Matches 1077; Conservative 46; Mismatches 32; Indels 570; Gaps 1;
QY 1 EPYCIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVTTFAPNRLKIWWQSENGVENV 60
Db 42 EPYCIVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVTTFAPNRLKIWWQSENGVENV 101
QY 61 TIQLDLEAEFFHFTLIMTFKTRPAAMLIERSSDFGKTGWVYRYFAYDCESFPFGISTGP 120
Db 102 TIQLDLEAEFFHFTLIMTFKTRPAAMLIERSSDFGKTGWVYRYFAYDCESFPFGISTGP 161
QY 121 MKKVDDIIICDSRYSDIEPSTEGEVIFFALDPAPFKIEDPSPRIQNLKLTNRIKFKVLH 180

Db 162 MKKVDDIICDSRYSIDIEPSTEGEVIIFRALDPFKIEDPYSPIRQNLKXITNLRIFKFKLH 221
Qy 181 TLGDNLLDSRMEIREKYYYAYVDMVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMCR 240
Db 222 TLGDNLLDSRMEIREKYYYAYVDMVRGNCFCYGHASECAPVDGFNEEVEGMVHGCMCR 281
Qy 241 HNTKGLNCELMDFFYHDLPRWPAEGRNSACKKNCNEHSSSCHFDMAVFLATGNVSGV 300
Db 282 HNTKGLNCELMDFFYHDLPRWPAEGRNSACKKNCNEHSSSCHFDMAVFLATGNVSGV 341
Qy 301 CDNCQNTMGRNCEQCKPFYFOHPERDIRPNLCEPCTCDPAGSENGICDGYTDFSVGL 360
Db 342 CDDCQNTMGRNCEQCKPFYFOHPERDIRPNLCEPCTCDPAGSENGICDGYTDFSTGL 401
Qy 361 IAGQCRCKLHVEGERCDVCKEGFYDLSAEDYGCCKSCACNPLGTIPGPNPCDSETGYCYC 420
Db 402 IAGQCRCKLHVEGERCDVCKEGFYDLSAEDYGCCKSCACNPLGTIPGPNPCDSETGYCYC 437
Qy 421 KRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCLGALNNSCEDSGQCSCLPHMIGRQCN 480
Db 438 ----- 437
Qy 481 EVESGYFTTLDHYIYEAEEANLPGVVVVERQYIQDRIPSWTGPGRVVRPEGAYLEFFI 540
Db 438 ----- 437
Qy 541 DNIPYSMEYEILIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTVPDDDNQVVSLSPGS 600
Db 438 ----- 437
Qy 601 RYVVLPRPVCFEKGMNTYVRLELPQYTAGSDVESPYTFIDSLVMPYCKSLDIFTVGS 660
Db 438 ----- 437
Qy 721 SSVCDPNGGQCQCRPNVVGRTNRCAPGTFGFGPNCKPCDCHLQGSASFDAITGQCH 780
Db 438 ----- 437
Qy 781 CFQGIYARQCDRLPGYWGFPSCQPCQCNGHALDCDVTGECCLSCQDYTTGHNCRCLAG 840
Db 438 ----- 437
Qy 841 YYGDPILGSDHCRPCPCPDGPDGSRQFARSCYQDPVTLQACVCDPGYIGSRCDDCASG 900
Db 438 ----- 437
Qy 901 FFGNPSDFGGSCQPCQCHNIDTDPACDKDTGRCLKCLYHTEGDHCLQCYGYGDAL 960
Db 438 ----- 437
Qy 961 RQDCRKCVCNYLGTVKEHNGSDCHCDKATGQCSCLPNVIGONCDRCAPNTWOLASGTGC 1020
Db 438 -----CVCNYLGTVQEHCHNGSDCQCDKATGQCLCLPNVIGONCDRCAPNTWOLASGTGC 491
Qy 1021 GPCNCNAAHSFGPSCNEFTGQCCQMPGFGGRTCSCEQLFWGDPDVECRACDPRGIET 1080
Db 492 DPCNCNAAHSFGPSCNEFTGQCCQMPGFGGRTCSCEQLFWGDPDVECRACDPRGIET 551
Qy 1081 PQCDQSTGQCVVEGVGPRCDKCTRGYSVGFDPCTPCHQCQFALWDAIIGELTNRTHKFL 1140
Db 552 PQCDQSTGQCVVEGVGPRCDKCTRGYSVGFDPCTPCHQCQFALWDAIIGELTNRTHRFL 611
Qy 1141 EKAKALISGVIGPYRETVDSEKKNVEIKDILAQSPAEBPLKNIGILFEEAEKTKDVT 1200
Db 612 EKAKALISGVIGPYRETVDSEKKNVEIKDILAQSPAEBPLKNIGILFEEAEKTKDVT 671
Qy 1201 EKMAQVEVKLTDASQSNSTAGELGALQAEASLDKTVKELAEQLEFIKNSDIQCALDSI 1260

Db 672 EMMAQVEVKLSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSI 731
Qy 1261 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLERESPFKEQOEEOARLLDEL 1320
Db 732 TKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVMMERESQFKEQOEEOARLLDEL 791
Qy 1321 AGKLQSLDLASAAQMTCTGPPGADCSSECGPNCRCTDEGEKCKGCGGGLVTVVAHSAW 1380
Db 792 AGKLQSLDLASAAQMTCTGPPGADCSSECGPNCRCTDEGERKCGGCGGGLVTVVAHSAW 851
Qy 1381 OKAMDFDRDVLASALAEVQSLKVMSEAKVRADEAKQNAQDVLTKTNATKVKDKSNEELR 1440
Db 852 OKAMDLQDVLASALAEVQSLKVMSEAKVRADEAKQNAQDVLTKTNATKVKDKSNEELR 911
Qy 1441 NLIKQIRNFLTQDSADLDSIEAVANEVLKSGNASTPQQLQNLTERIRERVETLSQVEVIL 1500
Db 912 NLIKQIRNFLTQDSADLDSIEAVANEVLKSGNASTPQQLQNLTERIRERVETLSQVEVIL 971
Qy 1501 QOSAAADIARAEELLEAEKRAKSKSATDVKVTADVMVKEALEEAEKAAQVAAEKAIKQADEDIQ 1560
Db 972 QOSAAADIARAEELLEAEKRAKSKSATDVKVTADVMVKEALEEAEKAAQVAAEKAIKQADEDIQ 1031
Qy 1561 GTQNLTSIESETAASEETLTNASORISKLERNVVEELKRAAQNSEAEYIEKVVYSVKQ 1620
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Qy 1621 NADDVKKTLDGELDEKYKVESLIAQKTESADARRKAELLONEAKTLLAQANSKLQLE 1680
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Qy 1681 DLERKYEDNQYLEDKQELVLRLEGEVRSLLKDISEKVAVYSTCL 1725
Db 1152 DLERKYEDNQYLEDKQELVLRLEGEVRSLLKDISEKVAVYSTCL 1196

RESULT 11
US-08-735-893-4
; Sequence 4, Application US/08735893
; Patent No. 5914317
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert E.
; APPLICANT: Wagman, David W.
; TITLE OF INVENTION: BLK CHAIN OF LAMININ AND METHODS OF USE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: United States
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/735,893
; FILING DATE: 18-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/144,121
; FILING DATE: 27-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: (MCH-0780.1) MGP-021DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:


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; LENGTH: 1196 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 1..250
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 251..437
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 438..807
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 808..840
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 841..1196
;
US-08-735-893-4

Query Match      58.2%; Score 5489; DB 2; Length 1196;
Best local Similarity 62.4%; Pred. No. 3.6e-316;
Matches 1077; Conservative 46; Mismatches 32; Indels 570; Gaps 1;

QY 1 EPYCIIVSHLQEDKKCFICDSRDPYHETLNPDShLIENVVTFEAPNRLKIWMQSENGVENV 60
Db 42 EPYCIIVSHLQEDKKCFICNSQDPYHETLNPDShLIENVVTFEAPNRLKIWMQSENGVENV 101
QY 61 TIQLDLAEAFHFTHLIMTFKTPRPAAMLIERSDFGKTGWVRYFYAYDCEASFPGISTGP 120
Db 102 TIQLDLAEAFHFTHLIMTFKTPRPAAMLIERSDFGKTGWVRYFYAYDCEASFPGISTGP 161
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Db 162 MKKVDDIICDSRYSYDIEPSTEGEVIFRALDPAFKIEDPYSPIQNLLKITNLRKFVKLH 221
QY 181 TLGDNLLDSRMEIREKYYIYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMCR 240
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QY 241 HNTKGLNCELMDFYHDLPRPAEGRNSNACKKNCNEHSSCHFDMAVFLATGNVSGGV 300
Db 282 HNTKGLNCELMDFYHDLPRPAEGRNSNACKKNCNEHSISCHFDMAVFLATGNVSGGV 341
QY 301 CDNCQHTMGRNCEQCKPFYFOHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 360
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QY 361 IAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGNPCDSETGYCYC 420
Db 402 IAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGNPCDSETGYCYC 437
QY 421 KRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCLGGLNNSCEDSGQSCCLPHMIGRCQN 480
Db 438 ----- 437
QY 481 EVESGYFTTLDHYIYEAEANLPGVVVVERQYIQDRIPSWTGRGFRVRVPEGAYLEFFI 540
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QY 541 DNIPYSMEYEILIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTVPDDNQVVSLSPGS 600
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Db 438 ----- 437
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QY 721 SSVCDPNGGQCCQCRPNVVGRTCNRCAPGTFTFGFPGNCKPCDCHLQGSASAFCDAITGQCH 780
Db 438 ----- 437
QY 781 CFQGIYARQCDRCLPGYWGFPSCQPCQCNGHALDCDVTVTGECCLSCQDYTTGHNCRCLAG 840
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Db 438 ----- 437
QY 961 RQDCRKVCNLYLGTVKEHCHNGSDCHCDKATGQCSCLPNVIGQNCDCRCAPNTWQLASGTGC 1020
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QY 1021 GPCNCNAAHSFGPSCNEFTGQCCQMPGFGGRTCSCEQLFWGDDPVECRACDCDPRGIET 1080
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QY 1201 EKMAQVEVKLTDTASQSNSTAGELGALQAEESLDKTVKELAEQLEFIKNSDIQGALDSI 1260
Db 672 EMMAQVEVKLTDTASQSNSTAGELGALQAEESLDKTVKELAEQLEFIKNSDIQGALDSI 731
QY 1261 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRVEDLMLERESPFKEQEEQARLLDEL 1320
Db 732 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRVEDLMLERESPFKEQEEQARLLDEL 791
QY 1321 AGKLSLDLSAAAQMTCTGTPPGADCESECGGNCRCTDEGEKKCGGCGGLVTVVAHSAW 1380
Db 792 AGKLSLDLSAAAQMTCTGTPPGADCESECGGNCRCTDEGEKKCGGCGGLVTVVAHSAW 851
QY 1381 QKAMDFDRDVLALAEVEQLSKMVSEAKVRADAKQNAQDVLKTNATKEKVDKSNEDLR 1440
Db 852 QKAMDFDRDVLALAEVEQLSKMVSEAKVRADAKQNAQDVLKTNATKEKVDKSNEDLR 911
QY 1441 NLIKQIRNFLTDSADLSIEAVANEVLKSGNASTPQQQLNLTEDIRERVETLSQVEVIL 1500
Db 912 NLIKQIRNFLTDSADLSIEAVANEVLKSGNASTPQQQLNLTEDIRERVETLSQVEVIL 971
QY 1501 QSAADIAARAELLLLEAKRASKSATDVKVTADMVKEALEEAEKAAQVAAEKAIQADEDIQ 1560
Db 972 QSAADIAARAELLLLEAKRASKSATDVKVTADMVKEALEEAEKAAQVAAEKAIQADEDIQ 1031
QY 1561 GTQNLLTSIESETAASEETLTNASQRISELRNVEELKRAAQAQNSGEAEYIEKVYVSVKQ 1620
Db 1032 GTQNLLTSIESETAASEETLTNASQRISELRNVEELKRAAQAQNSGEAEYIEKVYVSVKQ 1091
QY 1621 NADDVKKTLDGELDEKYKVKVESLIAQKTRESADARRKAELLQNEAKTLLAQANSKLQLE 1680
Db 1092 SAEDVKKTLDGELDEKYKVKVESLIAQKTRESADARRKAELLQNEAKTLLAQANSKLQLE 1151
QY 1681 DLERKYEDNQKYLEDKAQLVRLEGEVRSLLKDISEKVAIVYSTCL 1725
Db 1152 DLERKYEDNQKYLEDKAQLVRLEGEVRSLLKDISEKVAIVYSTCL 1196
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RESULT 12
US-09-845-583A-6
; Sequence 6, Application US/09845583A

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; Patent No. 6635616
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Brunken, William Joseph
; APPLICANT: Champlaud, Marie-France
; APPLICANT: Hunter, Dale
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
; FILE REFERENCE: 10287-056001
; CURRENT APPLICATION NUMBER: US/09/845,583A
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/200,863
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1799
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-845-583A-6

Query Match      52.1%; Score 4914; DB 4; Length 1799;
Best Local Similarity 51.0%; Pred. NO. 5.7e-282;
Matches 883; Conservative 297; Mismatches 534; Indels 18; Gaps 8;

QY      1 EPYCIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVVTFAPNRLKIHWQSENGVENV 60
DB      77 QPYCIVSHLQDEKKCFCLDSRRPFSARDNPNSHRIQNVTFSAPQRTAWQSENGVPMV 136

QY      61 TIQLDLAEFHFTHLINTFKTERPAAMLIERSDFGKTWGVYRYFAYDCESFPFGISTGP 120
DB      137 TIQLDLAEFHFTHLINTFKTERPAAMLVERSADFGRTWHVYRYFSYDCGADFPGIPLAP 196

QY      121 MKKVDDIIICDSRYSIEPSTEGEVIFFRALDPAFKIEDPYSPRIQNLLKITNLRKFVKLH 180
DB      197 PRRWDDVVCESRYSEIEPSTEGEVIYRVLDPAIPIDPYSSRIQNLLKITNLRVNLTRLH 256

QY      181 TLGDNLLDSRMEIREKYYAVYDMVVRGNCFYGHASECAPVDGVNEEVEGMVHGHCMC 240
DB      257 TLGDNLLDPRREIREKYYALYELVIRGNCFYGHASQCAPAPGAPAHAEGMVHGACICK 316

QY      241 HNTKGLNCELCMDYHDLPRPAPAEGRNSACKKCNCSHSSCHFDMAVFLATGNVSGGV 300
DB      317 HNTRGLNCEQCQDFYQDLPHWPAEDGHTHACKRCECNHGHTSCHFDMAVYLASGNVSGGV 376

QY      301 CDNCQHNTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 360
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; Sequence 11, Application US/09561709B
; Patent No. 6682911
; GENERAL INFORMATION:

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; Sequence 11, Application US/09561709B
; Patent No. 6682911
; GENERAL INFORMATION:

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

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Run on: May 18, 2004, 14:56:24 ; Search time 43.8855 Seconds
(without alignments)
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Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	8873	94.1	1765	14	US-10-037-182-8
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6	8873	94.1	1786	9	US-09-938-275-6
7	8873	94.1	1786	14	US-10-037-182-6
8	5482	58.1	1196	16	US-10-443-349-4
9	4936	52.3	1801	9	US-09-938-275-8
10	4914	52.1	1799	9	US-09-845-583-6
11	4890	51.9	1798	9	US-09-938-275-9
12	4778	50.7	1798	9	US-09-845-583-8
13	3646	38.7	1808	15	US-10-369-493-5986
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16	2154	22.8	527	14	US-10-102-806-703	Sequence 703, App
17	1730	18.3	3672	15	US-10-369-493-6146	Sequence 6146, Ap
18	1649	17.5	3712	12	US-10-037-417-48	Sequence 48, Appl
19	1649	17.5	3712	13	US-10-108-605-103	Sequence 103, App
20	1645	17.4	3712	12	US-10-037-417-51	Sequence 51, Appl
21	1637.5	17.4	1572	14	US-10-037-182-20	Sequence 20, Appl
22	1637.5	17.4	1605	14	US-10-037-182-18	Sequence 18, Appl
23	1622.5	17.2	1576	14	US-10-037-182-16	Sequence 16, Appl
24	1622.5	17.2	1609	14	US-10-037-182-14	Sequence 14, Appl
25	1622.5	17.2	1609	14	US-10-299-058-12	Sequence 12, Appl
26	1618.5	17.2	1609	9	US-09-938-275-11	Sequence 11, Appl
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43	1484	15.7	1587	12	US-10-262-839-210	Sequence 210, App
44	1482	15.7	3084	9	US-09-938-275-4	Sequence 4, Appli
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ALIGNMENTS

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; Sequence 12, Application US/10037182
; Publication No. US2003004899A1
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Doi, Masayuki
; APPLICANT: Thyboll, Jill
; TITLE OF INVENTION: Recombinant Laminin 10
; FILE REFERENCE: 99-274-F
; CURRENT APPLICATION NUMBER: US/10/037,182
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,449
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/279,282
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1725
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-037-182-12

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; Patent No. US20020111309A1
; GENERAL INFORMATION:
; APPLICANT: Gerardo Castillo
; APPLICANT: Alan Snow
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications
; TITLE OF INVENTION: Of Laminin and Laminin-Derived Protein Fragments
; FILE REFERENCE: PROTEO.P03
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; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
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; TYPE: PRT
; ORGANISM: Mus Musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Swissprot P02469
; DATABASE ENTRY DATE: 1989-07-01
US-09-938-275-7

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QY 421 KRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCDLGGALNNSCSEDSGQCSCLPHMIGRQCN 480
Db 482 KRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCDLGGALNNSCSEDSGQCSCLPHMIGRQCN 541
QY 481 EVESGYFTTLDHYIYEAEENLPGVWVVERQYIQDRIPSWTGPGRVPEGAYLEFFI 540
Db 542 EVESGYFTTLDHYIYEAEENLPGVWVVERQYIQDRIPSWTGPGRVPEGAYLEFFI 601
QY 541 DNIPYSMEYEILIRYEPQLPDHWEKAVITVORPGKIPASSRCGNTVPDDDNQVVSLSPGS 600
Db 602 DNIPYSMEYEILIRYEPQLPDHWEKAVITVORPGKIPASSRCGNTVPDDDNQVVSLSPGS 661
QY 601 RYVVLPRPVCFEKGMNYYTVRLELPQYTAGSDVESPYTFIDSLVMPYCKSLDIFTVGS 660
Db 662 RYVVLPRPVCFEKGMNYYTVRLELPQYTAGSDVESPYTFIDSLVMPYCKSLDIFTVGS 721
QY 661 GDGEVNTSAWETFORYRCLENSRSVVKTPMTDVCNRIIFSISALIHQTGLACECDPQGS 720
Db 722 GDGEVNTSAWETFORYRCLENSRSVVKTPMTDVCNRIIFSISALIHQTGLACECDPQGS 781
QY 721 SSVCDPNQGGQCCQCRPNVVGRTCNRCAPGTFGFGPNCGKPCDCHLQGSASAFCDAITGQCH 780
Db 782 SSVCDPNQGGQCCQCRPNVVGRTCNRCAPGTFGFGPNCGKPCDCHLQGSASAFCDAITGQCH 841
QY 781 CFQGIYARQCDRCLPGYWGFFPSCQCCNGHALDCDVTGFCLSQDYTTGHNCRERCLAG 840
Db 842 CFQGIYARQCDRCLPGYWGFFPSCQCCNGHALDCDVTGFCLSQDYTTGHNCRERCLAG 901
QY 841 YYGDPPIGSGDHCRPCPCPDGPDGSRQFARSCYQDPVTQLACVCDPQYIGSRCDDCASG 900
Db 902 YYGDPPIGSGDHCRPCPCPDGPDGSRQFARSCYQDPVTQLACVCDPQYIGSRCDDCASG 961
QY 901 FFGNPSDFGSGCQPCQCHNIDITDPEACDKDTGRCLKCLYHTEGDHCQLCQYGYGDAL 960
Db 962 FFGNPSDFGSGCQPCQCHNIDITDPEACDKDTGRCLKCLYHTEGDHCQLCQYGYGDAL 1021
QY 961 RQDCRKVCNLYLGTVKEHCNGSDCHCDKATGQCSCLPNVIGQNCDDRCAPNTWQLASGTGC 1020
Db 1022 RQDCRKVCNLYLGTVKEHCNGSDCHCDKATGQCSCLPNVIGQNCDDRCAPNTWQLASGTGC 1081
QY 1021 GPCNCNAAHSFGPSCNEFTGQCCQCMFGGRTCSQCQLFWGDPDVECRACDDPRGIET 1080
Db 1082 GPCNCNAAHSFGPSCNEFTGQCCQCMFGGRTCSQCQLFWGDPDVECRACDDPRGIET 1141
QY 1081 PQCDQSTGQVCVEGVEGPRCDKCTRGYSGVFPDCTPCHQCQFALWDIAIGELTNRTHKFL 1140
Db 1142 PQCDQSTGQVCVEGVEGPRCDKCTRGYSGVFPDCTPCHQCQFALWDIAIGELTNRTHKFL 1201
QY 1141 EKAKALKISGVIQPYRETVDVSVEKKVNEIKDILAQSPAAPLKNIGILFEEAEKLTKDVT 1200
Db 1202 EKAKALKISGVIQPYRETVDVSVEKKVNEIKDILAQSPAAPLKNIGILFEEAEKLTKDVT 1261
QY 1201 EKMAQVEVKLTDTASQSNSTAGELGALQAEASLDKTVKELABQLEFIKNSDIOGALDSI 1260
Db 1262 EKMAQVEVKLTDTASQSNSTAGELGALQAEASLDKTVKELABQLEFIKNSDIOGALDSI 1321
QY 1261 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLERESPFEKQEEQARLLDEL 1320

Db 1322 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLERESPFEKQEEQARLLDEL 1381
QY 1321 AGKLOSLDLSAAAQMTCTGTPPGADCESECGGNPCRTDEGEKKCGGPGCGGLVTVVAHSW 1380
Db 1382 AGKLOSLDLSAAAQMTCTGTPPGADCESECGGNPCRTDEGEKKCGGPGCGGLVTVVAHSW 1441
QY 1381 QKAMPDFDRDVLASAEVEQLSKVSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDLR 1440
Db 1442 QKAMPDFDRDVLASAEVEQLSKVSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDLR 1501
QY 1441 NLIKQIRNFLTSDADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVIL 1500
Db 1502 NLIKQIRNFLTSDADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVIL 1561
QY 1501 QQSAADTARAELLLLEAKRASKSATDVKVTDVMVKEALEEAEAKAQVAAEKAIKQADEDIQ 1560
Db 1562 QQSAADTARAELLLLEAKRASKSATDVKVTDVMVKEALEEAEAKAQVAAEKAIKQADEDIQ 1621
QY 1561 GTQNLITSIESETAASEETLTNASQRIKLERNVVELKRAAQNNGEAEYIEKVVSVKQ 1620
Db 1622 GTQNLITSIESETAASEETLTNASQRIKLERNVVELKRAAQNNGEAEYIEKVVSVKQ 1681
QY 1621 NADDVKKTLDGELDEKYYKKVESLIAQKTEESADARRKAEILLQNEAKTLLAQANSKLQLE 1680
Db 1682 NADDVKKTLDGELDEKYYKKVESLIAQKTEESADARRKAEILLQNEAKTLLAQANSKLQLE 1741
QY 1681 DLERKYEDNQKYLEDKAQLVRLGEVRSLLKDISEKVAVYSTCL 1725
Db 1742 DLERKYEDNQKYLEDKAQLVRLGEVRSLLKDISEKVAVYSTCL 1786

RESULT 3

US-10-037-182-10
; Sequence 10, Application US/10037182
; Publication No. US20030044899A1
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Doi, Masayuki
; APPLICANT: Thyboll, Jill
; TITLE OF INVENTION: Recombinant Laminin 10
; FILE REFERENCE: 99-274-F
; CURRENT APPLICATION NUMBER: US/10/037,182
; PRIOR APPLICATION NUMBER: 2001-12-21
; PRIOR FILING DATE: 2001-12-21
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/257,449
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-037-182-10

Query Match 100.0%; Score 9429; DB 14; Length 1786;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPYCIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVVTTTAPNRLKIWWQSENGVENV 60
Db 62 EPYCIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVVTTTAPNRLKIWWQSENGVENV 121
QY 61 TIQLDLEAEFHETHLIMTFKTRPAAAMLIERSDDFGKTGWVYRFAYDCESSFPGISTGP 120
Db 122 TIQLDLEAEFHETHLIMTFKTRPAAAMLIERSDDFGKTGWVYRFAYDCESSFPGISTGP 181
QY 121 MKKVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLLKITNLRKIFVKLH 180
Db 182 MKKVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLLKITNLRKIFVKLH 241
QY 181 TLGDNLLDSRMEIREKYYIAYVDMVVRGNCFCYGHASECAPVDGVNVEEGMVHGHCMCR 240

Db 242 TLGDNLLDSRMEIREKYYAVYDMVVRGNCFYGHASECAPVDGVNEEVEGMVGHCMCR 301
QY 241 HNTKGLNCEL CMDFYHDL PWRPAEGRNSNACKKNCNEHSSSCHFDMAVFLATGNVSGGV 300
Db 302 HNTKGLNCEL CMDFYHDL PWRPAEGRNSNACKKNCNEHSSSCHFDMAVFLATGNVSGGV 361
QY 301 CDNCQHTNMTGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 360
Db 362 CDNCQHTNMTGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 421
QY 361 IAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSKACNPLGTIPGGNPCDSETGYCYC 420
Db 422 IAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSKACNPLGTIPGGNPCDSETGYCYC 481
QY 421 KRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCDLGGALNNSCEDSGQCSCLPHMIGRQCN 480
Db 482 KRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCDLGGALNNSCEDSGQCSCLPHMIGRQCN 541
QY 481 EVESGYFTTLDHYIYEAEEANLPGVGVVVERQYIQDRIPSWTGPGRVPEGAYLEFFI 540
Db 542 EVESGYFTTLDHYIYEAEEANLPGVGVVVERQYIQDRIPSWTGPGRVPEGAYLEFFI 601
QY 541 DNIPYSMEYELLIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTVPDDDNQVVSLSPGS 600
Db 602 DNIPYSMEYELLIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTVPDDDNQVVSLSPGS 661
QY 601 RYVVLPRPVCPEKGMNYYTVRLELPQYTAGSDVESPYTFIDSLVLMPCYCKSLDIFTVGG 660
Db 662 RYVVLPRPVCPEKGMNYYTVRLELPQYTAGSDVESPYTFIDSLVLMPCYCKSLDIFTVGG 721
QY 661 GDGEVNTSAWETFQRYRCLENSRSVVKTPMTDVCNRIIFSISALIHQTGLACECDPOSSL 720
Db 722 GDGEVNTSAWETFQRYRCLENSRSVVKTPMTDVCNRIIFSISALIHQTGLACECDPOSSL 781
QY 721 SSVCDPNGGQOCQRPNVVGRTCNRCAPGTGFGPGNGCKPCDCHLQGSASAFCDAITGQCH 780
Db 782 SSVCDPNGGQOCQRPNVVGRTCNRCAPGTGFGPGNGCKPCDCHLQGSASAFCDAITGQCH 841
QY 781 CFQGIYARQCDRLPGYWGFPSPCQPCQNGHALDCDTVTGECUSCQDYTTGHCNRCIAG 840
Db 842 CFQGIYARQCDRLPGYWGFPSPCQPCQNGHALDCDTVTGECUSCQDYTTGHCNRCIAG 901
QY 841 YGDPPIIGSGDHCRPCPCPDGPDGSRQFARSYQDPVTLQACVCDPGYIGSRCDDCASG 900
Db 902 YGDPPIIGSGDHCRPCPCPDGPDGSRQFARSYQDPVTLQACVCDPGYIGSRCDDCASG 961
QY 901 FFGNPSDFGSGCQPCQCHNIDTTPDPEACDKDTGRCLKCLYHTEGDHCQLCQYGYGDAL 960
Db 962 FFGNPSDFGSGCQPCQCHNIDTTPDPEACDKDTGRCLKCLYHTEGDHCQLCQYGYGDAL 1021
QY 961 RQDCRKVCVNYLGTVKEHCNGSDCHCDKATGQCSCLPNVIGQNCDCRCAPNTWQLASGTGC 1020
Db 1022 RQDCRKVCVNYLGTVKEHCNGSDCHCDKATGQCSCLPNVIGQNCDCRCAPNTWQLASGTGC 1081
QY 1021 GPCNCNAAHSFGPSCNEFTGQCQCMPPGFGRTCSQCQLFWGDPDVECRACDCDPRGIET 1080
Db 1082 GPCNCNAAHSFGPSCNEFTGQCQCMPPGFGRTCSQCQLFWGDPDVECRACDCDPRGIET 1141
QY 1081 PQCDQSTGQCVCVEGVEGPRCDKCTRGYSVFPDCTPCHQCFAWDAIIGELTNRTHKFL 1140
Db 1142 PQCDQSTGQCVCVEGVEGPRCDKCTRGYSVFPDCTPCHQCFAWDAIIGELTNRTHKFL 1201
QY 1141 EKAKALKISGVI GPVRETVDVSVEKKVNEIKDILAQSPAAPLKNIGILFEEAEKLT KDVT 1200
Db 1202 EKAKALKISGVI GPVRETVDVSVEKKVNEIKDILAQSPAAPLKNIGILFEEAEKLT KDVT 1261
QY 1201 EKMAQVEVKLTDTASQSNSTAGELGALQAEAEKLT KDVTVEKELAEQLEFIKNSDIOGALDSI 1260
Db 1262 EKMAQVEVKLTDTASQSNSTAGELGALQAEAEKLT KDVTVEKELAEQLEFIKNSDIOGALDSI 1321
QY 1261 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRVEDLMLERESPKEQEQEARLLDEL 1320

Db 1322 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRVEDLMLERESPKEQEQEARLLDEL 1381
QY 1321 AGKQSLDLSAAAQMTCTGTPPGADCSSECGGPNCRTEGEKKCGGPGCGGLVTVHAWSA 1380
Db 1382 AGKQSLDLSAAAQMTCTGTPPGADCSSECGGPNCRTEGEKKCGGPGCGGLVTVHAWSA 1441
QY 1381 QKAMDFDRDVL SALAEVEQLSKMVSEAKVRADEAKQNAQDVLLKTNATKEKVKDSNEDLR 1440
Db 1442 QKAMDFDRDVL SALAEVEQLSKMVSEAKVRADEAKQNAQDVLLKTNATKEKVKDSNEDLR 1501
QY 1441 NLIKQIRNFLTEDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVIL 1500
Db 1502 NLIKQIRNFLTEDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVIL 1561
QY 1501 QCSAADIPARAELLLEAEKRAKRSATDVKVVTADMVKEALEEAEKQVAAEKAIKQADEDIQ 1560
Db 1562 QCSAADIPARAELLLEAEKRAKRSATDVKVVTADMVKEALEEAEKQVAAEKAIKQADEDIQ 1621
QY 1561 GTQNLTSIESETAASEETLTNASQRIKLERNVVEELKRKAQNSGEAEYIEKVVSVKQ 1620
Db 1622 GTQNLTSIESETAASEETLTNASQRIKLERNVVEELKRKAQNSGEAEYIEKVVSVKQ 1681
QY 1621 NADDVKKTLDGELDEKYYKKVESLIAQKTEESADARRKAEQLQNEAKTLQAANSKLQLE 1680
Db 1682 NADDVKKTLDGELDEKYYKKVESLIAQKTEESADARRKAEQLQNEAKTLQAANSKLQLE 1741
QY 1681 DLERKYEDNOKYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1725
Db 1742 DLERKYEDNOKYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1786

RESULT 4

US-10-037-182-8
; Sequence 8, Application US/10037182
; Publication No. US20030044899A1
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Doi, Masayuki
; APPLICANT: Thyboll, Jill
; TITLE OF INVENTION: Recombinant Laminin 10
; FILE REFERENCE: 99-274-F
; CURRENT APPLICATION NUMBER: US/10/037,182
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,449
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/279,282
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-037-182-8

Query Match 94.1%; Score 8873; DB 14; Length 1765;
Best Local Similarity 92.9%; Pred. No. 0;
Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

QY 1 EPYCIVSHLQEDKKCFICDSRDPYHETLNPDShLIENVVTTFAPNRLKIWWQSENGVENV 60
Db 41 EPYCIVSHLQEDKKCFICNSQDPYHETLNPDShLIENVVTTFAPNRLKIWWQSENGVENV 100
QY 61 TIQLDLAEAFHFTHLIMTFKTRPAAMLIERSSDFGKTGWVYRYFAYDCESSFPFGISTGP 120
Db 101 TIQLDLAEAFHFTHLIMTFKTRPAAMLIERSSDFGKTGWVYRYFAYDCEASFPFGISTGP 160
QY 121 MKKVDDIICDSRYSDIEPSTEGEVI FRALDPAFKIEDPSPRIQNLKITNLRIKFVKLH 180
Db 161 MKKVDDIICDSRYSDIEPSTEGEVI FRALDPAFKIEDPSPRIQNLKITNLRIKFVKLH 220
QY 181 TLGDNLLDSRMEIREKYYAVYDMVVRGNCFYGHASECAPVDGVNEEVEGMVGHCMCR 240

Db 221 TLGDNLLDSRMEIREKYYAVYDMVVRGNCFYGHASECAPVDGFNEBEVGMVHGCMCR 280
QY 241 HNTKGLNCELMDYFHDLPWRPAEGRNSNACKKCNNEHSSSCHFDMAVFLATGNVSGV 300
Db 281 HNTKGLNCELMDYFHDLPWRPAEGRNSNACKKCNNEHSSSCHFDMAVFLATGNVSGV 340
QY 301 CDNCQHNTMGRNCEQCKPFYQHPERDIRDPNICEPCTCDPAGSENGGICDGYTDFSVGL 360
Db 341 CDDCQHNTMGRNCEQCKPFYQHPERDIRDPNICEPCTCDPAGSQNEGICDSTYDFSTGL 400
QY 361 IAGQCRCKLHVEGERCDVCKEGFYDLAEDPYGCKSCACNPLGTIPGGNPNCDSETGYCYC 420
Db 401 IAGQCRCKLHVEGERCDVCKEGFYDLSSDPFGCKSCACNPLGTIPGGNPNCDSETGHCYC 460
QY 421 KRLVTGORCDQCLPQHWGLSNDLDGCRPCDCDLGGALNNSCEDSGQCSCLPHMIGRQCN 480
Db 461 KRLVTGOHCDQCLPEHWGLSNDLDGCRPCDCDLGGALNNSCFAESGQCSRPHMIGRQCN 520
QY 481 EVESGYFTTLDHYIYEAEANLPGVVVVERQYIQRIPSWTGPGRVPEGAYLEFFI 540
Db 521 EVEPGYFATLDHYLYEAEANLPGVSVIVERQYIQRIPSWTGAQFVRVPEGAYLEFFI 580
QY 541 DNIPYSMEYEILIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTVPDDNQVVSLSPGS 600
Db 581 DNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPSTSSRCGNTIPDDNQVVSLSPGS 640
QY 601 RYVVLPRPVCFEKGMNTYVRLLELPQYTAGSDVESPYTFIDSLVLMPCYCKSLDIFTVGS 660
Db 641 RYVVLPRPVCFEKGMNTYVRLLELPQYTAGSDVESPYTFIDSLVLMPCYCKSLDIFTVGS 700
QY 661 GDGEVNTSAWETFQRYRCLENSRSVVKTPMTDVCNLIIFISALIHQTLGACECDPQSSL 720
Db 701 GDGVNTSAWETFQRYRCLENSRSVVKTPMTDVCNLIIFISALLHOTGLACECDPQSSL 760
QY 721 SSVCDPNGGQCQCRPNVVGRTCNRCAPGTGFGPGNCKPCDCHLQGSASAFCDAITGQCH 780
Db 761 SSVCDPNGGQCQCRPNVVGRTCNRCAPGTGFGPGNCKPCDCHLQGSVNAFCNPVTGQCH 820
QY 781 CFQGYARQCDRCLPGYWGPFSPCQPCQCNHGLDCTVTGECCLSCQDYTTGHNCERCLAG 840
Db 821 CFQGYARQCDRCLPGHWPFPSCQPCQCNHGLDCTVTGECCLSCQDYTMGHNCERCLAG 880
QY 841 YYGDPPIIGSGDHCRPCPCPDGPDGSGRQFARSCYQDPVTQLACVCDPGLYIGSRCDDCASG 900
Db 881 YYGDPPIIGSGDHCRPCPCPDGPDGSGRQFARSCYQDPVTQLACVCDPGLYIGSRCDDCASG 940
QY 901 FFGNPSDFGGSCQPCQCHNIDTDPACDKOTGRCLKCLYHTEGDHCQLCQGYGGDAL 960
Db 941 YFGNPSVGGSCQPCQCHNIDTDPACDKOTGRCLKCLYHTEGEHCQFCRFGYGDAL 1000
QY 961 RQDCRKVCNYLGTVKEHNGSDCHCDKATGQCSCLPNVIGQNCDCRCAPNTWQLASGTGC 1020
Db 1001 RQDCRKVCNYLGTVQEHNGSDCQCDKATGQCLCLPNVIGQNCDCRCAPNTWQLASGTGC 1060
QY 1021 GPCNCNAAHSFGPSCNEFTGQCQCMGPGFGGRTCSQCQLFWGDPDVECRACDPCRGLET 1080
Db 1061 DPCNCNAAHSFGPSCNEFTGQCQCMGPGFGGRTCSQCQLFWGDPDVECRACDPCRGLET 1120
QY 1081 PQCDQSTGQCVCEGVEGPRCDKCTRGYSGVFPDCTPCHQCFALWDALIGELTNRTHKFL 1140
Db 1121 PQCDQSTGQCVCEGVEGPRCDKCTRGYSGVFPDCTPCHQCFALWDALIGELTNRTHKFL 1180
QY 1141 EKAKALKISGVIPYRETVDVSVEKKVNEIKDILAQSPAAEPLKNIGILFEEAEKLTKDVT 1200
Db 1181 EKAKALKISGVIPYRETVDVSVERKVSEIKDILAQSPAAEPLKNIGILFEEAEKLTKDVT 1240
QY 1201 EKMAQVEVKLTDTASQSNSTAGELGALQAEASLDKTVKELAEQLEFIKXNSDIQCALDSI 1260
Db 1241 EMMAQVEVKLSDTTSQSNSTAKELDSIQTEAESLDNTVTKELAEQLEFIKXNSDIRGALDSI 1300
QY 1261 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLERESPFEKQEEQARLDEL 1320
Db 1301 TKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVMMERESQFKEKQEEQARLDEL 1360

QY 1321 AGKLQSLDLSAAAQMTCTGTPPGADCSSECGGNCRCTDEGEKKCGGCGGLVTVHAWSA 1380
Db 1361 AGKLQSLDLSAAAQMTCTGTPPGADCSSECGGNCRCTDEGERKCGGCGGLVTVHAWSA 1420
QY 1381 OKAMDFDRDVLALAEVEQLSKMVSEAKVRADAEAKQADVLLKTNATKVKVDKSNEDLR 1440
Db 1421 OKAMDLDQDVLALAEVEQLSKMVSEAKVRADAEAKQADVLLKTNATKVKVDKSNEDLR 1480
QY 1441 NLIKQIRNFLTSDADLDSIEAVANEVLKSGNASTPQQLQNLNLTEDIRERVETLSQVEVIL 1500
Db 1481 NLIKQIRNFLTQDSDADLDSIEAVANEVLKSGNASTPQQLQNLNLTEDIRERVETLSQVEVIL 1540
QY 1501 QQSAADIARAELLLEAAKRAKSKSATDVKVTDVMVKEALEEAEAKQAAEAKAKQADEDIQ 1560
Db 1541 QHSAADIARAEMLLLEAAKRAKSKSATDVKVTDVMVKEALEEAEAKQAAEAKAKQADEDIQ 1600
QY 1561 GTONLLTSIESETAASEETLTNASQRIKSLERNVBEELKRAAQNNGEAEYIEKVYVSVKQ 1620
Db 1601 GTONLLTSIESETAASEETLTNASQRISELERNVBEELKRAAQNNGEAEYIEKVYVTVKQ 1660
QY 1621 NADVVKKTLDGELDEKYKVESLIAQKTEESADARRKAELLQNEAKTLLAQANSKLQLLK 1680
Db 1661 SAEDVKTLDGELDEKYKVENLIAKTEESADARRKAEMLQNEAKTLLAQANSKLQLLK 1720
QY 1681 DLERYEDNQKYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1725
Db 1721 DLERYEDNQRYLEDKAQELARLEGEVRSLLKDIQKVAVYSTCL 1765

RESULT 5

US-09-873-676-113
; Sequence 113, Application US/09873676
; Patent No. US20020077289A1
; GENERAL INFORMATION:
; APPLICANT: Macdonald, Nicholas J.
; APPLICANT: Sim, Kim L.
; TITLE OF INVENTION: Angiostatin and Endostatin Binding Proteins and Methods of Use
; FILE REFERENCE: 05213-0378 (43170-259333)
; CURRENT APPLICATION NUMBER: US/09/873,676
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 60/209,065
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/289,387
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 113
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-873-676-113

Query Match 94.1%; Score 8873; DB 9; Length 1786;

Best Local Similarity 92.9%; Pred. No. 0;
Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

QY 1 EPYCIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVVTFAPNRLKIWWQSENGVENV 60
Db 62 EPYCIVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVVTFAPNRLKIWWQSENGVENV 121
QY 61 TIQLDLEAEFHFTLIMTFKTRPAAMLIERSSDFGKTGWVRYFAYDCESSFPPISTGP 120
Db 122 TIQLDLEAEFHFTLIMTFKTRPAAMLIERSSDFGKTGWVRYFAYDCEASFPPISTGP 181
QY 121 MKKVDDIICDSRYSDIEPSTEGEVIFFRALDPAFKIEDPSPRIQNLKITNLRKFVKLH 180
Db 182 MKKVDDIICDSRYSDIEPSTEGEVIFFRALDPAFKIEDPSPRIQNLKITNLRKFVKLH 241
QY 181 TLGDNLLDSRMEIREKYYAVYDMVVRGNCFYGHASECAPVDGVNEEVEGMVHGCMCR 240
Db 242 TLGDNLLDSRMEIREKYYAVYDMVVRGNCFYGHASECAPVDGVNEEVEGMVHGCMCR 301

QY 241 HNTKGLNCELWDFYHDLPRPAEGRNSNACKKCNNEHSSSCHDFMAVFLATGNVSGV 300
Db 302 HNTKGLNCELWDFYHDLPRPAEGRNSNACKKCNNEHSSSCHDFMAVFLATGNVSGV 361
QY 301 CDNCOHNTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 360
Db 362 CDDCOHNTMGRNCEQCKPFYFQHPERDIRDPNFCERCTCDPAGSQNEGICDGYTDFSTGL 421
QY 361 IAGQCRCKLVHEGERCDVCKEGFYDLSEADPYGCKSCACNPLGTIPGNGPCDSETGYCYC 420
Db 422 IAGQCRCKLVHEGERCDVCKEGFYDLSEADPYGCKSCACNPLGTIPGNGPCDSETGYCYC 481
QY 421 KRLVTGQRCDQCLPQHWGLSLNDLDCRPPCDLGGALNNSCSEDSGQCSCLPHMIGRQCN 480
Db 482 KRLVTGQRCDQCLPQHWGLSLNDLDCRPPCDLGGALNNSCSEDSGQCSCLPHMIGRQCN 541
QY 481 EVESGYFTTLDHYIYEAEANLPGVGVVVERQYIQRIIPSWTGPFGFVRVPEGAYLEFFI 540
Db 542 EVEPGYFATLDHYLYEAEANLPGVSVIVERQYIQRIIPSWTGAFFVRVPEGAYLEFFI 601
QY 541 DNIPYSMEYZILIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTVPDDNQVSLSPGS 600
Db 602 DNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTIPDDNQVSLSPGS 661
QY 601 RYVLPFRPVCFEKGMYTYVRLELQYTAGSDVESPYTFIDSLVLMYPYCKSLDIFTVGG 660
Db 662 RYVLPFRPVCFEKGMYTYVRLELQYTAGSDVESPYTFIDSLVLMYPYCKSLDIFTVGG 721
QY 661 GDGEVNTSANETFORYRCLENSRSVVKTPMTDVCNIIFSISALIHQTLGACEDPQGS 720
Db 722 GDGVNTSANETFORYRCLENSRSVVKTPMTDVCNIIFSISALLHQTGLACEDPQGS 781
QY 721 SSVCDPNNGGQCCRPNVVGRTCNRKCAPGTGFGPNCKPCDCHLQGSASFDAITGQCH 780
Db 782 SSVCDPNNGGQCCRPNVVGRTCNRKCAPGTGFGPNCKPCDCHLQGSVNAFCNPVTGQCH 841
QY 781 CFQGIYARQDRCLPGYWGFPSCQPCQCNHGLDCTVTGECCLSCQDYTTGHNCERCLAG 840
Db 842 CFQGIYARQDRCLPGYWGFPSCQPCQCNHGLDCTVTGECCLSCQDYTTGHNCERCLAG 901
QY 841 YGDPPIIGSDHCRPCPCPDGPPSGRQFARSCYQDPVTQLQACVCDPVGIGSRCDCCASG 900
Db 902 YGDPPIIGSDHCRPCPCPDGPPSGRQFARSCYQDPVTQLQACVCDPVGIGSRCDCCASG 961
QY 901 FFGNPSDFGSCQPCQCHNIDITDPEACDKTGRCLKCLYHTEGHCQCYGYGDAL 960
Db 962 YFGNPSDFGSCQPCQCHNIDITDPEACDKTGRCLKCLYHTEGHCQCYGYGDAL 1021
QY 961 RQDCRKVCNLYGTVEHNGSDCHCDKATGQCSCLPNVIGQNCDCRCAPTWQLASGTGC 1020
Db 1022 RQDCRKVCNLYGTVEHNGSDCHCDKATGQCSCLPNVIGQNCDCRCAPTWQLASGTGC 1081
QY 1021 GPCNCAHSGFPGSCNEFTGQCCMPGFGGRTCSQELFWGDDPVECRACDDPRGIET 1080
Db 1082 DPCNCAHSGFPGSCNEFTGQCCMPGFGGRTCSQELFWGDDPVECRACDDPRGIET 1141
QY 1081 PQCDQSTGQCVCEGVEGPRCDKTRGYSGVFPDCTPCHQCFALWDALIGELTNRTHKFL 1140
Db 1142 PQCDQSTGQCVCEGVEGPRCDKTRGYSGVFPDCTPCHQCFALWDALIGELTNRTHKFL 1201
QY 1141 EKAKALKISGVIGPYRETVDSEKKNVNEIKDILAQSPAAEPLKNIGILFEEAEKLTQDVT 1200
Db 1202 EKAKALKISGVIGPYRETVDSEKKNVNEIKDILAQSPAAEPLKNIGILFEEAEKLTQDVT 1261
QY 1201 EKMAQVEVLTDTASQSNSTAGELGALQAEBSLDTVKELAEQLEFKNSDIQGALDSI 1260
Db 1262 EKMAQVEVLTDTASQSNSTAGELGALQAEBSLDTVKELAEQLEFKNSDIRGALDSI 1321
QY 1261 TKYFQMSLEAKRVNASTTDPNSTVEQSALTRDRVEDMLERESPFEQEQEQLLDEL 1320
Db 1322 TKYFQMSLEAKRVNASTTDPNSTVEQSALTRDRVEDMLERESPFEQEQEQLLDEL 1381
QY 1321 AGKLQSLDLASAAQMTCTGTPPGADCSSECGGPNCRTEDEGEKKCGGPGGLVTVVAHSAW 1380

Db 1382 AGKLQSLDLASAAQMTCTGTPPGADCSSECGGPNCRTEDEGEKKCGGPGGLVTVVAHSAW 1441
QY 1381 QKAMDFDRDVLASAEVQLSKMSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDLR 1440
Db 1442 QKAMDLQDVLASAEVQLSKMSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDLR 1501
QY 1441 NLIKQIRNFELTSDSADLDSIEAVANEVLKSGNASTPQQLQNLTDIEDIRERVETLSQVEVIL 1500
Db 1502 NLIKQIRNFELTSDSADLDSIEAVANEVLKSGNASTPQQLQNLTDIEDIRERVETLSQVEVIL 1561
QY 1501 QQSAADIARAEILLIEEAKRASKSATDVKVTDAMVKEALBEAEKAQVAAEKAQKQADEDIQ 1560
Db 1562 QHSAADIARAEILLIEEAKRASKSATDVKVTDAMVKEALBEAEKAQVAAEKAQKQADEDIQ 1621
QY 1561 GTQNLTSIESETAASEETLTNASQRIKSLERNVEELKPKAAQNSGEAEYIEKVYVSVKQ 1620
Db 1622 GTQNLTSIESETAASEETLTNASQRIKSLERNVEELKPKAAQNSGEAEYIEKVYVSVKQ 1681
QY 1621 NADDVKKTLDCGELDEKYYKKVESLIAQKTEESADARRKAEILLQNEAKTLLAQANSKILQLE 1680
Db 1682 SAEDVKKTLDCGELDEKYYKKVESLIAQKTEESADARRKAEILLQNEAKTLLAQANSKILQLE 1741
QY 1681 DLERKYEDNQYLEDKQAEVLRLGEVRSLLKDISEKVAVYSTCL 1725
Db 1742 DLERKYEDNQYLEDKQAEVLRLGEVRSLLKDISEKVAVYSTCL 1786

RESULT 6
US-09-938-275-6
; Sequence 6, Application US/09938275
; Patent No. US20020111309A1
; GENERAL INFORMATION:
; APPLICANT: Gerardo Castillo
; APPLICANT: Alan Snow
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications
; TITLE OF INVENTION: of Laminin and Laminin-Derived Protein Fragments
; FILE REFERENCE: PROTEO.P03
; CURRENT APPLICATION NUMBER: US/09/938,275
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Swissprot P07942
; DATABASE ENTRY DATE: 1988-08-01
US-09-938-275-6

Query Match 94.1%; Score 8873; DB 9; Length 1786;
Best Local Similarity 92.9%; Pred. No. 0;
Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

QY 1 EYCIIVSHLOEDKCKFCIDSRDYPHETLNPDSHLIENVVVTFAPNRLKIWQSENGVENV 60
Db 62 EYCIIVSHLOEDKCKFCIDSRDYPHETLNPDSHLIENVVVTFAPNRLKIWQSENGVENV 121
QY 61 TIQDLAEAFHFTHLIMTFTFRPAAMLIERSDFGKTGWVYRYFAYDCESFPFGISTGP 120
Db 122 TIQDLAEAFHFTHLIMTFTFRPAAMLIERSDFGKTGWVYRYFAYDCESFPFGISTGP 181
QY 121 MKKVDDIICDSRYSIDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLKTIKFKVVKLH 180
Db 182 MKKVDDIICDSRYSIDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLKTIKFKVVKLH 241
QY 181 TLGDNLLDSRMEIREKYYAVYVDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGHCMCR 240
Db 242 TLGDNLLDSRMEIREKYYAVYVDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGHCMCR 301
QY 241 HNTKGLNCELWDFYHDLPRPAEGRNSNACKKCNNEHSSSCHDFMAVFLATGNVSGV 300

Db 302 HNTKGLNCEL CMDFYHDL PWRPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGV 361
QY 301 CDNCOHNTMGRNCEQCKPFYFOHPERDIRBNLCEPCTCDPAGSENGGICDGYTDFSVGL 360
Db 362 CDDCOHNTMGRNCEQCKPFYFOHPERDIRBNLCEPCTCDPAGSQNEGICDSYTFDFSTGL 421
QY 361 IAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSKACNPLGTIPGPNPCDSETGYCYC 420
Db 422 IAGQCRCKLHVEGERCDVCKEGFYDLSSEDPFCKSKACNPLGTIPGPNPCDSETGHCYC 481
QY 421 KRLVTGQRCDQCLPQHGLNSNDLDGCRPCDCDLGGALNNSCEDSGQSCSLPHMIGROCN 480
Db 482 KRLVTGQHCDQCLPEHGLNSNDLDGCRPCDCDLGGALNNSCFAESGQSCSRPHMIGROCN 541
QY 481 EVESGYFTTLDHYIYEABEANLPGVVVVERQYIQDRIPSWTGPGRVVRPEGAYLEFFI 540
Db 542 EVEPGYFATLDHYLYEABEANLPGVSVIVERQYIQDRIPSWTGAGFVRVPEGAYLEFFI 601
QY 541 DNIPYSMEYEILIRYEPQPDHWEKAVITVQRPCKIPASSRCGNTVPDDNQVVSLSPGS 600
Db 602 DNIPYSMEYDILIRYEPQPDHWEKAVITVQRPGRIPTSRRCGNTIPDDNQVVSLSPGS 661
QY 601 RYVVLPRPVCFEKGMNVTYRLELPOYTASGSDVESPYTFIDSLVMPYCKSLDIFTVGS 660
Db 662 RYVVLPRPVCFEKGTNYTNRLELPOYTSSDSVESPYTLIDSLVMPYCKSLDIFTVGS 721
QY 661 GDGEVNTSAWETFQYRCLNRSRWKTPMTDVCNIIIFSALIHQTLGACECDPQGS 720
Db 722 GDGVNTSAWETFQYRCLNRSRWKTPMTDVCNIIIFSALLHQTGLACECDPQGS 781
QY 721 SSVCDPNGGQCQCRPNVVGRTNRCAPGTGFGPNCKPCDCHLQGSASAFCDAITGQCH 780
Db 782 SSVCDPNGGQCQCRPNVVGRTNRCAPGTGFGPSGCKPCCHLQGSVNAFNPVTGQCH 841
QY 781 CFQGIYARQCDRLPGYWGPFSCQPCQCNHGLDCTVTGECCLSCQDYTTGHNCERCLAG 840
Db 842 CFQGYVARQCDRLPGHWGPFSCQPCQCNHGLDCTVTGECCLSCQDYTMGHNCERCLAG 901
QY 841 YGDPFIIGSDHCRPCPCPDGSDGRQFARSQYQDPVTQLACVCDPDPYIGSRCDDCASG 900
Db 902 YGDPFIIGSDHCRPCPCPDGSDGRQFARSQYQDPVTQLACVCDPDPYIGSRCDDCASG 961
QY 901 FFGNPSDFGSCQPCQCHNIDTTPDPEACDKOTGRCLKCLYHTEGDHQCQCOGYGYGDAL 960
Db 962 YFGNPSDFGSCQPCQCHNIDTTPDPEACDKOTGRCLKCLYHTEGDHQCQCFRFGYGDAL 1021
QY 961 RQDCRKCVCNYLGTVKEHNGSDCHCDKATGQCSCLFNQVGNQCDRCAPNTWOLASGTGC 1020
Db 1022 RQDCRKCVCNYLGTVQEHNGSDCHCDKATGQCLCLFNQVGNQCDRCAPNTWOLASGTGC 1081
QY 1021 GPCNCAHSGFPCSCNEFTGQCCMPGFGGRTCEQBELFWGDEPDECRACDCDPRGIET 1080
Db 1082 DPCNCAHSGFPCSCNEFTGQCCMPGFGGRTCEQBELFWGDEPDECRACDCDPRGIET 1141
QY 1081 PQCDQSTGQCVCEGVEGPRCDKCTRGYSGVFPDCTPCHQCFALWDAIIIGELTNRTHKFL 1140
Db 1142 PQCDQSTGQCVCEGVEGPRCDKCTRGYSGVFPDCTPCHQCFALWDAIIAELTNRTHREL 1201
QY 1141 EKAKALKISGVIGPYRETVDVSVEKKVNEIKDILAQSPAABPLKNIGILFEEAEKLTKDVT 1200
Db 1202 EKAKALKISGVIGPYRETVDVSVERKVSEIKDILAQSPAABPLKNIGNLFEEAEKLTKDVT 1261
QY 1201 EKMAQVEVKLTDTASQSNSTAGELGALQAEBSLDTKTVKELABQLEFIKNSDIOGALDSI 1260
Db 1262 EMMAQVEVKLSDTTSQSNSTAKELDSLQTEAESLNTVXKELABQLEFIKNSDIRGALDSI 1321
QY 1261 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLERESPFEKQEEQARLLDEL 1320
Db 1322 TKYFQMSLEAEKRVNASTTDPNSTVEQSALMRDRVEDVMNERESQFKEKQEEQARLLDEL 1381
QY 1321 AGKLOSLDLASAAQMTCTGTPPGADCSSECGGNCRTEGKCKGPGCGGLVTVHAWSAW 1380
Db 1382 AGKLOSLDLASAAEMTCGTPPGASCSETECGGNCRTEGKCKGPGCGGLVTVAHNAW 1441

QY 1381 QKAMDFDRDVLSSALAEVEQLSKMVSEAKVRADEAKQNAQDVLTKTNATKEKVKDKSNEDLR 1440
Db 1442 QKAMDLQDVLSSALAEVEQLSKMVSEAKVRADEAKQSAEDILLKTNATKEKMDKSNEELR 1501
QY 1441 NLIKQIRNFLTQSDSADLDSIEAVANEVLKSGNASTPQQLQNLNLTEDIRERVETLSQVEVIL 1500
Db 1502 NLIKQIRNFLTQSDSADLDSIEAVANEVLKMEPSTPQQLQNLNLTEDIRERVESLSQVEVIL 1561
QY 1501 QQSAADIARAELLEEAKRASKSATDVKVTADVMKEALEEAEAKAQVAAEKAQKQADEDIQ 1560
Db 1562 QHSAADIARAELLEEAKRASKSATDVKVTADVMKEALEEAEAKAQVAAEKAQKQADEDIQ 1621
QY 1561 GTQNLITSIESETAASEETITNASQRIKSLERNVEELKRKAQNSGEAEYIEKVYVSVKQ 1620
Db 1622 GTQNLITSIESETAASEETLFNASQRISELERNVEELKRKAQNSGEAEYIEKVYVTVKQ 1681
QY 1621 NADDVKKTLDGELDEKVKVESLIAQKTEESADARRKAEELLQNEAKTLLAQANSKIQLLLE 1680
Db 1682 SAEDVKKTLDGELDEKVKVENLIAKTEESADARRKAEMLQNEAKTLLAQANSKIQLLK 1741
QY 1681 DLERKYEDNQYLEDKAQELVRLEGEVRSLLKDISQKVAVYSTCL 1725
Db 1742 DLERKYEDNQYLEDKAQELARLEGEVRSLLKDISQKVAVYSTCL 1786

RESULT 7
US-10-037-182-6
; Sequence 6, Application US/10037182
; Publication No. US20030044899A1
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Doi, Masayuki
; APPLICANT: Thybøll, Jill
; TITLE OF INVENTION: Recombinant Laminin 10
; FILE REFERENCE: 99-274-F
; CURRENT APPLICATION NUMBER: US/10/037,182
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,449
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/279,282
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-037-182-6

Query Match 94.1%; Score 8873; DB 14; Length 1786;
Best Local Similarity 92.9%; Pred. No. 0;
Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

QY 1 EPYCIVSHLQEDKKCFICDSRDPYHETLNPDASHLIENVVTFAPNRLKIWWQSENGVENV 60
Db 62 EPYCIVSHLQEDKKCFICNSQDPYHETLNPDASHLIENVVTFAPNRLKIWWQSENGVENV 121
QY 61 TIQLDLEAFHFTHLIMTFKTRPAAMLIERSSDFGKTGWYRYFAYDCESSFPGISTGP 120
Db 122 TIQLDLEAFHFTHLIMTFKTRPAAMLIERSSDFGKTGWYRYFAYDCEASFPGISTGP 181
QY 121 MKKVDDIICDSRYSIDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLLKITNLRIKFVKLH 180
Db 182 MKKVDDIICDSRYSIDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLLKITNLRIKFVKLH 241
QY 181 TLGDNLLDSRMEIREKYYAVYAVDMVVRGNCFCYGHASECAPVDGWNEEVEGMVHGHCMCR 240
Db 242 TLGDNLLDSRMEIREKYYAVYAVDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGHCMCR 301
QY 241 HNTKGLNCEL CMDFYHDL PWRPAEGRNSNACKKNCNEHSCHFDMAVFLATGNVSGV 300
Db 302 HNTKGLNCEL CMDFYHDL PWRPAEGRNSNACKKNCNEHSCHFDMAVFLATGNVSGV 361

QY	301	CDNCQHNTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL	360
Db	362	CDDCQHNTMGRNCEQCKPFYFQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFDFSTGL	421
QY	361	IAGQCRCKLHVEGERCDVCKEGFDYDLSAEDPYGCKSCACNPLGTIPGPNPCDSETGYCYC	420
Db	422	IAGQCRCKLNVEGECHDCVKEGFDYDLSSEDPFGCKSCACNPLGTIPGPNPCDSETGHCYC	481
QY	421	KRLVTGQRCDQCLPQHGLSNDLDGCRPCDCDLGGALNNSCSEDSGQCSCLPHMIGRQCN	480
Db	482	KRLVTGQHCDQCLPEHWGLSNDLDGCRPCDCDLGGALNNSCPAESGQCSRPHMIGRQCN	541
QY	481	EVESGYYFTTLDHYIYEAEEANLPGVWVVERQYIQDRIPSWTGPGRVVRPEGAYLEPFI	540
Db	542	EVEPGYYFATLDHYLYEAEEANLPGVSIIVERQYIQDRIPSWTGPGRVVRPEGAYLEPFI	601
QY	541	DNIPYSMEYEILIRYEPQLPDHWEKAVITVQRPKIPASSRCNGTVPDDDNQVVSLSPGS	600
Db	602	DNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPSSRCNGTIPDDDNQVVSLSPGS	661
QY	601	RYVVLPRPVCFEKGMNYYVRLLELPQYTASGSDVESPYTFIDSLVLMYPYCKSLDIFTVGGS	660
Db	662	RYVVLPRPVCFEKGTNTYVRLLELPQYTSSDSDVESPYTLIDSLVLMYPYCKSLDIFTVGGS	721
QY	661	GDGEVNTSAWETFQYRCLENSRSVWKTPTMTDVCRNIIIFSALIHQTLGACEDCPQSSL	720
Db	722	GDGWVNTSAWETFQYRCLENSRSVWKTPTMTDVCRNIIIPSISALLHQTGLACEDCPQSSL	781
QY	721	SSVCDPNGGCQCQCRPNVVGRTCNRCAPGTFGFGPNCKPCDCHLQGSASAFCDAITGQCH	780
Db	782	SSVCDPNGGCQCQCRPNVVGRTCNRCAPGTFGFGPSGCKPCECHLQGSVNAFCNPVTGQCH	841
QY	781	CFQGIYARQCDCRLPGYWGFPSPCQPCQCNHGHALDCDTVTGECLSCQDYTTGHNCCERCLAG	840
Db	842	CFQGVYARQCDCRLPGHWGFPSPCQPCQCNHGADDCTPVTGECLNCQDYTMGHNCCERCLAG	901
QY	841	YYGDPPIIGSGDHCRPCPCPDGPDSDGRQFARSCYQDPVTTLQACVCDPGYIGSRCDDCASG	900
Db	902	YYGDPPIIGSGDHCRPCPCPDGPDSDGRQFARSCYQDPVTTLQACVCDPGYIGSRCDDCASG	961
QY	901	FFGNPSDFGGSCQPCQCHNIDTTDPEACDKJTRCLKCLYHTEGDHCOLCQYGYYGDAL	960
Db	962	YFGNPSSEVGGSCQPCQCHNIDTTDPEACDKJTRCLKCLYHTEGHCQCFRFGYYGDAL	1021
QY	961	RQDCRKVCVNYLGTVKEHONGSDCHCDKATGQCSCLPNVIGQNCDCRCAPNTWOLASGTGC	1020
Db	1022	RQDCRKVCVNYLGTVOEHONGSDCQCCKATGQCLCLPNVIGQNCDCRCAPNTWOLASGTGC	1081
QY	1021	GPCNCNAAHSFGPSCNEFTGQCQCMPPFGGRTCEQBELFWGDDPDVECRACDCDPRGIET	1080
Db	1082	DPNCNAAHSFGPSCNEFTGQCQCMPPFGGRTCEQBELFWGDDPDVECRACDCDPRGIET	1141
QY	1081	PQCDQSTGQCVCEGVGPRCDKCTRGYSGVFPDCTPCHQCFCALWDIAIIGELTNRTHKFL	1140
Db	1142	PQCDQSTGQCVCEGVGPRCDKCTRGYSGVFPDCTPCHQCFCALWDVIIAELTNRTHRFL	1201
QY	1141	EKAKALKISGVIOPYRETVDVSVEKKVNEIKDILAQSPAAEPLKKNIGILFEEAEKLTKDVT	1200
Db	1202	EKAKALKISGVIOPYRETVDVSVERKVSEIKDILAQSPAAEPLKKNIGNLFEEAEKLTKDVT	1261
QY	1201	EKVAQVEVKLTDITASQSNSTAGELGALQAEAESLDKTVKELAEQLEFIKNSDIQSALDSI	1260
Db	1262	EMMAQVEVKLSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDINGALDSI	1321
QY	1261	TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLERESPFKQEQQEQARLLDEL	1320
Db	1322	TKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVMMERESQFKEKQEQQARLLDEL	1381
QY	1321	AGKLQSLDLSAAAQMTGTPPGADCSSECGGPNCRCTDEGEKKCGGPGCGGLVTVAHSAW	1380
Db	1382	AGKLOSLDLSAAAEWMTGTPPGASCSETECGGPNCRCTDEGERKCGGPGCGGLVTVAHNAW	1441

[illegible]

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RESULT 8
US-10-443-349-4
: Sequence 4, Application US/10443349
: Publication No. US20040023856A1
: GENERAL INFORMATION:
: APPLICANT: Burgeson, Robert E.
: APPLICANT: Wagan, David W.
: TITLE OF INVENTION: BLK CHAIN OF LAMININ AND METHODS OF USE
: FILE REFERENCE: 10287/021003
: CURRENT APPLICATION NUMBER: US/10/443,349
: CURRENT FILING DATE: 2003-05-22
: PRIOR APPLICATION NUMBER: US/09/161,872
: PRIOR FILING DATE: 1998-09-28
: PRIOR APPLICATION NUMBER: US 08/735,893
: PRIOR FILING DATE: 1996-10-23
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 4
: LENGTH: 1196
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: NAME/KEY: DOMAIN
: LOCATION: (1)...(250)
: OTHER INFORMATION: Human B1 chain
: FEATURE:
: NAME/KEY: DOMAIN
: LOCATION: (251)...(437)
: OTHER INFORMATION: Human B1 chain
: FEATURE:
: NAME/KEY: DOMAIN
: LOCATION: (438)...(807)
: OTHER INFORMATION: Human B1 chain
: FEATURE:
: NAME/KEY: DOMAIN
: LOCATION: (808)...(840)
: OTHER INFORMATION: Human B1 chain
: FEATURE:
: NAME/KEY: DOMAIN
: LOCATION: (841)...(1196)
: OTHER INFORMATION: Human B1 chain
: US-10-443-349-4

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Query Match 58.1%; Score 5482; DB 16; Length 1196;
Best Local Similarity 62.4%; Pred. No. 1.4e-300;
Matches 1076; Conservative 46; Mismatches 33; Indels 570; Gaps 1;

OV 1 EPYCIVSHLOEDKKCFICDSRDPYHETLNPDSHLIENVVTTFAPNRLKIHWQSENGVENV 60

QY 61 TIQLDLEAEFHTLIMTKTRPAAMLIERSSDFGKTGWVYRYFAYDCESPPGISTGP 120
Db 137 TIQLDLEAEFHTLIMTKTRPAAMLVERSADFGRTWRVYRFSYDCGADFPGLAP 196
QY 121 MKKVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLLKITNLRKFVXLH 180
Db 197 PRWDVWCESRYSEIEPSTEGEVYRVLDPAIPIPDYPSSRIQNLLKITNLRVNLTRLH 256
QY 181 TLGDNLLDSRMEIREKYVYAVYDMVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMCR 240
Db 257 TLGDNLLDPRREIREKYVYALVELVIRGNCFCYGHASQCAPAPGAPAHAEGMVHGACICK 316
QY 241 HNTKGLNCELMDYHDLPRPAEGRNSNACKKNCNEHSSSCHFDMAVFLATGNVSGV 300
Db 317 HNTKGLNCEQCQDFYQDLPWHPAEDGHTHACRCKECNGHSHSCHFDMAVFLASGNVSGV 376
QY 301 CDNCOHNTMGRNCEQCKPFYFQHPERDIRDNLCEPCTCDPAGSENGGICDGYTDFSVGL 360
Db 377 CDGCOHNTAGHCELCPFFYVRDPTKDMRDPAAACRPDCDPMGSDGGRCDSDHDDFVLGL 436
QY 361 IAGQCRCKLHVEGERCDVCKEGFYDLSDAEDPYGCKSCACNPLGTIPGGNCPDSETGYCYC 420
Db 437 VSGQCRCKEHVVGTRCQCRDGFGLSASNPRGQCRCQCNRGTVPGGTPCDSSSGTCFC 496
QY 421 KRLVTGRCDCQCLPOHWGLSNDLDCRCPDCDLGGALNNSCEDSGQSCSLPHMIGRCQN 480
Db 497 KRLVTGDCDRCLPGHWGLSHDLLGCRPCDCDVGALDPCQDEATGQCPCRPHMIGRCE 556
QY 481 EVESGYFTILDHYIYEAEEANLPGVWVVERQYIQDIRIPSWTGGFVRVPEGAYLEFFI 540
Db 557 QVQPGYFRPFLDHLTWEAGAH-QQVLEVVRLVNTNRETFSWTGFGVRLREGQVEFLV 615
QY 541 DNIPYSMEVEILIRYEPOLPDHWEKAVITVORPGKIPASSRCGNTPVDDDNQVVSLSPGS 600
Db 616 TSLPRAMDYDILLRWEPQVPEQWAELELVQRPVSAHSPFGHVLPRDDRIQGMHPNT 675
QY 601 RYVVLPRPVCFEKGMYTVRLELPQYTASGSDVESPYT----FIDSLVMPYCKSLDIFT 656
Db 676 RVLVFRPVVCLPEPGLSYKLKLTG-TGGRAPHPETPYSGSGILIDSLVLQPHVLMLEMF- 733
QY 657 VGGSGDGEVNTSAWETFQYRCLENSRSVVKTPMTDVCNIIIFSALIHQTLGACECDP 716
Db 734 ---SGGDAALERRTTFRYRCHEEGLMPSKTLPLSEACVPLLISASSLVYNGALPCQCDP 790
QY 717 QGSLSSVCDPNQGCQCRPNVGRTCNRCAPGTGFGPNGKPCDCDCHLQGSASAFCDAIT 776
Db 791 QGSLSECNPHGQCRCKPGVWVRRCDACATGYGFGPAGCQACQCSPDGALSALCEGTS 850
QY 777 GQCHCFQGIYARQDRCLPGYWGFPSCPCQCNHGDCTVTGECLSQDYTTGHNCE 836
Db 851 GQCLCRTGAFGLRCDHCQRGQWGFNCRPCVNCGRADCAHTGACLGCRDYGHECER 910
QY 837 CLAGYGDPIIGSGDHCRPCPCPDGPDSCGFARSCYQDPVTLQACVCDPVGYSRCD 896
Db 911 CIAGFHGDPRLPYGQCRPCPCPEGPGSORHFPATSCHRDGYSQQIVCHCRAGYTGLRCE 970
QY 897 CASGFFGNPSDFGSGCQPCQCHNIDTIDPEACDKDTGRCLKCLYHTEGDHCOLCQGY 956
Db 971 CAPGHGDPSPKPGRCQLCECSGNIDPTDPCADPHTGQCLRLHTEGPHCGHCKPGFH 1030
QY 957 GDALRQDCRCKVCNVLGTVKEHNCNGSD-CHCDKATGQCSCLPNVIGONCDRCAPNTWOLA 1015
Db 1031 GQARQSCHRCTCNLLGTDPPQRCPSDLCDCDPTGQCPCLPHVQGLSCDRCAPNFWNT 1090
QY 1016 SGTGCGPCNCAHSGFPCSNFTGQCCQCMGPGGRTCECQELFWGDPDVECRACDCDP 1075
Db 1091 SGRGQCPACHPSPARGPTCNEFTGQCHCHAGFGGRTCECQELHWGDPGLQCRACDCDP 1150
QY 1076 RGIETPQCDQSTGQCVVEGVEGPRCDKCTRGYSGVFPDCTPCHQCQFALWDIAIIGELTNR 1135
Db 1151 RGIDKPCQCHRSTGHCSCTPGVSGVRCQDCQARGSGVFPACHPCHACFGDWRVQDLAAR 1210

QY 1136 THKFLKAKALKISGVIGPYRETVDVSEKKNVEIKDILA--QSPAAEPLKNIGILFEEAE 1193
Db 1211 TERLEQWAELOQTGVLGAFESSFLNLQGLGMVQAIVAARNTSAASTAK----LVEATE 1266
QY 1194 KLTQDV--TEKMAQVEVKLTDTASQSNSTAGELGALQAEASLDKTVKELAEQLEFIKN 1250
Db 1267 GLRHEIGKTTERTLTQLEABLTVDQDENFNANHALSGLERDGLALNLTLRQLDQHLILKH 1326
QY 1251 SDIQGALDSITKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMERESPFEQQ 1310
Db 1327 SNFLGAYDSIRHAHSQSTAEARRANASTFAIPSPVNSADTRRRRAEVLMAQRENFNRQH 1386
QY 1311 EQARLLDELAKGLQSLDLSAAAQMTCTGPPGADCESECGGNCRDTDEGEKKCGGPGCG 1370
Db 1387 LANQOALGRLSTHTTSLTGVNELVCGAPGAPDAPCATSPCGGAGCRDEDDGQPRCGGLCS 1446
QY 1371 GLVTVAHSAWQKAMDFDRDVLALAEVEQLSKMVSEAKVRADAEAKQNAQDVLTKTNATKE 1430
Db 1447 GAAATADLALGRARHTQAEQALVEGGGILSRVSETRRQAEAAQQAALDKANASRG 1506
QY 1431 KVDKSNEDLRNLIKQIRNFLTEDSADLDSIEAVANEVLKSGNASTPQQLQNLNLTEDIRERV 1490
Db 1507 QVEQANQELRELINQVDFLSQEGADPDSIEMVATRVLDISIPASPEIQIRLASEIAERV 1566
QY 1491 ETLQVEVILQQSAADIAARAEILLLEAKRASKSATDVKVTADMVKEALEEAEAKQVAAEK 1550
Db 1567 RSLADVDTILAHMTMGDVRRAEQQLQDAQRARSRAEGRQKAETVQAALEEAQRAQAAQG 1626
QY 1551 AIKQADEDIQGTQNLNLTISSETAAASEETLTNASQRIKSLERNVEELKRKAQNGSEAEY 1610
Db 1627 AIRGAVVDTKNTQTLQVQVERMAGTEQSLNSASERARQHLALLEALKKRAGNSLAAS 1686
QY 1611 IEKVYVSVQNADDVKKTLGDELDEKVKKVESLIAQKTEESADARRKAELLQNEAKTLILA 1670
Db 1687 AEETAGSAQSRAREAEKQLREQVGDQYQTVRALAERKAEGVLAQAQAEQRLDEARGLLQ 1746
QY 1671 QANSKLQLELDERKYEDNQVLEDKAQELVRLEGEVRSLLKIDISEKVAVYSTC 1724
Db 1747 AAQDKLQRLQLEGTYYEENERERELEVKAQQLDGLAARMRSVLQAINLQVQIYNTC 1800

RESULT 10
US-09-845-583-6
; Sequence 6, Application US/09845583
; Patent No. US20020142954A1
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Brunken, William Joseph
; APPLICANT: Champiaud, Marie-France
; APPLICANT: Hunter, Dale
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
; FILE REFERENCE: 10287-056001
; CURRENT APPLICATION NUMBER: US/09/845,583
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/200,863
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1799
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-845-583-6

Query Match 52.1%; Score 4914; DB 9; Length 1799;
Best Local Similarity 51.0%; Pred. No. 2.5e-268;
Matches 883; Conservative 297; Mismatches 534; Indels 18; Gaps 8;
QY 1 EPYCIIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVVTTFAPNRLKIWQSENGVENV 60
Db 77 QPYCIIVSHLQDEKKCFICDSRRPFSARDNPNSHRIQNVVTSFAPQRTAWQSENGVPMV 136
QY 61 TIQLDLEAEFHTLIMTKTRPAAMLIERSSDFGKTGWVRYFAYDCESFPGISTGP 120

Db 137 TIQLDLEAEFHTLIMTKTFRPAAMLVERSADFGRTWHVRYESYDCGADFPGIPLAP 196
QY 121 MKKVDDIICDSRYSDIEPSTEGEVIIFRALDPAFKIEDPYSPIRQNLKITNLRKFVKLH 180
Db 197 PRRWDDVVCESRYSEIEPSTEGEVIYRVLDPAIPDPYSSRIQNLKITNLRVNLRLH 256
QY 181 TLGDNLLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMCR 240
Db 257 TLGDNLLDPRREIREKYYALYELVIRGNCFCYGHASQCAPAPAPAHAEGMVHGACICK 316
QY 241 HNTKGLNCELMDPFYHDLWPRAEGRNSACKKNCNEHSSSCHDFMAYFLATGNVSGV 300
Db 317 HNTRGLNCEQCQDFYQDLPWHPAEDGHTHACKKCECNHGHTHSCHDFMAYVLASGNVSGV 376
QY 301 CDNCQHTMTGRNCEQCKPFYFQHPERDIRDNLCEPCTCDPAGSENGGICDGYTDFSVGL 360
Db 377 CDGQCHNTAGRHCFRCRPFYRDPTKDMRPAVCRPCDCDPMGSDGGRCDSDHDDPVLGL 436
QY 361 IAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGPNPCDSETGYCYC 420
Db 437 VSGQCRCKEHVVGTRCQCRDGFGLSASDRPGRCQRCQNSRGTVPGSSPCDSSSGTCFC 496
QY 421 KRLVTGQRCDQCLPQHGLSLNDLGRPCDCLGALNNSCEDSGQCSCLPHMIGROCN 480
Db 497 KRLVTGHGCDRCLPGHWGLSHDLLGCRPCDGVGALDPQCDEATGQCPCRQHMGIRRC 556
QY 481 EVESGYFTTLDHYIYEAEANLPGVVVVERQYIQDRIPSWTGPGRVPEGAYLEFFI 540
Db 557 QVQPGYFRPFLDHLTWAEAAQ-GQVLEVVERLVNRETPTSPWTGPFVRLREGQEVFLV 615
QY 541 DNIPYSMEYEILIRYEPOLPDHWEKAVITVORPGKIPASSRCGNTPVDDNQVVSLSPGS 600
Db 616 TSLPRAMDYDLLRWEPQVPEQWAELELMVQRPVSAHSPCGHVLPKDDRIQGMHPNT 675
QY 601 RYVVLPRPVCFEKGMNVTVRLELPQYTAGSDVESPYT--FIDSLVMPYCKSLDIFTVG 658
Db 676 RVLVFRPVCLEPGISYKLLKLG-TGGRAQPEYSYGLLIDSLVLPVHVLVLEMF--- 731
QY 659 GSGDGEVNTSAWETFQYRCLENSRSVVKTPMTDVCNRIIFSISALIHQTGLACECDPQ 718
Db 732 -SGGDAALERRTTTFERYCHEEGLMPSKAPLSETCAPLLISVSALIYNGALPCQCDPQ 790
QY 719 SLSSVCDPNGGQCCQCRNVVGRTCNRCAPGTFGPGNGCKPCDCDCHLQGSASAFCDAITG 778
Db 791 SLSSCSPHGGQCRCKPGVVGRRCDVCATGYGFGPAGCQACQCSPDGALSALCEGTSG 850
QY 779 CHCFQGIYARQCDRLPGYWGFPSPCQPCQNGHALDCDVTGECILSCQDYTTGHNCECL 838
Db 851 CPCRPAFGLRCDHCQRCQGWGFPCNCRPCVNCNGRADECDDHTGACLGCRDYGEGHCERC 910
QY 839 AGYVGDPPIIGSDHCRPCPCPDGSDGRQFARSYQDPVTLQACVCDPGYIGSRCDCA 898
Db 911 AGPHGDPRLPYGGQCRPCPCPEGPGSGRHFATSHRDSYQQIVCHCRAGYTLGRCEACA 970
QY 899 SGFFGNPSDFGSGCQPCQCHHNIDTTDPEACDKTGRCLKCLYHTEGHCQLCOYGYGD 958
Db 971 PGPPGDPSPKPGGRCLCECSGNIDPMDPDACDHTGQCLRLCLHNTGEGHCGYCKPFGHQ 1030
QY 959 ALRQDCRKCVCNYLGTVKEHNGSD-CHCDKATGQCSCLPNVIGQNCRCAPNTWQLASG 1017
Db 1031 AARQSCHRCTCNLLGTDPRRCFSTDLCCHCDPSTIGQCPCLPHVQGLNCDHCAPNFWNFTSG 1090
QY 1018 TGGPCNCNAHSGFSPCNEFTGQCQCMPPGFGRTCSCEQLFWGDDPVECRACDPRG 1077
Db 1091 RGCQPCACHPSRRAGPTCNEFTGQCHAGFGGRTCSCEQLYWGDPGLQCRACDPRG 1150
QY 1078 IETPQCDQSTGQVCVEGVEGPRCDKCTRGYSGVFPDCTPCHQCFCALWDALIGELTNRTH 1137
Db 1151 IDKPOCHRSTGHCSRCRPGSVGRCDQCARGFSGVFPACHPCFACFGDWRVVDLAARTR 1210
QY 1138 KFLEKAKALKISGVIGPYRETVDVSVEKKVNEIKDILA--QSPAAEPLKNIGILFEEAEKL 1195

Db 1211 RLEQWAQELQQTGVLGAFESSFLNQKLGVMVQAIMSARNASASTAK---LVEATEGL 1266
QY 1196 TKDV---TERMAQVEVKLTDTASQSNSTAGELGALQAEAESLDKTVKELAEQLEFIKNSD 1252
Db 1267 RHEIGKTTTERLTQLEAELTAVQDENFNANHALSGLERDGFALNLTILRQLDQHLKHSN 1326
QY 1253 IQGALDSITKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLERESPFKEQEE 1312
Db 1327 FLGAYDSIRHAHSQSTEAEERRANASTFAVPSVNSADTRRRTEVLGMAQKENFNQHLA 1386
QY 1313 QARLLDELAKGLQSLDLSAAQMTCTGTPGADCSESECGPNCRTEDEGKCGGPGCGGL 1372
Db 1387 NQALGRLSAHAHTLSLTGINELVCGAPGAPCATSPCGGAGCRDEDEGPRCGGLGCSGA 1446
QY 1373 VTVAHSAWQKAMDFDRDVLALAEVEQLSKMVSEAKVRADEAKQNAQDVLLKTNATKEV 1432
Db 1447 AAPADLALGRARHSAELQALVEGGGILSRVSETRRQAEAAQQAALDKANASRGQV 1506
QY 1433 DKSNEDLRNLIKQIRNFELTSDADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVET 1492
Db 1507 EQANQELRELIONVKDFLSQEGADPDSIEMVATRVLDISIPASPEIQIRLASEIAERVRS 1566
QY 1493 LSQVEVILQQAADIAFAEALLLEAKRAKSKSATDVKVVTADMVKEALEEAEKAAQVAEKAI 1552
Db 1567 LADVDTILAHMTMGVRRAEQLQDAHRARSRAEGERQKAETVQAALAEQRAQGAAGAI 1626
QY 1553 KQADEDIQGTQNLTSIESETAASEETLTNASQISKLERNVEELKRKAQNSGEAEYIE 1612
Db 1627 RGAVVDTQNTQEQTLQVQERMAGAEKSLNSAGERARQLDALLEALKRAGNSLAATAE 1686
QY 1613 KVYYSVKQNAADDVKKTLDELDEKYYKKVESLIAQKTEESADARRKAEALLQNEAKTLLAQ 1672
Db 1687 ETAGSAQSRAREAEKQLEQVGDQYQTVRALAEKAEGLVAAQAEQLRDEARDLLQAA 1746
QY 1673 NSKLQLEDLERKYNQKYLEDKAQELVRLGEVRSLLKDISEKAVAVYSTC 1724
Db 1747 QDKLQRLQLEGTGYEENERALEGKAAQLDGLAEARMRSVLQAINLQVQIYNTC 1798

RESULT 11

US-09-938-275-9
; Sequence 9, Application US/09938275
; Patent No. US20020111309A1
; GENERAL INFORMATION:
; APPLICANT: Gerardo Castillo
; APPLICANT: Alan Snow
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications
; TITLE OF INVENTION: of Laminin and Laminin-Derived Protein Fragments
; FILE REFERENCE: PROTEO.P03
; CURRENT APPLICATION NUMBER: US/09/938,275
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1798
; TYPE: PRT
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Swissprot P55268
; DATABASE ENTRY DATE: 1996-10-01
US-09-938-275-9

Query Match 51.9%; Score 4890; DB 9; Length 1798;
Best Local Similarity 50.3%; Pred. No. 5.7e-267;
Matches 871; Conservative 305; Mismatches 542; Indels 12; Gaps 6;
QY 1 EPYCIVSHLQEDKKCFICSDRDPYHETLNPDSHLIENVVTFAPNRLKIWWQSENGVENV 60
Db 74 QPYCIVSHLQEDKKCFCLDSRRPFSARDNPHSHRIQNVVTSFAPQRRAAWQSENGIPAV 133
QY 61 TIQLDLEAEFHTLIMTKTFRPAAMLIERSSDFGKTGWGVRYFAYDCSSFPGISGTP 120
Db 134 TIQLDLEAEFHTLIMTKTFRPAAMLVERSADFGRTWHVRYFSYDCGADFPGVPLAP 193

Db 194 PRHWDVVCESRYSEIEPSTEGEVIYRVLDPAIPDPYSSRIQNLLKITNLRVNLTRLH 253
QY 181 TLGDNLLDSRMEIREKYYAYVDMVRGNCFCYGHASECAPVDGVNVEEVMVGHGCMCR 240
Db 254 TLGDNLLDPRREIREKYYALYELVVRGNCFCYGHASECAPAPGAPAHAGMVGACICK 313
QY 241 HNTKGLNCELCMDFYHDLPRWPAEGRNSNACKKNCNEHSSSCHFDMVFLATGNVSGGV 300
Db 314 HNTRGLNCEQCQDFYRDLPRWPAEDGHSHACRCKDRHGHTHSCFDMVYLGSGNVSGGV 373
QY 301 CDNCQHTMGRNCEQCKPFYFQHPERDIRDNLCEPCTCDPAGSENGGICDGYTDFSVGL 360
Db 374 CDGCQHNTAWRHCELCRPFYRDPTKDLRDPAYCRSCDCDPMGSDQDGGRCDSHDDPALGL 433
QY 361 IAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGNGPCDSETGYCYC 420
Db 434 VSGQCRCKEHVVGTRCQCQCRDGFGLSISDPSPGCRRCQCNARGTVPGSTPCDPNSGSCYC 493
QY 421 KRLVTGQRCDQCLPQHWSGLSNDLDGCRPCDCDLGGALNNSCEDSGQCSCLPHMIGRQCN 480
Db 494 KRLVTGRGCDRCLPGHWSGLSNDLDGCRPCDCDVGGALDPQCEGTGQCRCRQHVMVGRRC 553
QY 481 EVESGYFTTLDHYIYEABEANLPGVVVVERQYIQDRIPSWTGPGFVRVPEGAYLEFFI 540
Db 554 QVQPGYFRPFLDHLIWEAENR-GQVLDVVERLVTPGETPSTWTSWGSFVRLQEGQTLFLV 612
QY 541 DNIPTSMEMEILIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTPVDDNQVVSLSPGS 600
Db 613 ASVPNAMDYDLLRLPEQVPEQWAELELIVQRPVPFAHSLCGHLVPRDRRIQGTLPQPHA 672
QY 601 RYVVLPRPVCFEKGMNVTVRLPQYTAGSDVESPT- ---FIDSLVLMPYCKSLDIFT 656
Db 673 RYLIFPNPVCLEPGISYKHLKLV-R-TGSAQAPETPYSGPGLLIDSLVLLPRVLVLEMF- 730
QY 657 VGSBGDEVNTSAWETFQRYRCLNSRSRVVTKPMTDVCRNIIIFSIALIHOTGLACECDP 716
Db 731 ---SGDAAALERQATFERYQCHEEGLVPSKTSPEACAPLLISLSTLIYNGALPCQCNP 787
QY 717 QGSLSSVCDPNGGQCQCRPNVVGRTCNRCAPGTGFGPNGCKPCDCCHLQGSASAFCDAIT 776
Db 788 QGSLSSSECNPHGGQCLCKPGVVGRRCDTCAPGYYGFGTGCQACQCSPRGALSCLERTS 847
QY 777 GQCHCFQGIYARQCDRCLPGYMGFPSPCQPCQCNHGLDCTVTGECLSQDVTGHNCR 836
Db 848 GQCLCRTGAFGLRCDACQRGWGFPSCRPCVCNCGHAEBCNTHTGACLGCRDLTGGEHCR 907
QY 837 CLAGYGDPIIGSDHCRPCPCPDGSDSGRQFARSCYQDPVTLQACVCDPFGYISRCDD 896
Db 908 CIAGFHGDPRLPYGAQCRPCPCPEGPGSORHFATSCHQDEYSQIIVCHCRAGYTLRCEA 967
QY 897 CASGFGNPSDFGSGCQPCQCHNIDTTDPEACDKDTGRCLKCLYHTEGDHCOLCQYGY 956
Db 968 CAPGQFGDPSRPGRCQLCECSGNIDPMDPDACDPHFGQCLRCLHHTGPHCAHSPGFH 1027
QY 957 GDALRQDCRKCVCNYLGTVKEHNGSD-CHCDKATGQCSCLPNVIGQNCDCRCAPNTWOLA 1015
Db 1028 GQAARQSCHRCTCNLLGTNPQQCPSPDQCHCDPSSGGQCPCLPNVQALAVDRCAPFWNLT 1087
QY 1016 SGTGCGPCNCNAHSGFSPSCNEFTGQCQCMFGFGRTCSECQELFWGDPDVECRACDCDP 1075
Db 1088 SGHGQPCACLPSPEEGPTCNFTGQCHCLCGFGGRTCSECQELHWGDPGLQCHACDCDS 1147
QY 1076 RGIEPTQDQSTGQCVCVEGPRCDKCTRGYSGVFPDCTPCHQCFCALWDALIGELTNR 1135
Db 1148 RGIDTPQCHRFTGHTCTCRPGVSGVRCDQCARGFSGIFPACHPCFACFCGWDWRVQDLAAR 1207
QY 1136 THKFLKAKALKISGVIQPYRETVDSEVKKVNEIKDIL-AQSPAAEPLKNIGILFEEAEK 1194
Db 1208 TORLEQRAQELQQTGVLGAFESSPFWMQEKLGIVQGIVGARNTSAASTAQLVEATEELRR 1267
QY 1195 LTKDVTBEKMAQVEVKLTDITASQSNSTAGELGALQAEASLDKTVKELAEQLEFTKNSDIQ 1254

Db 1268 EIGEATEHLTQLEADLTDVDQDENFNANHALSGUERDLALNLTLRQLDQHLDLLKHSNFL 1327
QY 1255 GALDSITKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLERESPFEQEEQA 1314
Db 1328 GAYDSIRHAHSQSAEABERRANTSALAVSPVSNASARHRTALMDAQEKEDFNSKHMNQ 1387
QY 1315 RLLDELAKGLQSLDLSAAQMTCTGTPPGADCESECCGPNCRCTDEGEKKCGPGCGGLVT 1374
Db 1388 RALGKLSAHTHTLSLTINELVCGAQLHHDRTSPCGGAGCRDEDEGQPRCGGLSCNGAAA 1447
QY 1375 VAHSAWQKAMDFFDRVLSALAEVEQLSKMVSEAKVRADEAKQNAQDVLTKTNATKXVDK 1434
Db 1448 TADLALGRARHTQAEQLRALAEGGSILSRVAETRRQASEAQQAALDKANASRGQVEQ 1507
QY 1435 SNEDLRNLIKQIRNFLTEDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLS 1494
Db 1508 ANQELQELIQSVKDFLNQEGADPDSIEMVATRVLELSIPASAEQIQHLAGAIARVRSLA 1567
QY 1495 QVEVILQQAADIARAEALLLEAEAKRASKSATDVKVTADMVKEALEEAEKAQVAAEKAQK 1554
Db 1568 DVDAILARTVGDVRRAEQLLDARRARSWAEDEKQKAEVQAALEEAQRAQGIQAQAIRG 1627
QY 1555 ADEDIQTQNLTSIESETAASEETLTNASQRIKLERNVVEELKRKAAQNSGEAEYIEKV 1614
Db 1628 AVADTRDTEQTLYQVQERMAGAEALSSAGERARQLDALLEALKLRAGNSLAATAEET 1687
QY 1615 VYSVKQNAADVKTLDGELDEKVKVESLIAQKTEESADARRKAELLQNEAKTLLAQANS 1674
Db 1688 AGSAQGRAQEAELLRGPLGQYQTVKALAERKAQGVLAQAARAEQLPDEARDLLQAQD 1747
QY 1675 KLQLEDLERKYEDNQKYLEDKAQELVRLGEVRSLLKDISKVAVYSTC 1724
Db 1748 KLQRLQLEGTYEENERALESKAAQLDGLREARMRSVLQAINLQVQIYNTC 1797

RESULT 13

US-10-369-493-5986
; Sequence 5986, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5986
; LENGTH: 1808
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5986

Query Match 38.7%; Score 3646; DB 15; Length 1808;
Best Local Similarity 39.5%; Pred. No. 8.5e-197;
Matches 720; Conservative 307; Mismatches 613; Indels 184; Gaps 37;

QY 3 YCIVSHLQEDKKCFICDSRDPHYETLNPD--SHLIENVVTFAPNRLKIWQSENGVENV 60
Db 66 FCIVSHLEEQTCKFCYCDSTRTEWKPOREPRLSHRIENVVTEVMDDKNRNWWYQSENGAQN 125
QY 61 TIQDLEABFHTHLIMTFKTRPAAMLIERSSDFGKTGWYRYFAYDCSSFFGISTGP 120
Db 126 SISFDLEABFHTHLIMTFKSRPAAMIERSADFGKTQWYRYFAYDCSSFFGIEGP 185
QY 121 MKKVDDIICDSRYSDIETPSTEGEVIERALDPAFKIEDPVSRIQNLKITNLRIFVKLH 180

Db 186 PKKHTDVICTSQSDVAPSTGGEIYVKVISHPIVTENPYADEISTLLKITNLRFNFTKLH 245
QY 181 TLGDNLLDSRMEIREKYYIYAVYDMVVRGNCFCYGHASECAPVD---GVNEEVE--GMVHG 235
Db 246 TLGDDLLDYRPEIDEKYYIYAIYEVVRGSCSYGHASRCIPIDPHVSPNTVMERADIVHG 305
QY 236 HMCRRHNTKGLNCELMDFFHDLPPWRPAEGRNSNACKKNCNEHSSCHFDMVFLATGN 295
Db 306 RCECMHNTGLNCEKCKAFYNDLPWRPAIGDEKNECRQCNRRHALRCHFDRAVYESGT 365
QY 296 -----VSGGVCDNCQHNTMGRNCEQCKPFYFQHPERDIRDPNLCEPC 337
Db 366 NSSFSKSFYSFSGVSGVCDCHMNTQGNCEQCKPFFYRDPRTIDDPHVCLPC 425
QY 338 TCDPAGSENGGICDGYTDFSVGLIAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSC 397
Db 426 ECDKAGSQNGKICEGEEDAERGLVAGKYCKTNVDGNRCDRCCKNGYWNLTETNVDGCVAC 485
QY 398 ACNPLGTIPGPNPCDSETGYCYCKRLVTGQRCDQCCLPQHGLSNDLDGCRPCDCDLGGAL 457
Db 486 TCNLLGTY--NNEGCDKYTGMCCTCKRLVTGENCDQCLPEHYGLSEHVDGCKACDCDIGSY 544
QY 458 NNSCEDSGQCSCPLPHMIGRQCNVEVESGYFTTLDHYIYEAEEANLPGVVVVERQYIQD 517
Db 545 DNTCEITTGQCKCREGFSRRCEADSSFCADITHYVYEAAYANLTRGEVKTREWPSQP 604
QY 518 RIPSWTGPGFVRVPEGAYLEFFIDN--IPYSMEYEILLRYE-PQLPDHWEKAVITVQRP 574
Db 605 HEQTFTEGGAQAVEGTIITV---NPIVEVSQKYNVIRHDGARDPVGWENIQTIVRP- 660
QY 575 KIPASSRCGNTVPDDNQVVSLSPGSRYVVLPRPVCPEKGMNVTVRLEL-----PQY 626
Db 661 EAEGDSCSDAPPSDDFLIARIYPGSRYIEVQPAICLEAGVQYELRIQFNEKRGNSHPQE 720
QY 627 TAGSDVESPYTFIDSLVLMPCYKSLDIFTVGGSGDGEVNTSAWETFQRYRC--LENSRS 684
Db 721 RAAAN-----ILIDSILLAPPTSELHIFQGSARAEQHLE-----YNRYQCRHLALSLS 769
QY 685 VVKTPMTDVCERNIIPISALIHQTLACEDPQGSLSVCDPNGGQCQCRPNVVGRTCNR 744
Db 770 LFXDQRNEVCERYVCPIAAALLNKTSECNCDATGSVSGICNVQGGQCECKPNVVGRRCDQ 829
QY 745 CAPGTFGFGNGCKPCDCHLQGSASAFCDAITGQCHCFQ-GIYARQCDRLCPGYWGFPPSC 803
Db 830 CAIGTYGFGSPGCKKCDCAVAVSLGNDCKDQSGQCVCREKGIYGRQCNCQCPGFWGFPEC 889
QY 804 QPCQCNHGLDCTVTGECCLSCQDYTTGHNCCERCLAGYVGDPIIGSGDHCRCPCPCPDGPD 863
Db 890 RTCQCNDRANICDQSSGACIECRDLTTGHYCDRCQDGYIGDPRLGVIPIKPCPCPGGPT 949
QY 864 SGRQFARSCY---QDPVTLQACVCDPPGYIGSRCDDCASGFFGNPSPDFGGSCQPCQCHHN 920
Db 950 SGYQHADTCYLRNSGNNTQDIVCNCKSGYQGERCGEACQNHWSPREVGGTCERCDCNGN 1009
QY 921 IDTTDPEACDKDTRCLKCLYHTEGHCQLCQGYGYGDALRQDCRKCVCNVLGTVKEHCN 980
Db 1010 IDMAMEGSCDAATGECLKCLHHTEGAQCEHCVDGYYGDAKLKTCQRCVCNELGT-----N 1064
QY 981 GSDCHCDKATGQCSCLPNVIGQNCNDRCAPNTWOLASGTGCGPCNCNA-----AHSFGP-- 1033
Db 1065 STKGACDRVSGQCPCHDNIIGMQCQCAENHFNLASGAGCEAGCDSNGVVLNHEGVPHL 1124
QY 1034 SCNEFTGQCQCMGFGGRTCESECQELFWGDPDVE--CRACDCDPRGIETPQCQSTGQCV 1091
Db 1125 QCNIFDQCQCKPGRGKCDQCEDLYWGPPTPDGCHRCENPTGSKSLQCHRNNGTCE 1184
QY 1092 CVEGVEGPRCKXTRGYSGVFPDCTPCHQCFALWDAIIGELTNRTHKFLEKAKALKISGV 1151
Db 1185 CQAGSGGALCNECARGYTGOWPYCNPCGECFHQWDNIMQLQKVHALIDTANNIEDTGV 1244
QY 1152 IGPYRETVDSEVKVNEIKDILAQSPAAEPLKNIGILFEEAEKLTKDVT-----E 1201
Db 1245 ASAYDADFKEKMEETLKETK-----KALSDANISKEDIEEMSKLALLKKQVIAGRE 1295

QY 1202 KMAQVEVKLTDITASQSNSTAGELGALQAEAESLDKTVKELAEQLEFIKNSDIQCALDSIT 1261
Db 1296 KLGAIETRISNITQAVDPAQKDLEHLQKEVDKVTKATIELEDKASKIKEADVLGAFNITR 1355
QY 1262 KYFQMSLEAEKRVNASTDPNSTVQSALTRDRVEDLMLERESPFFKEQQEQEARLLDE-- 1319
Db 1356 ESASKSLDAQRRRTDAA-IGKLAAAEENQAL---RASELLEKNKDNDFEKQYVENEALNEAE 1411
QY 1320 -LAGKLQSLDLSAAQMTCGTPPGADCESECEGPGNCRDTDEGEKCGGPG---CGGLVT 1374
Db 1412 TLLGGLSV-LPKLNEQVCG-----ASSAPC-----DALCGPGSGCGCGG--- 1451
QY 1375 VAHSAWQKAMDFDRDVLSSALAEVEQLSKMVSEAKVRADEAKQNAQ-----DVLKKTNA 1427
Db 1452 -----QSCME-----GAVSKANQAKSFATEADTRLDEKQKEAEVLSIVRDVLTETTK 1499
QY 1428 TKEKVDKSNE-----DLRNLKIQIRNFELTDSADLDSIEAVANEVLKSGNA 1473
Db 1500 AKAKAEKAYEVAKNTAQANSSRAELDKIAEEIGEFTLQAKSSPEQIRNLAEEVLKKEIS 1559
QY 1474 STPQQLQNLTEDIRERVETILSQVEVILQQSAADIAARABLLLEAKRASKSATDVKVTADM 1533
Db 1560 LTPDQITDLTGKIKESLAKINNIDEILNETRGNKSTAAANLESRAVKANKEAELLQKAMBE 1619
QY 1534 VKEALEEAEKAQVAEAKAIQADEDIQGTQNLITSIESETAASEETLTNASQRISKLEARN 1593
Db 1620 IREALQLADQAYNNVTSVLEEDTDMQVQARELIDKARNSTEAVEGKAQAANTTLAELEGV 1679
QY 1594 VEELKRKAAQNSGEAEYIEKVYVSVKQADDDVKKTLDDGEL-----DEKYKVKVES----- 1642
Db 1680 MSGVK-----VEYLO-----ISEAKNALTTVDAALAAATAAEQKNKQIQTDLERA 1725
QY 1643 --LIAQKTEESADARRKAEILLQNEAKTLLAQANSKLQLELDERKYEDNQKYLEDKAQEL 1700
Db 1726 TELLEKXMEGNVAPQORAEKLEPRAAKLLYQAOQRHNDIDNLSK--DSTEMRLDDYETIL 1783
QY 1701 VRLEGEVRSLLKDISSEKVAVYSTC 1724
Db 1784 ADLSRLERVTRDIHEKTDHFATC 1807

RESULT 14

US-10-287-971-18
; Sequence 18, Application US/10287971
; Publication No. US20040067882A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD:
; FILE REFERENCE: 21402-480A
; CURRENT APPLICATION NUMBER: US/10/287,971
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 09/997,425
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 10/035,568
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/338,626
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 60/401,479
; PRIOR FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/333,072
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 60/348,283
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/393,262
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: 60/406,181
; PRIOR FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 397
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 18
; LENGTH: 1101
; TYPE: PRT

QY	1210	LTDITASQSNSTAGELGALQAEBSLDKTVKELAEQLEFIKNSDIOGALDSITKYFQMSLE	1269
Db	121	LSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLE	180
QY	1270	AEKRYNASTTDPNSTVEQSALETDRVEDLMLERESPFKEQOEEOARLLDELACKLQSLDL	1329
Db	181	AEERYNASTTEPNSTVEQSALEMDRVEDVMMERESQFKEKQOEEOARLLDELACKLQSLDL	240
QY	1330	SAAQWTCGTPPGADCSESECGGNCRTDEGEKKCGGPGCGGLVTVAHSAWQKAMDFFDRD	1389
Db	241	SAXAEMTCGTPPGASCXEXECCGGNCRTDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQD	300
QY	1390	VLSALAEVEQLSKMVSEAKVRADEAKQNAQDVLLKTNATYKVKVDSNEDLRNLKQIRNF	1449
Db	301	VLSALAEVEQLSKMVSEAKLRADAKQSAEDILLKTNATKEMDKSNEELRNLIKQIRNF	360
QY	1450	LTEDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVILQOSAADIAR	1509
Db	361	LTQDSADLDSIEAVANEVLKMEMPESTPQQLQNLTEDIRERVESLSQVEVILQHSAADIAR	420
QY	1510	AELLLLEEAKRASKSATDVKVTADMVKEALEEAEAKQVAAEKAIKQADEDIQGTQNLTSI	1569
Db	421	AEMLLLEEAKRASKSATDVKVTADMVKEALEEAEAKQVAAEKAIKQADEI-----	470
QY	1570	ESETAASEETLTNASQRISKLERNVE---ELKRKAAQNSGEAEYIEKVVSVKQONADDV	1625
Db	471	-----XRNPEPXNFLEFXKQQLSG-GNLVQRPVPRASSEFREDV	508
QY	1626	KKTLDGEL	1633
Db	509	GRXLGKL	516

Search completed: May 18, 2004, 15:42:45
Job time : 50.8855 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:26:08 ; Search time 10.0352 Seconds
(without alignments)
9158.169 Million cell updates/sec

Title: US-10-037-182-8

Perfect score: 9654

Sequence: 1 QEPFSGYCAEGSCYPATGD.....EVRSLKDISQKAVYSTCL 1765

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	9654	100.0	1786	1 LMB1_HUMAN	P07942 homo sapien
2	9092	94.2	1786	1 LMB1_MOUSE	P02469 mus musculus
3	5084	52.7	1801	1 LMB2_RAT	P15800 rattus norv
4	5048	52.3	1798	1 LMB2_HUMAN	P55268 homo sapien
5	5046	52.3	1799	1 LMB2_MOUSE	Q61292 mus musculus
6	3844.5	39.8	1790	1 LMB1_DROME	P11046 drosophila
7	1759	18.2	1639	1 LMG1_DROME	P15215 drosophila
8	1729.5	17.9	3672	1 LML2_CAEEL	Q21313 caenorhabdi
9	1696.5	17.6	1535	1 LML1_CAEEL	Q18823 caenorhabdi
10	1676.5	17.4	1609	1 LMG1_HUMAN	P11047 homo sapien
11	1653	17.1	1607	1 LMG1_MOUSE	Q02468 mus musculus
12	1637	17.0	3712	1 LMA_MOUSE	Q00174 drosophila
13	1617	16.7	3718	1 LMA5_MOUSE	Q61001 mus musculus
14	1583	16.4	303	1 LMB1_CHICK	Q01635 gallus gall
15	1560.5	16.2	3695	1 LMA5_HUMAN	O15230 homo sapien
16	1559.5	16.2	3110	1 LMA2_HUMAN	P24043 homo sapien
17	1558.5	16.1	1581	1 LMG3_MOUSE	Q9r0b6 mus musculus
18	1552.5	16.1	1172	1 LMB3_HUMAN	Q13751 homo sapien
19	1535.5	15.9	3106	1 LMA2_MOUSE	Q60675 mus musculus
20	1525	15.8	3075	1 LMA1_HUMAN	P25391 homo sapien
21	1515.5	15.7	1587	1 LMG3_HUMAN	Q9y6n6 homo sapien
22	1507.5	15.6	3084	1 LMA1_MOUSE	P19137 mus musculus
23	1483.5	15.4	1168	1 LMB3_MOUSE	Q61087 mus musculus
24	1372	14.2	3333	1 LMA3_MOUSE	Q61789 mus musculus
25	891	9.2	1191	1 LMG2_MOUSE	Q61092 mus musculus
26	873	9.0	1193	1 LMG2_HUMAN	Q13753 homo sapien
27	695.5	7.2	604	1 NET1_HUMAN	Q95631 homo sapien
28	695.5	7.2	604	1 NET1_MOUSE	O09118 mus musculus
29	690.5	7.2	606	1 NET1_CHICK	Q90922 gallus gall
30	666	6.9	3707	1 PGBM_MOUSE	Q05793 mus musculus
31	657	6.8	4391	1 PGBM_HUMAN	P98160 homo sapien
32	600	6.2	581	1 NET2_CHICK	Q90923 gallus gall
33	582.5	6.0	1816	1 LMA4_HUMAN	Q16363 homo sapien

34	579	6.0	612	1 UNC6_CAEEL	P34710 caenorhabdi
35	576.5	6.0	1816	1 LMA4_MOUSE	P97927 mus musculus
36	556.5	5.8	727	1 NETA_DROME	Q24567 drosophila
37	541	5.6	400	1 LMB_HIRME	Q25092 hirudo medi
38	526	5.4	3375	1 UNC2_CAEEL	Q06561 caenorhabdi
39	524.5	5.4	2556	1 NTC1_HUMAN	P46531 homo sapien
40	518.5	5.4	2524	1 NOTC_XENLA	P21783 xenopus lae
41	515.5	5.3	2319	1 NTC3_RAT	Q9r172 rattus norv
42	511	5.3	198	1 LMBV_CHICK	Q01636 gallus gall
43	506.5	5.2	2703	1 NOTC_DROME	P07207 drosophila
44	506	5.2	2531	1 NTC1_MOUSE	Q01705 mus musculus
45	505.5	5.2	2437	1 NTC1_BRARE	P46530 brachydanio

ALIGNMENTS

RESULT 1
LMB1_HUMAN
ID LMB1_HUMAN STANDARD; PRT; 1786 AA.
AC P07942;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Laminin beta-1 chain precursor (Laminin B1 chain).
GN LAMB1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90368768; PubMed=1975589;
RA Vuolteenaho R., Chow L.T., Tryggvason K.;
RT "Structure of the human laminin B1 chain gene."
RL J. Biol. Chem. 265:15611-15616(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87280097; PubMed=3611077;
RA Pikkarainen T., Eddy R., Fukushima Y., Byers M., Shows T.,
RA Pihlajaniemi T., Saraste M., Tryggvason K.;
RT "Human laminin B1 chain. A multigene protein with gene (LAMB1)
locus in the q22 region of chromosome 7."
RL J. Biol. Chem. 262:10454-10462(1987).
RN [3]
RP SEQUENCE OF 1276-1709 FROM N.A.
RX MEDLINE=88021029; PubMed=3661559;
RA Jaye M., Modi W.S., Ricca G.A., Mudd R., Chiu I.M., O'Brien S.J.,
RA Drohan W.N.;
RT "Isolation of a cDNA clone for the human laminin-B1 chain and its
gene localization."
RL Am. J. Hum. Genet. 41:605-615(1987).
CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
is thought to mediate the attachment, migration and organization
of cells into tissues during embryonic development by interacting
with other extracellular matrix components.
CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
different polypeptide chains (alpha, beta, gamma), which are bound
to each other by disulfide bonds into a cross-shaped molecule
comprising one long and three short arms with globules at each
end. The beta-1 chain is a subunit of laminin-1 (EHS laminin),
laminin-2 (merosin), and laminin-6 (K-laminin).
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Found in the basement membranes (major
component).
CC -!- DOMAIN: The alpha-helical domains I and II are thought to interact
with other laminin chains to form a coiled coil structure.
CC -!- DOMAIN: Domains VI and IV are globular.
CC -!- SIMILARITY: Contains 1 laminin N-terminal domain.
CC -!- SIMILARITY: Contains 13 laminin EGF-like domains.
CC -!- SIMILARITY: Contains 1 laminin IV domain.

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CC -----

DR EMBL; M61951; AAA59486.1; --
DR EMBL; M58147; AAA59486.1; JOINED.
DR EMBL; M61917; AAA59486.1; JOINED.
DR EMBL; M61918; AAA59486.1; JOINED.
DR EMBL; M61921; AAA59486.1; JOINED.
DR EMBL; M61922; AAA59486.1; JOINED.
DR EMBL; M61923; AAA59486.1; JOINED.
DR EMBL; M61924; AAA59486.1; JOINED.
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DR EMBL; M61926; AAA59486.1; JOINED.
DR EMBL; M61927; AAA59486.1; JOINED.
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DR EMBL; M55371; AAA59485.1; JOINED.
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DR EMBL; M55369; AAA59485.1; JOINED.

DR EMBL; M61916; AAA59482.1; --
DR EMBL; M20206; AAA59487.1; --
DR PIR; S13547; MHUB1.
DR HSP; P02468; IKLO.
DR Genew; HGNC:6486; LAMB1.
DR MIM; I50240; --
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR008211; LamNT.
DR Pfam; PF00053; laminin_EGF; 13.
DR Pfam; PF00055; laminin_Nterm; 1.
DR PRINTS; PR00011; EGFLAMININ.
DR SMART; SM00180; EGF Lam; 12.
DR SMART; SM00136; LamNT; 1.
DR PROSITE; PS00022; EGF 1; 9.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01248; LAMININ TYPE EGF; 11.
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
Laminin EGF-like domain; Cell adhesion; Repeat; Signal; Polymorphism.
FT SIGNAL 1 21
FT CHAIN 22 1786 LAMININ BETA-1 CHAIN.
FT DOMAIN 271 334 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 335 397 LAMININ EGF-LIKE 1.
FT DOMAIN 398 457 LAMININ EGF-LIKE 2.
FT DOMAIN 458 509 LAMININ EGF-LIKE 3.
FT DOMAIN 510 540 LAMININ EGF-LIKE 4.
FT DOMAIN 541 771 LAMININ EGF-LIKE 5 (INCOMPLETE).
FT DOMAIN 773 820 LAMININ DOMAIN IV.
FT DOMAIN 821 866 LAMININ EGF-LIKE 6.
FT DOMAIN 867 916 LAMININ EGF-LIKE 7.
FT DOMAIN 917 975 LAMININ EGF-LIKE 8.
FT DOMAIN 976 1027 LAMININ EGF-LIKE 9.
FT DOMAIN 1028 1083 LAMININ EGF-LIKE 10.
FT DOMAIN 1084 1131 LAMININ EGF-LIKE 11.
FT DOMAIN 1132 1178 LAMININ EGF-LIKE 12.
FT DOMAIN 1179 1397 LAMININ EGF-LIKE 13.
FT DOMAIN 1398 1430 DOMAIN II.
FT DOMAIN 1431 1786 DOMAIN ALPHA.
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FT DOMAIN 1353 1388 COILED COIL (POTENTIAL).
FT DOMAIN 1442 1781 COILED COIL (POTENTIAL).
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FT DISULFID 917 933 BY SIMILARITY.
FT DISULFID 919 944 BY SIMILARITY.
FT DISULFID 946 955 BY SIMILARITY.

Query Match		100.0%;	Score 9654;	DB 1;	Length 1786;
Best local Similarity		100.0%;	Pred. No. 0;		
Matches 1765;		Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
QY	1	QEPFSGCAGSCYPATGDL	LLIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICNS	60	
Db	22	QEPFSGCAGSCYPATGDL	LLIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICNS	81	
QY	61	QDPYHETLNPDSHLIEN	VVTFAPNRLKIWQSENGVENVTIQLDLEAEFFHFLIMTFK	120	
Db	82	QDPYHETLNPDSHLIEN	VVTFAPNRLKIWQSENGVENVTIQLDLEAEFFHFLIMTFK	141	
QY	121	TFRPAAMLIERSDDFGK	TWGVRYFAYDCEASFPGISTGPMKKVDDIICDSRYSDIEPST	180	
Db	142	TFRPAAMLIERSDDFGK	TWGVRYFAYDCEASFPGISTGPMKKVDDIICDSRYSDIEPST	201	
QY	181	EGEVIFRALDPAFKIED	PYSPRIQNLKTIITNLR	IKFVKLHTLGDNLDSRMEIREKYVYA	240
Db	202	EGEVIFRALDPAFKIED	PYSPRIQNLKTIITNLR	IKFVKLHTLGDNLDSRMEIREKYVYA	261
QY	241	YDVMVRGNCFCYGHASE	CAPVDGFEVEEGMVHGHCMCRHNTKGLNCEL	CMDFYHDLPW	300
Db	262	YDVMVRGNCFCYGHASE	CAPVDGFEVEEGMVHGHCMCRHNTKGLNCEL	CMDFYHDLPW	321
QY	301	RPAEGRNSNACKKNCNEH	ISISCHFDMAVYLATGNVSGVCDCCQHNMTWGRNCEQCKPFY	360	
Db	322	RPAEGRNSNACKKNCNEH	ISISCHFDMAVYLATGNVSGVCDCCQHNMTWGRNCEQCKPFY	381	
QY	361	YQHPERDIRDPNFCER	CTCDPAGSQNEGICDSYTDFTSTGLIAGQCRCKLNVEGEHCDVCK	420	
Db	382	YQHPERDIRDPNFCER	CTCDPAGSQNEGICDSYTDFTSTGLIAGQCRCKLNVEGEHCDVCK	441	
QY	421	EGFYDLSSDPFGCKSC	ACNPLGTIPGGNCPDSETHCYCKRLVTGQHCDCQCLPEHWGLS	480	
Db	442	EGFYDLSSDPFGCKSC	ACNPLGTIPGGNCPDSETHCYCKRLVTGQHCDCQCLPEHWGLS	501	
QY	481	NDLDGCRPCDCLGGLN	NSCFAESGQCSCRPHMIGRCNEVEPGYFATLDHYLYEAE	540	
Db	502	NDLDGCRPCDCLGGLN	NSCFAESGQCSCRPHMIGRCNEVEPGYFATLDHYLYEAE	561	
QY	541	ANLPGVSIIVERQYIQ	DRIPSWTGAQFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP	600	
Db	562	ANLPGVSIIVERQYIQ	DRIPSWTGAQFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP	621	
QY	601	DHWEKAVITVQRPGR	IPTSSRCGNTIPDDNQVVSLSPGSRYVVLPRPVCFEKGNTYTVR	660	
Db	622	DHWEKAVITVQRPGR	IPTSSRCGNTIPDDNQVVSLSPGSRYVVLPRPVCFEKGNTYTVR	681	
QY	661	LELPQYTSSDSDVES	PYTLIDSLVMPYCKSLDIFTVGGSGDGVVWNSAWETFYRYRCLE	720	
Db	682	LELPQYTSSDSDVES	PYTLIDSLVMPYCKSLDIFTVGGSGDGVVWNSAWETFYRYRCLE	741	
QY	721	NSRSVVKTPMTDVCR	NIIFSIALLHQTLGACEDCPQGSLSVCDPNGGQCQCRPNVVG	780	
Db	742	NSRSVVKTPMTDVCR	NIIFSIALLHQTLGACEDCPQGSLSVCDPNGGQCQCRPNVVG	801	
QY	781	TCNRCAPGTFGFGPS	GCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDRCLPGHWGF	840	
Db	802	TCNRCAPGTFGFGPS	GCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDRCLPGHWGF	861	
QY	841	PSCQPCQCNHADD	CDPVTGECINCDQYTMGHNCBRCCLAGYGDPIIGSGDHCRPCPCPD	900	
Db	862	PSCQPCQCNHADD	CDPVTGECINCDQYTMGHNCBRCCLAGYGDPIIGSGDHCRPCPCPD	921	
QY	901	GPDGGRQFARSCYQ	DPVTILQACVCDPQYIGSRCDDCASGYFGNPSVGGSCQPCQCHNN	960	
Db	922	GPDGGRQFARSCYQ	DPVTILQACVCDPQYIGSRCDDCASGYFGNPSVGGSCQPCQCHNN	981	
QY	961	IDTDPACDKETGRCL	CKLYHTEGEHCQCFRFGYIGDALRQDCKKVCVNLGTVOEHCHN	1020	
Db	982	IDTDPACDKETGRCL	CKLYHTEGEHCQCFRFGYIGDALRQDCKKVCVNLGTVOEHCHN	1041	

QY	1021	GSDCQCDKATGQCLCL	PNVIGQNCDCRCAPNTWQLASGTGCDPCNCAAHSGPSCNEFTG	1080	
Db	1042	GSDCQCDKATGQCLCL	PNVIGQNCDCRCAPNTWQLASGTGCDPCNCAAHSGPSCNEFTG	1101	
QY	1081	QCQCMGFGGRTCECQ	ELFWGDPDVECRACDCDPRGIETPQCDQSTGCQCVCEGVEGPR	1140	
Db	1102	QCQCMGFGGRTCECQ	ELFWGDPDVECRACDCDPRGIETPQCDQSTGCQCVCEGVEGPR	1161	
QY	1141	CDKCTRGYSGVFPD	CTPCHQCFCALWDVIAELTNRTHRFLEKAKALKISGIVGYPYRETVD	1200	
Db	1162	CDKCTRGYSGVFPD	CTPCHQCFCALWDVIAELTNRTHRFLEKAKALKISGIVGYPYRETVD	1221	
QY	1201	SVERKVSEIKDILAQ	SPAAEPLKNIGNLFEEAEKLIKDVTEMMAQVEVKLSDTTSQSNST	1260	
Db	1222	SVERKVSEIKDILAQ	SPAAEPLKNIGNLFEEAEKLIKDVTEMMAQVEVKLSDTTSQSNST	1281	
QY	1261	AKELDSLQTEAESL	DNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEBERVNASTTE	1320	
Db	1282	AKELDSLQTEAESL	DNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEBERVNASTTE	1341	
QY	1321	PNSTVEQSALMRD	RVEDVMMERESQFKEKQEBEQARLLDELAKGLQSLDLSAAAEAMTCGTP	1380	
Db	1342	PNSTVEQSALMRD	RVEDVMMERESQFKEKQEBEQARLLDELAKGLQSLDLSAAAEAMTCGTP	1401	
QY	1381	PGASCSETECGGPN	CTDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLALAEVEQL	1440	
Db	1402	PGASCSETECGGPN	CTDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLALAEVEQL	1461	
QY	1441	SKVNSEAKLRAD	EAKQSAEDILLKTNATKEMDKSNEELRNLIKQIRNFLTQDSADLDSI	1500	
Db	1462	SKVNSEAKLRAD	EAKQSAEDILLKTNATKEMDKSNEELRNLIKQIRNFLTQDSADLDSI	1521	
QY	1501	EAVANEVLKMEM	PTPQQLQNLTEDIRERVESLSQVEVILQHSAAADIARAEMLLEEAKRA	1560	
Db	1522	EAVANEVLKMEM	PTPQQLQNLTEDIRERVESLSQVEVILQHSAAADIARAEMLLEEAKRA	1581	
QY	1561	SKSATDVKVTA	DMVKEALAEAEAKQAQAAEKAIQADEDIQGTQNLTSISEETAASEETL	1620	
Db	1582	SKSATDVKVTA	DMVKEALAEAEAKQAQAAEKAIQADEDIQGTQNLTSISEETAASEETL	1641	
QY	1621	FNASQRIS	ELELERNVEELKRAAQNNGEAEYIEKVYTVKQSAEDVKKTLDGELDEKYYKV	1680	
Db	1642	FNASQRIS	ELELERNVEELKRAAQNNGEAEYIEKVYTVKQSAEDVKKTLDGELDEKYYKV	1701	
QY	1681	ENLIAKTEES	ADARRKAEMLQNEAKTLLAQANSKLQLLKDLERKYEDNQRYLEDKAQEL	1740	
Db	1702	ENLIAKTEES	ADARRKAEMLQNEAKTLLAQANSKLQLLKDLERKYEDNQRYLEDKAQEL	1761	
QY	1741	ARLEGEVRS	LLKDISQKVAVYSTCL	1765	
Db	1762	ARLEGEVRS	LLKDISQKVAVYSTCL	1786	

RESULT 2
LMB1_MOUSE
ID LMB1_MOUSE STANDARD; PRT; 1786 AA.
AC P02469;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Laminin beta-1 chain precursor (Laminin B1 chain).
GN LAMB1-1 OR LAMB-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87147212; PubMed=3493487;
RA Sasaki M., Kato S., Kohno K., Martin G.R., Yamada Y.;
RT "Sequence of the cDNA encoding the laminin B1 chain reveals a
multidomain protein containing cysteine-rich repeats."
RL Proc. Natl. Acad. Sci. U.S.A. 84:935-939(1987).

RN [2] SEQUENCE OF 1292-1786 FROM N.A.
RP MEDLINE=85051302; PubMed=6209134;
RX Barlow D.P., Green N.M., Kurkinen M., Hogan B.L.M.;
RA "Sequencing of laminin B chain cDNAs reveals C-terminal regions of
RT coiled-coil alpha-helix";
RL EMBO J. 3:2355-2362(1984).
RN [3]
RP SEQUENCE OF 165-172; 539-547 AND 712-719.
RC STRAIN=BALB/c; TISSUE=Endothelial cells;
RX MEDLINE=97363207; PubMed=9219532;
RA Frieser M., Noeckel H., Pausch F., Roeder C., Hahn A., Deutzmann R.,
RA Sorokin L.M.;
RT "Cloning of the mouse laminin alpha 4 cDNA. Expression in a subset of
RL endothelium";
RL Eur. J. Biochem. 246:727-735(1997).
CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components.
CC -!- SUBUNIT: laminin is a complex glycoprotein, consisting of three
CC different polypeptide chains (alpha, beta, gamma), which are bound
CC to each other by disulfide bonds into a cross-shaped molecule
CC comprising one long and three short arms with globules at each
CC end. The beta-1 chain is a subunit of laminin-1 (BHS laminin),
CC laminin-2 (merosin), and laminin-6 (K-laminin).
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Found in the basement membranes (major
CC component).
CC -!- SIMILARITY: Contains 1 laminin N-terminal domain.
CC -!- SIMILARITY: Contains 13 laminin EGF-like domains.
CC -!- SIMILARITY: Contains 1 laminin IV domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M15525; AAA39407.1; ALT_INIT.
DR EMBL; X05212; CAA28839.1; -.
DR PIR; A26413; MMSB1.
DR HSSP; P02468; IKLO.
DR MGD; MGI:96743; Lamb1-1.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR008211; LamNT.
DR Pfam; PF00053; laminin_EGF; 13.
DR Pfam; PF00055; laminin_Nterm; 1.
DR PRINTS; PR00011; EGFLAMININ.
DR SMART; SM00180; EGF_Lam; 11.
DR SMART; SM00136; LamNT; 1.
DR PROSITE; PS00022; EGF_1; 9.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01248; LAMININ TYPE EGF; 11.
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
FT SIGNAL 1 21
FT CHAIN 22 1786 LAMININ BETA-1 CHAIN.
FT DOMAIN 22 270 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 271 334 LAMININ EGF-LIKE 1.
FT DOMAIN 335 397 LAMININ EGF-LIKE 2.
FT DOMAIN 398 457 LAMININ EGF-LIKE 3.
FT DOMAIN 458 509 LAMININ EGF-LIKE 4.
FT DOMAIN 510 540 LAMININ EGF-LIKE 5 (INCOMPLETE).
FT DOMAIN 541 772 LAMININ DOMAIN IV.
FT DOMAIN 773 820 LAMININ EGF-LIKE 6.
FT DOMAIN 821 866 LAMININ EGF-LIKE 7.
FT DOMAIN 867 916 LAMININ EGF-LIKE 8.
FT DOMAIN 917 975 LAMININ EGF-LIKE 9.
FT DOMAIN 976 1027 LAMININ EGF-LIKE 10.

FT DOMAIN 1028
FT DOMAIN 1084
FT DOMAIN 1132
FT DOMAIN 1178
FT DOMAIN 1397
FT DOMAIN 1430
FT DOMAIN 1431
FT DOMAIN 1216
FT DOMAIN 1368
FT DOMAIN 1448
FT DISULFID 271
FT DISULFID 273
FT DISULFID 300
FT DISULFID 312
FT DISULFID 335
FT DISULFID 337
FT DISULFID 365
FT DISULFID 377
FT DISULFID 398
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FT DISULFID 440
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FT DISULFID 1182
FT DISULFID 1785
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FT CARBOHYD 356
FT CARBOHYD 519
FT CARBOHYD 677
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FT CARBOHYD 1336
FT CARBOHYD 1343
FT CARBOHYD 1487
FT CARBOHYD 1533
FT CARBOHYD 1542
FT CARBOHYD 1643
FT CONFLICT 1531
FT CONFLICT 1749
SQ SEQUENCE 1786
1083 LAMININ EGF-LIKE 11.
1131 LAMININ EGF-LIKE 12.
1178 LAMININ EGF-LIKE 13.
1397 DOMAIN II.
1430 DOMAIN ALPHA.
1431 DOMAIN I.
1216 COILED COIL (POTENTIAL).
1368 COILED COIL (POTENTIAL).
1448 COILED COIL (POTENTIAL).
271 BY SIMILARITY.
273 BY SIMILARITY.
300 BY SIMILARITY.
312 BY SIMILARITY.
335 BY SIMILARITY.
337 BY SIMILARITY.
365 BY SIMILARITY.
377 BY SIMILARITY.
398 BY SIMILARITY.
400 BY SIMILARITY.
428 BY SIMILARITY.
440 BY SIMILARITY.
458 BY SIMILARITY.
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481 BY SIMILARITY.
493 BY SIMILARITY.
773 BY SIMILARITY.
775 BY SIMILARITY.
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806 BY SIMILARITY.
821 BY SIMILARITY.
823 BY SIMILARITY.
842 BY SIMILARITY.
854 BY SIMILARITY.
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886 BY SIMILARITY.
898 BY SIMILARITY.
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958 BY SIMILARITY.
976 BY SIMILARITY.
978 BY SIMILARITY.
1000 BY SIMILARITY.
1012 BY SIMILARITY.
1084 BY SIMILARITY.
1086 BY SIMILARITY.
1105 BY SIMILARITY.
1117 BY SIMILARITY.
1132 BY SIMILARITY.
1134 BY SIMILARITY.
1153 BY SIMILARITY.
1165 BY SIMILARITY.
1179 INTERCHAIN (PROBABLE).
1182 INTERCHAIN (PROBABLE).
1785 INTERCHAIN (PROBABLE).
120 N-LINKED (GLCNAC. . .)
356 N-LINKED (GLCNAC. . .)
519 N-LINKED (GLCNAC. . .)
677 N-LINKED (GLCNAC. . .)
1041 N-LINKED (GLCNAC. . .)
1195 N-LINKED (GLCNAC. . .)
1279 N-LINKED (GLCNAC. . .)
1336 N-LINKED (GLCNAC. . .)
1343 N-LINKED (GLCNAC. . .)
1487 N-LINKED (GLCNAC. . .)
1533 N-LINKED (GLCNAC. . .)
1542 N-LINKED (GLCNAC. . .)
1643 N-LINKED (GLCNAC. . .)
1531 SGNA -> MEMP (IN REF. 2).
1749 D -> N (IN REF. 2).
1786 AA; 196904 MW; 846671B7BF41A474 CRC64;

Query Match		94.2%;	Score 9092;	DB 1;	Length 1786;			
Best Local Similarity		93.0%;	Pred. No. 0;					
Matches 1642;		Conservative 71;	Mismatches 52;	Indels 0;	Gaps 0;			
QY	1	QEPEFSYGCAEGSCYPATGDL	LLIGRAQKLSVTSTCGLHKP	PEPYCI	VSHLQEDKKCFICNS 60			
Db	22	QEPEFSYGCAEGSCYPATGDL	LLIGRAQKLSVTSTCGLHKP	PEPYCI	VSHLQEDKKCFICDS 81			
QY	61	QDPYHETLNPDSHLIENV	VTTFAPNRLKI	WQSENGVENVTI	QLDLEAEFHFTHLIMTFK 120			
Db	82	QDPYHETLNPDSHLIENV	VTTFAPNRLKI	WQSENGVENVTI	QLDLEAEFHFTHLIMTFK 141			
QY	121	TFRPAAMLIERSSDFGKT	GWYRYFAYDCEAS	PPGISTGPMKKVDDI	ICDSRYSDIEPST 180			
Db	142	TFRPAAMLIERSSDFGKT	GWYRYFAYDCESS	PPGISTGPMKKVDDI	ICDSRYSDIEPST 201			
QY	181	EGEVIFRALDPAPKIEDP	YSPRIQNLKITNLR	IKFVKLHTL	GNLDDSRMEIREKYIYA 240			
Db	202	EGEVIFRALDPAPKIEDP	YSPRIQNLKITNLR	IKFVKLHTL	GNLDDSRMEIREKYIYA 261			
QY	241	VYDMVVRGNCFCYGHASE	CAPVDGFNEEVEGMV	HGCMCRHNTKGLN	CMLCFYHDLPW 300			
Db	262	VYDMVVRGNCFCYGHASE	CAPVDGVNEEVEGMV	HGCMCRHNTKGLN	CMLCFYHDLPW 321			
QY	301	RPAEGRNSNACKKCN	NEHSISCHFDMA	VVLATGNVSGGVCDD	COHNTMGRNCEQCKPFY 360			
Db	322	RPAEGRNSNACKKCN	NEHSSSCHFDMA	VVLATGNVSGVCDNC	QHNTMGRNCEQCKPFY 381			
QY	361	YQHPERDIRDPNFC	RCTCDPAGSQNEGIC	SDYTFDSTGLI	AGQCRCKLNVEGEHCDVCK 420			
Db	382	FQHPERDIRDPNLC	EPTCDPAGSENGGIC	SDYTFD	SVGLIAGQCRCKLHVEGERCDVCK 441			
QY	421	EGFYDLSSDPFGCK	SCACNPLGTIPG	GNPCDSETHCYCK	RLVTGQCHDQCLPEHWGLS 480			
Db	442	EGFYDLSSDPFGCK	SCACNPLGTIPG	GNPCDSETHCYCK	RLVTGQCHDQCLPEHWGLS 501			
QY	481	NDLDGCRPCDCLG	GALNNSCF	FAESGQCS	CRPHMIGRQCNEVEPGYVFATLDHYLYEAE 540			
Db	502	NDLDGCRPCDCLG	GALNNSCF	FAESGQCS	CRPHMIGRQCNEVEPGYVFATLDHYLYEAE 561			
QY	541	ANLGPVSVIVERQ	YIQDRIPSWT	GAGFVRVPEGA	YLEFFIDNIPYSMEYDILIRYEPQLP 600			
Db	562	ANLGPVSVIVERQ	YIQDRIPSWT	GPGFVRVPEGA	YLEFFIDNIPYSMEYDILIRYEPQLP 621			
QY	601	DHWEKAVITVOR	PGRIPTSSRCGNT	IPDDNQV	VSLSPGSRVYVLP	PRPVCFEKGNTYTVR 660		
Db	622	DHWEKAVITVOR	PGKI	PASSRCGNTVP	DDNQV	VSLSPGSRVYVLP	PRPVCFEKGNTYTVR 681	
QY	661	LELPQYTSSD	SVESPYTLIDSL	VLMPYCKSLD	IFTVGGSGDVVTNS	AWETFORYRCLE 720		
Db	682	LELPQYTASG	SVESPYTFIDSL	VLMPYCKSLD	IFTVGGSGDGEVTNS	AWETFORYRCLE 741		
QY	721	NSRSVVKTPMTD	VCRNII	IFSI	SALLHQTGLACE	DPQGSLSVCDP	NGGQCRPNVVG 780	
Db	742	NSRSVVKTPMTD	VCRNII	IFSI	SALI	HQTGLACE	DPQGSLSVCDP	NGGQCRPNVVG 801
QY	781	TGNRCAPGTF	FGPGSGCKPCE	CHLQGS	VNAFCNPVTG	QCHCFQGVYAR	QCDRCLPGHWGF 840	
Db	802	TGNRCAPGTF	FGPGSGCKP	CDCHLQGS	AFCD	AITGQCHCFQGI	YARQCDRCLPGYWG 861	
QY	841	PSCQPCQCNGH	ADDCDPVT	GECLNCQDY	TMGHNC	BRCLAGYGDPI	IGSGDHCRPCPCPD 900	
Db	862	PSCQPCQCNGH	ALDCDVT	GECLSCQDY	TTGHNC	BRCLAGYGDPI	IGSGDHCRPCPCPD 921	
QY	901	GPSGGRQFAR	SCYQDPVT	LQACVCDP	PGYIG	SRCDDCASGYFG	GNPSEVGSCQPCQCHN 960	
Db	922	GPSGGRQFAR	SCYQDPVT	LQACVCDP	PGYIG	SRCDDCASGFF	GNPSDFGSGCQPCQCHN 981	
QY	961	IDTTDPEACD	KETGRCLKCLY	HTEGEHCQ	CFRFGY	GDALRQD	CRKVCVNLGTVOEHCN 1020	
Db	982	IDTTDPEACD	KETGRCLKCLY	HTEGDH	CQLCQY	GYGDALRQD	CRKVCVNLGTVOEHCN 1041	
QY	1021	GSDCQCDKAT	GQCICLP	PNVIGQNC	DRCAPNTW	QLASGTGCD	PCNCAAHSFGPSCNEFTG 1080	

Db	1042																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
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RESULT 3
LMB2 RAT
ID LMB2 RAT STANDARD; PRT; 1801 AA.
AC P15800;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Laminin beta-2 chain precursor (S-laminin) (Laminin chain B3).
GN LAMB2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89159410; PubMed=2922051;
RA Hunter D.D., Shah V., Merlie J.P., Sanes J.R.;
RT "A laminin-like adhesive protein concentrated in the synaptic cleft of the neuromuscular junction."
RL Nature 338:229-234 (1989).

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:28 ; Search time 47.8797 Seconds
(without alignments)
11631.021 Million cell updates/sec

Title: US-10-037-182-8
Perfect score: 9654
Sequence: 1 QEPFSYGAEGSCYPATGD.....EVRSLKDISQKAVYSTCL 1765

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	6794	70.4	1785	13 Q8JHV7	Q8jlv7 brachydanio
2	5808	60.2	1086	4 Q8TAS6	Q8tas6 homo sapien
3	5321	55.1	1792	13 Q57484	Q57484 gallus gall
4	5059	52.5	1799	11 Q8R0Y0	Q8r0y0 mus musculu
5	4891	50.7	984	11 Q8K271	Q8k271 mus musculu
6	4527	46.9	911	11 Q9CRX6	Q9crx6 mus musculu
7	3832.5	39.7	1761	4 Q86XN2	Q86xn2 homo sapien
8	3785.5	39.2	1827	13 Q8JHV6	Q8jlv6 brachydanio
9	3625.5	37.6	1631	4 Q9Y6U6	Q9y6u6 homo sapien
10	2835	29.4	1067	5 Q44565	Q44565 caenorhabdi
11	2297.5	23.8	1168	5 Q967S8	Q967s8 schistocerc
12	2034	21.1	761	4 Q9UHI2	Q9uhi2 homo sapien
13	1921	19.9	1026	5 Q8SWY0	Q8swy0 drosophila
14	1847	19.1	1069	5 Q9BPS2	Q9bps2 bombyx mori
15	1729.5	17.9	3704	5 P91904	P91904 caenorhabdi
16	1684.5	17.4	1593	13 Q8JHV8	Q8jlv8 brachydanio

17	1674.5	17.3	1623	5 Q9U3U7	Q9u3u7 anopheles g
18	1633	16.9	3712	5 Q9VRW0	Q9vrw0 drosophila
19	1564.5	16.2	3695	4 Q8TDF8	Q8tdf8 homo sapien
20	1491.5	15.4	1168	11 Q91V90	Q91v90 mus musculu
21	1380	14.3	1007	13 Q90ZN3	Q90zn3 gallus gall
22	1307.5	13.5	3102	5 Q45614	Q45614 caenorhabdi
23	1217	12.6	2731	5 Q9VJT5	Q9vjt5 drosophila
24	1217	12.6	3367	5 Q9XZC9	Q9xzc9 drosophila
25	1217	12.6	3375	5 Q8IP51	Q8ip51 drosophila
26	1101.5	11.4	1546	4 Q9NS27	Q9ns27 homo sapien
27	1099.5	11.4	1546	4 Q75445	Q75445 homo sapien
28	1064	11.0	1486	4 Q14637	Q14637 homo sapien
29	1041.5	10.8	1461	11 Q9JLP3	Q9jlp3 mus musculu
30	1040	10.8	750	4 Q86TP7	Q86tp7 homo sapien
31	1001.5	10.4	616	4 Q15483	Q15483 homo sapien
32	1001	10.4	628	11 Q9J133	Q9j133 mus musculu
33	993	10.3	628	4 Q9HB63	Q9hb63 homo sapien
34	991	10.3	628	4 Q9BZP1	Q9bzp1 homo sapien
35	975	10.1	605	4 Q7Z5B6	Q7z5b6 homo sapien
36	964	10.0	1512	11 Q8K3K1	Q8k3k1 rattus norv
37	889	9.2	1190	6 Q8HZI9	Q8hzi9 equus cabal
38	880	9.1	1196	6 Q867A2	Q867a2 canis famil
39	695.5	7.2	604	11 Q924Z9	Q924z9 rattus norv
40	680	7.0	1664	5 Q9TVQ2	Q9tvq2 caenorhabdi
41	678.5	7.0	569	13 Q57339	Q57339 xenopus lae
42	678	7.0	602	13 Q42203	Q42203 brachydanio
43	675.5	7.0	529	4 Q8N2D6	Q8n2d6 homo sapien
44	674	7.0	603	13 Q42140	Q42140 brachydanio
45	669.5	6.9	1574	11 Q88281	Q88281 rattus norv

ALIGNMENTS

RESULT 1
Q8JHV7
ID Q8JHV7 PRELIMINARY; PRT; 1785 AA.
AC Q8JHV7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Laminin beta 1.
GN LAMB1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22065263; PubMed=12070089;
RA Parsons M.J., Pollard S.M., Saude L., Feldman B., Coutinho P.,
RA Hirst E.M., Stemple D.L.;
RT "Zebrafish mutants identify an essential role for laminins in
RT notochord formation."
RL Development 129:3137-3146(2002).
DR EMBL; AF48049; AAM61767.1;...
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR008211; LamNT.
DR Pfam; PF00053; laminin_EGF; 13.
DR Pfam; PF00055; laminin_Nterm; 1.
DR PRINTS; PR00011; EGFLAMININ.
DR SMART; SM00180; EGF_Lam; 13.
DR SMART; SM00136; LamNT; 1.
DR PROSITE; PS00022; EGF_1; 10.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 12.
KW Laminin EGF-like domain.
SQ SEQUENCE 1785 AA; 197279 MW; 1BD338A0B6AB9F26 CRC64;

Query Match				70.4%;	Score 6794;	DB 13;	Length 1785;
Best Local Similarity				67.3%;	Pred. No. 1.4e-288;		
Matches 1189;				Conservative 253;	Mismatches 319;	Indels 6;	Gaps 6;
QY	3	PEPSYGCAEGSCYPATGDLIIIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICNSQD	62				
Db	20	PELGDVCTEGSCYPATGDLIIIGRAQQLLATSTCGVHKPEPFPCIVSHLQEEKCFVCDSRQ	79				
QY	63	PYHETLNP-DSHLIENVVTFAPNRLKIWQSENGVENVTIQLDLAEFHFTHLIMTFKT	121				
Db	80	AYNETAHQVTSHSIENVVTFAPNRLKIWQSENGLENVTIQLDLAEFHFTHLIMTFKT	139				
QY	122	FRPAAMLIERSSDFGKTGWVYRYFAYDCEASPPGISTGPMKKVDDIICDSRYSDIEPSTE	181				
Db	140	FRPAAMVIERSADFGNTWQVYRYFAYDCESSPFVSHGPMTKVDVDCDTRYSDIEPSTE	199				
QY	182	GEVIFRALDPAFKIEDPSPRIQNLLKITNLRIKPVKLHTLGDNLDSRMEIREKYYIAY	241				
Db	200	GEVIFRVLDPAFRIEDPSPRIQNMLKITNLRVKFTKLHTLGDNLDSRIEIKEKYYIAY	259				
QY	242	YDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGCMCRHNTKGLNCELCMDYFHDLPWR	301				
Db	260	YDMVVRGNCFCYGHASECAPVDGTGEAVEGMVHGCMCNHNTIGLNCERCQDFYHDLPLWR	319				
QY	302	PABGRNSNACKKCNNEHSISCHFDMAVYLATGNVSGGVCDCCQHNTWGRNCEQCKPFYY	361				
Db	320	PABGRNTNACKKCHCNHSHSCHFDMAVYRASGNVSGGVCDCCQHNTWGRNCEQCKPFFH	379				
QY	362	QHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSTGLIAGQCRCKLNVEGEHCDVCKE	421				
Db	380	QHPEKDIRDPNICEPCNCDPVGSLNGGVCDPMTDVSGLISGQCRCKPNVEGERCDQCKQ	439				
QY	422	GFYDLSSDPFGCKSCACNPLGTIPGPNPCDSETHCYCKRLVTGQHCDQCLPEHWGLSN	481				
Db	440	GHYGL-SEDPLGCPCTCNALGTVPGGSPCDTDSGNCYCKRLVTGRNCDQCLPQHWGLSN	498				
QY	482	DLDGCRPCDCLGGLANNSCFAESGQCSCRPHMIGRCNEVEPGYYFATLDHYLYAEAEA	541				
Db	499	DMGCRPCDCHGGAINNNSCPVSGQCQCREHMFGRCDQVESGFYFIALDHYTYAEAEA	558				
QY	542	NLGPVSVIVERQYIQDIRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLPD	601				
Db	559	KFGPGVTVVPRNHQDRSPPTWTGIGFVNVPEGAFLFESIDNIPYSMEYDILIRYEPQLPE	618				
QY	602	HWEKAVITVQRPGRIPTRSSRCGNTIPDDNQVWSLSPGSRYVWLPRPVCFEKGTNYTVRL	661				
Db	619	QWEEVLMTVIRPRVITADSRCAANTMPDDNQMVSLHPSGRYVWLPRPVCFEGLNYTVRL	678				
QY	662	ELPQYTSDDSDVESPYTLIDSLVLMYPYCKSLDIFTVGGGSDGVVWTSNASETFRQYRCLE	720				
Db	679	SLSLY-SALSDVQSPYTLIDSLVLMYPYCKSLDIFTVGGGSDGVVWTSNASETFRQYRCLE	737				
QY	721	NSRSVVKTPMTDVCRNIIIFSISALLHOTGLACECDPQSSLSVCDPNGGQCQCRPNVVG	780				
Db	738	NSQAVVKTPTMTDVCRNIIIFSISALLHOTGLACECDPQSSLSVCDPNGGQCQCRPNVVG	797				
QY	781	TCNRCAPGTGFGPGSGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDCRCLPGHWGF	840				
Db	798	NCDRCAPATFLFXPQGRPCDCSPGSHVSYCHEATGQCECIAGAYGRQCDCRCLPGYWG	857				
QY	841	PSCQPCQCNCHADDCDPTVTGECNLNQDYMTHNCCERCLAGYGDPIIGSGDHCPCCPD	900				
Db	858	PNCRPCTCNHAEQCDPQTGQCLSCRDHTTGHNCERCLGGYGDPIIGSGDHCPCCPD	917				
QY	901	GPDSGRQFARSCYQDPVTTLQACVCDPVGIGSRCDCCASGFGNPSFVGGSCQPCQCHNN	960				
Db	918	GPDSGRQFARSCYQDPVTTLQACVCDPVGIGSRCDCCASGFGNPSFVGGSCQPCQCHNN	977				
QY	961	IDTTPDPEACDKETGRCLKLYHTEGEHCQCFRFGYVGDALRQDCRCKVCNVLGTVEHC-	1019				
Db	978	IDMDPESCDARTGACVKCLYHTEGESNCRCLGYGNALYQSCRKVCNQMGTVEEMCP	1037				
QY	1020	NGSDCCQCDKATGQCLPLPNVIGQNCRCRCAPTWQLASGTGCDPCNCAHSGFPGSCNEFT	1079				

RESULT 2			
Q8TAS6	PRELIMINARY; PRT; 1086 AA.		
ID	Q8TAS6		
AC	Q8TAS6;		
DT	01-JUN-2002 (TrEMBLrel. 21, Created)		
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)		
DE	Similar to laminin, beta 1 (Fragment).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Muscle;		
RA	Strausberg R.;		
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBSJ databases.		
DR	EMBL; BC026018; AAH26018.1; -.		
DR	GO; GO:0005198; F:structural molecule activity; IEA.		
DR	InterPro; IPR006209; EGF like.		
DR	InterPro; IPR002049; Laminin_EGF.		

Db	1739	ELARLEGEVRSLLKDISQKVAVYSTCL	1765
Db	1758	ELVDLEKAVKELLQEIHSKVTYVYSTCL	1784

QY	1038	SPGNCNCDLTSGQCLCLPNVVGQHCDCAPDTWNMASGKGCEDCDPNHSGSSCNEIM	1097
QY	1080	GQCQCMPPGFGGRTCSCEQLFWGDDPDVECRACDCDPRGIETPQCDSFGQCVCEGVEGP	1139
Db	1098	GQCSCKPGFGGRTCRECRELFWGNPEVKCHACDCDPRGIAEQQCNKVTGHCVCVEGSGP	1157
QY	1140	RCDKCTRGYSGVFPDCTPCHQCFAFDWVIAELTNRTHRFLEKAKALKISGVIGPYRET	1199
Db	1158	RCDTCARGYTGEFPQCHQCFAEWDDIIVGLDNTQTHRLVQKVNTIKATGITPYQATI	1217
QY	1200	DSVERKVSEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDVTEMMAQVEVKLSDTTSQSN	1259
Db	1218	NNVENSANSIRNILAQNPAQPLTEIQGLLEQATALMAEMNSNLNLTTELTSEISSD	1277
QY	1260	TAKELDSLOTEAESLDNTVKELAEQLEFIKNSDIRGALDSDITKYFQMSLEAEERVNAST	1319
Db	1278	TDTKLKSLKEEAQKLEQTVKDLREQVEFVNKSDIRGARASVTRYEYEQSNAEIRANAST	1337
QY	1320	EPNSTVEQSALMRDVEDVMMERESQFKEKEEQEQAARLLDELAKLQSLDLSAAAE	1379
Db	1338	DPYNLVNQSATLRTETEELMNQTKKEFNQRFQFSSKLDNLAGQLETLDELSELSEK	1397
QY	1380	PPGA-SCSETECGGPNCRDTEGERKCGGPGGLVTVAHNAWQAKMDLDQDVL	1438
Db	1398	PAGSENCADSRGGLSCVDMQSGRKCQGGEGCDGLTTLAHNAWQAKAKDFLEISAMEE	1457
QY	1439	QLSKMVSEAKLRADAEAKQSAEDILLKTNATKEKMDKSNEELRNLIKQIRNFLTQDSAD	1498
Db	1458	KLKSKMVSEAKVKADEAKLNAQEVLAQTNKTRVDSNEELRLQIKQIRDFLTQDGADLE	1517
QY	1499	SIEAVANEVLKMEMPTPQQLQNLTEDIRERVESLSQVEVILQHSAAADIARAEMLL	1558
Db	1518	SIEAVANEVLQMQMPTTPAQQLQNLTEIRERVSGLTDVEDILNQSAADILRAESLLEQ	1577
QY	1559	RASKSATDVKVTADMVKEALEEAEAKQAAEKAQADEDIQGTQNLTSIESETAASEE	1618
Db	1578	KARKEASDVKSTAEVMVKEALQHAERAQNSVAEALQAAVDIKGTQDLLVSVESETSD	1637
QY	1619	TLFNASQRISELERNVVEELKRAAQNNGEAEYIEKVYTVKQSAEDVKKTLDCGELDEK	1678
Db	1638	KLNATRRLLKLESDVALLKEKALNTSISANSTEXEAEINALEQKKDLDELSELKOKYS	1697
QY	1679	KVENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLLKOLKERYEDNQRYLEDKAQ	1738
Db	1698	TVEELITQKAEGVAEAKKGAELQEEARNLLQASEKLLKNLEKNYDQNKLLKEDKAN	1757

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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:25:32 ; Search time 48.4494 Seconds
(without alignments)
10415.614 Million cell updates/sec

Title: US-10-037-182-10
Perfect score: 9758
Sequence: 1 MGLLQVFAFGVLALWGTRVC.....EVRSLKDISKVAVYSTCL 1786

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query			DB ID	Description
	Score	Match	Length		
1	9758	100.0	1786	3 AAB19799	Aab19799 Mouse lam
2	9758	100.0	1786	3 AAB48450	Aab48450 Mouse lam
3	9758	100.0	1786	5 ABB81592	Abb81592 Mouse lam
4	9692	99.3	1776	2 AAW50894	Aaw50894 Mouse lam
5	9517.5	97.5	1764	1 AAP91672	Aap91672 Primary a
6	9429	96.6	1725	3 AAB19800	Aab19800 Mouse lam
7	9429	96.6	1725	3 AAB48451	Aab48451 Mouse lam
8	9429	96.6	1725	5 ABB81593	Abb81593 Mouse lam
9	9144	93.7	1786	2 AAW50893	Aaw50893 Human lam
10	9144	93.7	1786	3 AAB16522	Aab16522 Human lam
11	9144	93.7	1786	3 AAB19797	Aab19797 Human lam
12	9144	93.7	1786	3 AAB48448	Aab48448 Human lam
13	9144	93.7	1786	4 AAB90788	Aab90788 Human she
14	9144	93.7	1786	5 ABB81590	Abb81590 Human lam
15	9131	93.6	1786	5 AAM48896	Aam48896 Laminin p
16	9108.5	93.3	1785	2 AAY15461	Aay15461 Human lam
17	9092	93.2	1765	3 AAB19798	Aab19798 Human lam
18	9092	93.2	1765	3 AAB48449	Aab48449 Human lam
19	9092	93.2	1765	5 ABB81591	Abb81591 Human lam
20	5087.5	52.1	1801	2 AAW50895	Aaw50895 Rat lamin
21	5087.5	52.1	1801	7 ADE60383	Ade60383 Rat Prote
22	5066.5	51.9	1799	5 AAM50359	Aam50359 Mouse lam
23	5031.5	51.6	1798	2 AAW50896	Aaw50896 Human lam
24	5031.5	51.6	1798	7 ADE60385	Ade60385 Human Pro
25	4902	50.2	1798	5 AAU84346	Aau84346 Protein L

26	4902	50.2	1798	5 AAM50360	Aam50360 Human lam
27	3861.5	39.6	1788	4 ABB62995	Abb62995 Drosophil
28	3813.5	39.1	1761	2 AAY15457	Aay15457 Human lam
29	3616	37.1	822	5 AAM48897	Aam48897 Laminin p
30	3610	37.0	1670	7 ADE07851	Ade07851 Novel pro
31	3068.5	31.4	1101	7 ADE28641	Ade28641 Human NOV
32	3046.5	31.2	1105	2 AAY15459	Aay15459 SEQ ID 5
33	2640	27.1	466	2 AAR07447	Aar07447 Human lam
34	2154	22.1	527	3 AAB58995	Aab58995 Breast an
35	1940	19.9	434	1 AAP60109	Aap60109 Human Bl
36	1708	17.5	1639	4 ABB59807	Abb59807 Drosophil
37	1681	17.2	315	6 ABU70520	Abu70520 Human adi
38	1671	17.1	3712	4 ABB64954	Abb64954 Drosophil
39	1661.5	17.0	1572	3 AAB19806	Aab19806 Mouse lam
40	1661.5	17.0	1572	3 AAB48455	Aab48455 Mouse lam
41	1661.5	17.0	1572	5 ABB81597	Abb81597 Mouse lam
42	1661.5	17.0	1605	3 AAB19805	Aab19805 Mouse lam
43	1661.5	17.0	1605	3 AAB48454	Aab48454 Mouse lam
44	1661.5	17.0	1605	5 ABB81596	Abb81596 Mouse lam
45	1651	16.9	1609	3 AAB19801	Aab19801 Human lam

ALIGNMENTS

RESULT 1
AAB19799
ID AAB19799 standard; protein; 1786 AA.
XX
AC AAB19799;
XX
DT 05-MAR-2001 (first entry)
XX
DE Mouse laminin 2 beta-1 chain.
XX
KW Laminin 2; mouse; nerve regeneration; angiogenic; cell adhesion;
KW degenerative muscle disorder; muscular dystrophy; cell therapy.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Peptide 1..21 /label= Signal_peptide
FT Protein 22..1786 /label= Mature_protein
FT
XX
PN WO200066730-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US011378.
XX
PR 30-APR-1999; 99US-0131720P.
PR 15-JUN-1999; 99US-0139198P.
PR 12-JUL-1999; 99US-0143289P.
PR 24-SEP-1999; 99US-0155945P.
XX
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
PI Yurchenco P;
XX
DR WPI; 2000-687537/67.
DR N-PSDB; AAB88899.
XX
PT Purified laminin 2 protein, useful for research and therapeutic purposes
PT including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.
XX
PS Claim 5; Page 212-218; 305pp; English.
XX
CC The present sequence is that of the beta-1 chain of mouse laminin 2.
CC Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1
CC (100 kDa) chains. It is thought to be specifically required for

CC stabilizing myotubes during skeletal muscle development, and for
CC preventing apoptosis. Genetic defects in human laminin 2 structure or
CC expression are associated with a major type of congenital muscular
CC dystrophy. Laminin 2 is also thought to be important in Schwann
CC cell/basal lamina interactions. The invention provides laminin 2 alpha-2,
CC beta-1 and gamma-1 chain polypeptides (see AAB19791-806) and the
CC polynucleotides encoding them (see AAA8891-906), methods for making
CC recombinant laminin 2, cells that express recombinant laminin 2, and
CC methods for using purified laminin 2 for research and therapeutic
CC purposes including peripheral nerve regeneration, treatment of
CC degenerative muscle disorders, and angiogenesis regulation, promoting cell
CC attachment and migration, ex vivo cell therapy, improving the take of
CC grafts, improving the biocompatibility of medical devices and preparing
CC improved culture devices and media
XX

SQ Sequence 1786 AA;

Query Match 100.0%; Score 9758; DB 3; Length 1786;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLLQVFAFGVIALWGRVCAQEPESYGAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60
Db 1 MGLLQVFAFGVIALWGRVCAQEPESYGAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60
QY 61 PEPYCIIVSHLQEDKKCFICDSRDPYHETINPDSHLIENVVTFAPNRLKIWQSENGVEN 120
Db 61 PEPYCIIVSHLQEDKKCFICDSRDPYHETINPDSHLIENVVTFAPNRLKIWQSENGVEN 120
QY 121 VTIOLDLEAEFHTLIMTFKTRPAAMLIERSDDFGKTGWVRYFAYDCESFPFGISTG 180
Db 121 VTIOLDLEAEFHTLIMTFKTRPAAMLIERSDDFGKTGWVRYFAYDCESFPFGISTG 180
QY 181 PMKKVDDIIICDSRYSIDIEPSTEGEVIFRALDPFAFKIEDPYSPIQNLLKITNLRIFVKL 240
Db 181 PMKKVDDIIICDSRYSIDIEPSTEGEVIFRALDPFAFKIEDPYSPIQNLLKITNLRIFVKL 240
QY 241 HTLGDNLDSRMEIREKYYYAYVDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMC 300
Db 241 HTLGDNLDSRMEIREKYYYAYVDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMC 300
QY 301 RHNTKGLNCELMDPFYHDLWPRAEGRNSNACKKNCNEHSSSCHDFDPAFLATGNVSGG 360
Db 301 RHNTKGLNCELMDPFYHDLWPRAEGRNSNACKKNCNEHSSSCHDFDPAFLATGNVSGG 360
QY 361 VCDNCQHNTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVG 420
Db 361 VCDNCQHNTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVG 420
QY 421 LIAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGPNPCDSETGYCY 480
Db 421 LIAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGPNPCDSETGYCY 480
QY 481 CKRLVTGQRCDQCLPQHGLSNDLDGCRPCDCLGGALNNSCEDSGQCSCLPHMIGRQC 540
Db 481 CKRLVTGQRCDQCLPQHGLSNDLDGCRPCDCLGGALNNSCEDSGQCSCLPHMIGRQC 540
QY 541 NEVESGYFTTLDHYIYEAEANLPGVVVVERQYIQDRIPSWTGPGRVVRVPEGAYLEFF 600
Db 541 NEVESGYFTTLDHYIYEAEANLPGVVVVERQYIQDRIPSWTGPGRVVRVPEGAYLEFF 600
QY 601 IDNIPYSMEYEILIRVEPQLPDHWEKAVITVQRPCKIPASSRRCGNTVPDDNQVWSLSPG 660
Db 601 IDNIPYSMEYEILIRVEPQLPDHWEKAVITVQRPCKIPASSRRCGNTVPDDNQVWSLSPG 660
QY 661 SRYVVLPRPVCFEKGMNVTVRLELPQYTAGSDVESPYTFIDSLVLMPCYCKSLDIFTVGG 720
Db 661 SRYVVLPRPVCFEKGMNVTVRLELPQYTAGSDVESPYTFIDSLVLMPCYCKSLDIFTVGG 720
QY 721 SGDGEVTNSAWETFORYRCLENSRSVVKTPMTDVCRNIIIFSISALIHQTGLACECDPQGS 780
Db 721 SGDGEVTNSAWETFORYRCLENSRSVVKTPMTDVCRNIIIFSISALIHQTGLACECDPQGS 780

RESULT 2
AAB48450
ID AAB48450 standard; protein; 1786 AA.
XX

QY 781 LSSVCDPNGGQCQCRPNVVGRTCNRCAPGTGFGPNGCKPCDCHLQGSASAFCDAITQC 840
Db 781 LSSVCDPNGGQCQCRPNVVGRTCNRCAPGTGFGPNGCKPCDCHLQGSASAFCDAITQC 840
QY 841 HCFQGIYARQCDRCLPGYWGFPSPCQCNGHALDCDVTGECCLSCQDYTTGHNCRCLA 900
Db 841 HCFQGIYARQCDRCLPGYWGFPSPCQCNGHALDCDVTGECCLSCQDYTTGHNCRCLA 900
QY 901 GYGDPIIGSGDHCRCPCPCPDGSDGRQFARSCYQDPVTQLACVCDPGYIGSRCDCCAS 960
Db 901 GYGDPIIGSGDHCRCPCPCPDGSDGRQFARSCYQDPVTQLACVCDPGYIGSRCDCCAS 960
QY 961 GFFGNPSDFGSGCQPCQCHHNIDTTDPEACDKDTGRCLKCLYHTEGDHCQLCQYGYGDA 1020
Db 961 GFFGNPSDFGSGCQPCQCHHNIDTTDPEACDKDTGRCLKCLYHTEGDHCQLCQYGYGDA 1020
QY 1021 LRQDCRKVCNVLGTVKEHCNGSDCHCDKATGQCSCLPNVIGONCDRCAPNTWQLASGTG 1080
Db 1021 LRQDCRKVCNVLGTVKEHCNGSDCHCDKATGQCSCLPNVIGONCDRCAPNTWQLASGTG 1080
QY 1081 CGPCNCAHSGFSPSCNEFTGQCQCMPFGGRTCECQELFWGDPDVECRACDCDPRGIE 1140
Db 1081 CGPCNCAHSGFSPSCNEFTGQCQCMPFGGRTCECQELFWGDPDVECRACDCDPRGIE 1140
QY 1141 TPQCDQSTGQVCVEGVEGPRCDKCTRGYSGVFPDCTPCHQCFALWDAIIGELTNRTHKF 1200
Db 1141 TPQCDQSTGQVCVEGVEGPRCDKCTRGYSGVFPDCTPCHQCFALWDAIIGELTNRTHKF 1200
QY 1201 LEKAKALKISGVIGPYRETVDSEKKNVNEIKDILAQSPAAPLKNIGILFEEAEKLTADV 1260
Db 1201 LEKAKALKISGVIGPYRETVDSEKKNVNEIKDILAQSPAAPLKNIGILFEEAEKLTADV 1260
QY 1261 TEKMAQVEVKLTDTASQSNSTAGELGALQAEASLDKTVKELAEQLEFIKNSDIQALDS 1320
Db 1261 TEKMAQVEVKLTDTASQSNSTAGELGALQAEASLDKTVKELAEQLEFIKNSDIQALDS 1320
QY 1321 ITKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLESPFKEQEEQARLLDE 1380
Db 1321 ITKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLESPFKEQEEQARLLDE 1380
QY 1381 LAGKLSLDLSAAAQMTCTGTPPGADCESECGGPNCRDTDEGEKCGGPGCGGLVTVHSA 1440
Db 1381 LAGKLSLDLSAAAQMTCTGTPPGADCESECGGPNCRDTDEGEKCGGPGCGGLVTVHSA 1440
QY 1441 WQKAMDFDRDVLALAEVEQLSKMVSEAKVRADEAKQNAQDVLKTNATKEKVDKSNEDL 1500
Db 1441 WQKAMDFDRDVLALAEVEQLSKMVSEAKVRADEAKQNAQDVLKTNATKEKVDKSNEDL 1500
QY 1501 RNLIKQIRNFLTEDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVI 1560
Db 1501 RNLIKQIRNFLTEDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVI 1560
QY 1561 LQQAADIAARAEELLEAEAKRASKSATDVKVTADMVKEALEEAEKAQVAAEKAIKQADEDI 1620
Db 1561 LQQAADIAARAEELLEAEAKRASKSATDVKVTADMVKEALEEAEKAQVAAEKAIKQADEDI 1620
QY 1621 QGTQNLITSIESETAASEETLTNASQRIKSLERNVEELKRKAQNSGEAEYIEKVVSVK 1680
Db 1621 QGTQNLITSIESETAASEETLTNASQRIKSLERNVEELKRKAQNSGEAEYIEKVVSVK 1680
QY 1681 QNADDVKKTLDGELDEKVKVESLIAQKTEESADARRKAELLQNEAKTLLAQANSKLQLL 1740
Db 1681 QNADDVKKTLDGELDEKVKVESLIAQKTEESADARRKAELLQNEAKTLLAQANSKLQLL 1740
QY 1741 EDLERKYEDNQKYLEDKAQLVRLGEVRSLLKDISEKVAVYSTCL 1786
Db 1741 EDLERKYEDNQKYLEDKAQLVRLGEVRSLLKDISEKVAVYSTCL 1786

AC AAB48450;
XX
DT 02-MAR-2001 (first entry)
XX
DE Mouse laminin 8 polypeptide, SEQ ID NO: 18.
XX
KW Mouse; laminin 8; neuroprotective; angiogenic; osteopathic;
KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;
KW vascular tissue injury; neural injury; angiogenesis regulation.
XX
OS Mus musculus.
XX
PN WO200066732-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US011543.
XX
PR 30-APR-1999; 99US-0131720P.
PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.
PR 11-FEB-2000; 2000US-0182012P.
XX
PA (BIOS-) BIOSTRATUM INC.
XX
XX Kortessmaa J, Tryggvason K;
PI
XX
DR WPI; 2000-687539/67.
DR N-PSDB; AAC83711.
XX
PT Purified laminin 8 protein, useful for research and therapeutic purposes
PT including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.
XX
PS Claim 5; Page 176-182; 245pp; English.
XX
CC The present sequence is a laminin 8 polypeptide chain. Laminins are a
CC family of heterotrimeric glycoproteins that function via binding
CC interactions with neighbouring cell receptors and by forming laminin
CC networks. They are signalling molecules which influence cellular
CC function. Laminin 8 is useful for treating injuries to tissue of
CC mesenchymal origin, such as bone, cartilage, tendon, and ligament,
CC treating injuries to vascular tissue, promoting cell attachment and
CC migration, ex vivo cell therapy, improving the biocompatibility of
CC medical devices, and preparing improved cell culture devices and media.
CC Laminin 8 is also useful for promoting re-endothelialisation at the site
CC of vascular injuries, improving the take of grafts, improving the
CC biocompatibility of medical devices, treating neural injuries (neural
CC regeneration), regulating angiogenesis, and promoting cell attachment and
CC migration
XX
SQ Sequence 1786 AA;

Query Match 100.0%; Score 9758; DB 3; Length 1786;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLQVFAFGVLALWGTRVCAQEPFESYGCAGSCYPATGDLIGRAQKLSVTSTCGLHK 60
Db 1 MGLQVFAFGVLALWGTRVCAQEPFESYGCAGSCYPATGDLIGRAQKLSVTSTCGLHK 60

Qy 61 PEPYCIIVSHLQEDKKCFICDSRDYPYHETLNPDNPSHLIENVVTTTFAPNRLKIWWQSENGVEN 120
Db 61 PEPYCIIVSHLQEDKKCFICDSRDYPYHETLNPDNPSHLIENVVTTTFAPNRLKIWWQSENGVEN 120

Qy 121 VTIQDLLEAEFHTLIMTFKTRPAAMLIERSDFTGKTGWVRYFYAYDCSSFPFGISTG 180
Db 121 VTIQDLLEAEFHTLIMTFKTRPAAMLIERSDFTGKTGWVRYFYAYDCSSFPFGISTG 180

Qy 181 PMKKVDDIIICDSRYSDIEPSTEGEVIFRALDPAPFKIEDPSPRIQNLLKITNLRKIFVKL 240
Db 181 PMKKVDDIIICDSRYSDIEPSTEGEVIFRALDPAPFKIEDPSPRIQNLLKITNLRKIFVKL 240

Qy 241 HTLGDNLLDSRMEIREKYYAYVDMVVRGNCFYGHASECAPVDGVNEEVGMVHGHC 300
Db 241 HTLGDNLLDSRMEIREKYYAYVDMVVRGNCFYGHASECAPVDGVNEEVGMVHGHC 300

Qy 301 RHNTKGLNCELMDFYHDLPRPAEGRNSNACKKNCNEHSSSCHFDMAVFLATGNVSGG 360
Db 301 RHNTKGLNCELMDFYHDLPRPAEGRNSNACKKNCNEHSSSCHFDMAVFLATGNVSGG 360

Qy 361 VCDNCQHNTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVG 420
Db 361 VCDNCQHNTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVG 420

Qy 421 LIAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGGNPCDSETGYCY 480
Db 421 LIAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGGNPCDSETGYCY 480

Qy 481 CKRLVTGQRCDQCLPOHWGLSNDLDGCRPCDCLGGALNNSCEDSGQCSCLPHMIGRQC 540
Db 481 CKRLVTGQRCDQCLPOHWGLSNDLDGCRPCDCLGGALNNSCEDSGQCSCLPHMIGRQC 540

Qy 541 NEVESGYFTTLDHYIYEAEANLPGVVVVERQYIQDRIPSWTGPFGFVRVPEGAYLEFF 600
Db 541 NEVESGYFTTLDHYIYEAEANLPGVVVVERQYIQDRIPSWTGPFGFVRVPEGAYLEFF 600

Qy 601 IDNIPYSMEYEILIRYEPQLPDHWEKAVITVQRPKIPASSRCNGTVPDDDNQVVSLSPG 660
Db 601 IDNIPYSMEYEILIRYEPQLPDHWEKAVITVQRPKIPASSRCNGTVPDDDNQVVSLSPG 660

Qy 661 SRYVLP RPVCFEKGMNVTYVLELPQYTASGSDVESPYTFIDSLVLMYPYCKSLDIFTVGG 720
Db 661 SRYVLP RPVCFEKGMNVTYVLELPQYTASGSDVESPYTFIDSLVLMYPYCKSLDIFTVGG 720

Qy 721 SGDEVTNSAWETFORYRCLENSRSVVKTPMTDVCRNIIFISALIHQTGLACECDPQGS 780
Db 721 SGDEVTNSAWETFORYRCLENSRSVVKTPMTDVCRNIIFISALIHQTGLACECDPQGS 780

Qy 781 LSSVCDPNGGQCQCRPNVVGRTCNRCAPGTFGFGNGCKPCDCHLQGSASAFDAITGQC 840
Db 781 LSSVCDPNGGQCQCRPNVVGRTCNRCAPGTFGFGNGCKPCDCHLQGSASAFDAITGQC 840

Qy 841 HCFQGIYARQCDRCLPGYWGFPSPCQPCQNGHALDCDVTGECSCQDYTTGHCERCLA 900
Db 841 HCFQGIYARQCDRCLPGYWGFPSPCQPCQNGHALDCDVTGECSCQDYTTGHCERCLA 900

Qy 901 GYVGDPIIGSGDHCRPCPCPDGSDSGRQFARSCYQDPVTQLACVCDPGYIGSRCDDCAS 960
Db 901 GYVGDPIIGSGDHCRPCPCPDGSDSGRQFARSCYQDPVTQLACVCDPGYIGSRCDDCAS 960

Qy 961 GFFGNPSDFGGSCQPCQCHNIDTTPDPEACDKDTGRCLKLYHTEGDHQCQLCYGYGDA 1020
Db 961 GFFGNPSDFGGSCQPCQCHNIDTTPDPEACDKDTGRCLKLYHTEGDHQCQLCYGYGDA 1020

Qy 1021 LRQDCKKVCNLYLGTVKEHNGSDCHCDKATGQCCLPNVIGQNCDRCAPNTWQLASGTG 1080
Db 1021 LRQDCKKVCNLYLGTVKEHNGSDCHCDKATGQCCLPNVIGQNCDRCAPNTWQLASGTG 1080

Qy 1081 CGPCNCAAAHSFGPSCNEFTGQCQCMFGGRTCSSECQELFWGDPDVECRACDCDPRGIE 1140
Db 1081 CGPCNCAAAHSFGPSCNEFTGQCQCMFGGRTCSSECQELFWGDPDVECRACDCDPRGIE 1140

Qy 1141 TPQCDQSTGQCVCVEGVEGPRCDKCTRGYSVGFPPDCTPCHQCFCALWDIAIIGELTNRTHKF 1200
Db 1141 TPQCDQSTGQCVCVEGVEGPRCDKCTRGYSVGFPPDCTPCHQCFCALWDIAIIGELTNRTHKF 1200

Qy 1201 LEKAKALKISGVIQPYRETVDSEKKNVEIKDILAQSPAAEPLKNIIGILFEEAEKLTQDV 1260
Db 1201 LEKAKALKISGVIQPYRETVDSEKKNVEIKDILAQSPAAEPLKNIIGILFEEAEKLTQDV 1260

Qy 1261 TERMAQVEVKLTDTASQSNSTAGELGALQAEAESLDKTVKELAEQLEFIKNSDIQGALDS 1320
Db 1261 TERMAQVEVKLTDTASQSNSTAGELGALQAEAESLDKTVKELAEQLEFIKNSDIQGALDS 1320

Qy 1321 ITRYFQMSLEAEKRVNASITDPNSTVEQSALTDRDRVEDLMLERESPFEKEQEEQARLLDE 1380

Db 1321 ITKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLERESPFEKQEEQARLLDE 1380
QY 1381 LAGKLSLDLSAAQMTCTGTPPGADCSESECGGPNCRRTDEGEKKCGGPGCGGLVTVAHSA 1440
Db 1381 LAGKLSLDLSAAQMTCTGTPPGADCSESECGGPNCRRTDEGEKKCGGPGCGGLVTVAHSA 1440
QY 1441 WQKAMDFDRDVLALAEVEQLSKMVSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDL 1500
Db 1441 WQKAMDFDRDVLALAEVEQLSKMVSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDL 1500
QY 1501 RNLIKQIRNFELTSDADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVI 1560
Db 1501 RNLIKQIRNFELTSDADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVI 1560
QY 1561 LQQSAADIARAELLLEAEKRAKSKSATDVKVTADMVKEALEEAEKAQVAAEKAIKQADEDI 1620
Db 1561 LQQSAADIARAELLLEAEKRAKSKSATDVKVTADMVKEALEEAEKAQVAAEKAIKQADEDI 1620
QY 1621 QGTQNLTSISETAASEETLTNASQRIKSLERNVEELKRAKAQNSGEAEYIEKVVISVK 1680
Db 1621 QGTQNLTSISETAASEETLTNASQRIKSLERNVEELKRAKAQNSGEAEYIEKVVISVK 1680
QY 1681 QNADDVKKTLDGELDEKYYKVESLIAQKTESADARRKAEELLQNEAKTLLAQANSKLQLL 1740
Db 1681 QNADDVKKTLDGELDEKYYKVESLIAQKTESADARRKAEELLQNEAKTLLAQANSKLQLL 1740
QY 1741 EDLERKYEDNQYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1786
Db 1741 EDLERKYEDNQYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1786

RESULT 3

ABB81592
ID ABB81592 standard; protein; 1786 AA.
XX ABB81592;
AC ABB81592;
XX 19-SEP-2002 (first entry)
DT Mouse laminin 10 second chain protein sequence SEQ ID NO:10.
DE Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;
KW tissue repair development; laminin; healing; vascular tissue;
KW re-endothelialisation; vascular injury; cell attachment; cell stasis;
KW proliferation; migration.
XX Mus musculus.
OS
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT /label= signal
FT Protein 22..1786
FT /label= laminin_10_second_chain
XX WO200250111-A2.
PN
XX
PD 27-JUN-2002.
XX
XX 21-DEC-2001; 2001WO-US051035.
PF
XX 21-DEC-2000; 2000US-0257449P.
PR 28-MAR-2001; 2001US-0279282P.
PR 13-NOV-2001; 2001US-00279282.
XX
XX (BIOS-) BIOSTRATUM INC.
PA
XX Tryggvason K, Doi M, Thyboll J;
PI
XX WPI; 2002-557650/59.
DR N-PSDB; ABQ72910.
DR
XX New human laminin-10 proteins, useful for accelerating the healing of
PT

PT vascular tissue, improving the biocompatibility of grafts, or for
PT promoting re-endothelialization at the site of vascular injuries.
XX
PS Claim 9; Page 140-145; 231pp; English.
XX
CC The present invention describes human laminin alpha 5. Also described is
CC an isolated laminin 10. Laminin 10 has vulnery activity. Laminins are
CC useful in maintaining cell/tissue phenotype as well as promoting cell
CC growth and differentiation in tissue repair development. Specifically,
CC laminin 10 can be used for accelerating the healing injuries of vascular
CC tissue, improving the biocompatibility of grafts useful for treating such
CC injuries, for promoting re-endothelialisation at the site of vascular
CC injuries, and promote cell attachment and subsequent cell stasis,
CC proliferation, differentiation, and/or migration. The present sequence
CC encodes a second chain protein of laminin 10, from the present invention
XX
SQ Sequence 1786 AA;
Query Match 100.0%; Score 9758; DB 5; Length 1786;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLLQVFAFGVLALWGTRVCAQEPFSYGAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60
Db 1 MGLLQVFAFGVLALWGTRVCAQEPFSYGAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60
QY 61 PEPYCIVSHLQEDKKCFICDSRDPVHETLNPDSLHJENVTTPAPNRLKIWQSENGVEN 120
Db 61 PEPYCIVSHLQEDKKCFICDSRDPVHETLNPDSLHJENVTTPAPNRLKIWQSENGVEN 120
QY 121 VTIOLEAEFFHFTLIMTFTFRPAAMLIERSDDFKTGWYRYFAYDCSSFPFGISTG 180
Db 121 VTIOLEAEFFHFTLIMTFTFRPAAMLIERSDDFKTGWYRYFAYDCSSFPFGISTG 180
QY 181 PMKKVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPIQNLLKITNLRKFVKL 240
Db 181 PMKKVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPIQNLLKITNLRKFVKL 240
QY 241 HTLGDNLDSRMEIREKYYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMC 300
Db 241 HTLGDNLDSRMEIREKYYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMC 300
QY 301 RHNTKGLNCELMDFYHDLWPRAEGRNSNACKKCNNEHSSSCHDFMAVFLATGNVSGG 360
Db 301 RHNTKGLNCELMDFYHDLWPRAEGRNSNACKKCNNEHSSSCHDFMAVFLATGNVSGG 360
QY 361 VCDNCQHNMTGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVG 420
Db 361 VCDNCQHNMTGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVG 420
QY 421 LIAGQCRCRLHVEGERCDVCKEGFYDLAEDPYGCKSCACNPLGTIPGPNPCDSETGYCY 480
Db 421 LIAGQCRCRLHVEGERCDVCKEGFYDLAEDPYGCKSCACNPLGTIPGPNPCDSETGYCY 480
QY 481 CKRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCLDGGALNNSCEDSGQCSCLPHMIGRQC 540
Db 481 CKRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCLDGGALNNSCEDSGQCSCLPHMIGRQC 540
QY 541 NEVESGYFTTLDHYIYEAEANLPGVWVVERQYIQDRIPSWTGPVVRVPEGAYLEFF 600
Db 541 NEVESGYFTTLDHYIYEAEANLPGVWVVERQYIQDRIPSWTGPVVRVPEGAYLEFF 600
QY 601 IDNIPYSMEYEILIRYEPQLPDHWEKAVITVQRPKIPASSRCNTVPDDDNQVVSLSPG 660
Db 601 IDNIPYSMEYEILIRYEPQLPDHWEKAVITVQRPKIPASSRCNTVPDDDNQVVSLSPG 660
QY 661 SRYVVLPRPVCFEKGMNYYVRLELPQYTAGSDVESPYTFIDSLVLMYPYCKSLDIFTVGG 720
Db 661 SRYVVLPRPVCFEKGMNYYVRLELPQYTAGSDVESPYTFIDSLVLMYPYCKSLDIFTVGG 720
QY 721 SGDGEVNTSAWETPQRYRCLENSRSVVKTPMTDVCRNIIIFSALIHQTGLACECDPQGS 780
Db 721 SGDGEVNTSAWETPQRYRCLENSRSVVKTPMTDVCRNIIIFSALIHQTGLACECDPQGS 780

QY	781	LSSVCDP	NGGQCCQCRPNVVGRTCNRCAPGTFGPGNGCKPCDCHLQGSASAFCDAITGQC	840
Db	781	LSSVCDP	NGGQCCQCRPNVVGRTCNRCAPGTFGPGNGCKPCDCHLQGSASAFCDAITGQC	840
QY	841	HC	FQGIYARQCDCRLPGYWGFPSCQPCQCNHGALDCDVTGECILSCDYTTGHCNRCCLA	900
Db	841	HC	FQGIYARQCDCRLPGYWGFPSCQPCQCNHGALDCDVTGECILSCDYTTGHCNRCCLA	900
QY	901	GYGDP	PIIGSGDHCPCCPDGPDGDSGRQFARSCYQDPVTLQACVCPGYIGSRCDDCAS	960
Db	901	GYGDP	PIIGSGDHCPCCPDGPDGDSGRQFARSCYQDPVTLQACVCPGYIGSRCDDCAS	960
QY	961	GFFGN	PSDFGGSCQPCQCHNIDTTDPEACDKDTGRCLKCLYHTEGHCQLCQYGYYGDA	1020
Db	961	GFFGN	PSDFGGSCQPCQCHNIDTTDPEACDKDTGRCLKCLYHTEGHCQLCQYGYYGDA	1020
QY	1021	LRQDC	RKVCNVLGTVEHCNGSDCHCDKATGQCSCLPNVIGQNCDCRCAPNTWQLASGTG	1080
Db	1021	LRQDC	RKVCNVLGTVEHCNGSDCHCDKATGQCSCLPNVIGQNCDCRCAPNTWQLASGTG	1080
QY	1081	CGPCN	CNAHSFGPSCNEFTGQCQCMPPGFGGRTGTCSEQELFWGDPDVECRACDCDPRGIE	1140
Db	1081	CGPCN	CNAHSFGPSCNEFTGQCQCMPPGFGGRTGTCSEQELFWGDPDVECRACDCDPRGIE	1140
QY	1141	TPQCD	QSTGQVCVGEVGPGRCDKCTRGYSGVFPDCTPCHQCFALWDIAIGELTNRTHKF	1200
Db	1141	TPQCD	QSTGQVCVGEVGPGRCDKCTRGYSGVFPDCTPCHQCFALWDIAIGELTNRTHKF	1200
QY	1201	LEKAK	KISGVIGPYRETVDSEKKNVEIKDILAQSPAAEPLKNIGILFEEAEKLTQDV	1260
Db	1201	LEKAK	KISGVIGPYRETVDSEKKNVEIKDILAQSPAAEPLKNIGILFEEAEKLTQDV	1260
QY	1261	TERMA	QVEVKLTDTASQSNSTAGELGALQAEESLDKTVKELAEQLEFIKNSDIQGALDS	1320
Db	1261	TERMA	QVEVKLTDTASQSNSTAGELGALQAEESLDKTVKELAEQLEFIKNSDIQGALDS	1320
QY	1321	ITKYP	QMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLERESPFEQEEQARLLDE	1380
Db	1321	ITKYP	QMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLERESPFEQEEQARLLDE	1380
QY	1381	LAGKL	QSLDLASAAQMTCTGTPPGADCSSECGGPNCRIDEGEKKCGGPGCGGLVTVHAHA	1440
Db	1381	LAGKL	QSLDLASAAQMTCTGTPPGADCSSECGGPNCRIDEGEKKCGGPGCGGLVTVHAHA	1440
QY	1441	WQKAM	DFRDLVLSALAEVEQLSKMVSSEAKVRADEAKQNAQDVLLKTNAATKEKVDKSNEDL	1500
Db	1441	WQKAM	DFRDLVLSALAEVEQLSKMVSSEAKVRADEAKQNAQDVLLKTNAATKEKVDKSNEDL	1500
QY	1501	RNLIK	QIRNFILTEDSADLDSIEAVANEVLKSGNASTPQOIQNLTEDIRERVETLSQVEVI	1560
Db	1501	RNLIK	QIRNFILTEDSADLDSIEAVANEVLKSGNASTPQOIQNLTEDIRERVETLSQVEVI	1560
QY	1561	LQOSA	ADTARAELLLEAEKRAKRSATDVKVTDVMVKEALEAEAKQAQVAEAKIAQADEDI	1620
Db	1561	LQOSA	ADTARAELLLEAEKRAKRSATDVKVTDVMVKEALEAEAKQAQVAEAKIAQADEDI	1620
QY	1621	OGTQN	LLTSIETASAEETLTNASQRIKSLERNVEELKRAAQNQSGEAEYIEKVYYSVK	1680
Db	1621	OGTQN	LLTSIETASAEETLTNASQRIKSLERNVEELKRAAQNQSGEAEYIEKVYYSVK	1680
QY	1681	QNADD	VKKTLDGELDEKYYKKVESLIAQKTEESADARRKABELLQNEAKTLQAQNSKIQLL	1740
Db	1681	QNADD	VKKTLDGELDEKYYKKVESLIAQKTEESADARRKABELLQNEAKTLQAQNSKIQLL	1740
QY	1741	EDLER	KYEDNQKYLEDKAQELVRLGEVRSLLKDISKVAVYSTCL	1786
Db	1741	EDLER	KYEDNQKYLEDKAQELVRLGEVRSLLKDISKVAVYSTCL	1786

RESULT 4
AAW50894
ID AAW50894 standard; protein; 1776 AA.

XX	AC	AAW50894;
XX	DT	07-DEC-1998 (first entry)
XX	DE	Mouse laminin B1 chain.
XX	KW	Laminin; mouse; beta-amyloid; amyloidosis; Alzheimer's disease; Down's syndrome; hereditary cerebral haemorrhage; inflammation; malignancy; Familial Mediterranean Fever; multiple myeloma; type II diabetes; prion disease; Creutzfeldt-Jacob disease; CJD; Gertsmann-Straussler syndrome; kuru; scrapie; haemodialysis; carpal tunnel syndrome; senile cardiac amyloid polyneuropathy; Familial Amyloidotic Polyneuropathy; thyroid carcinoma; diagnosis; therapy.
XX	OS	Mus sp.
XX	PN	WO9815179-A1.
XX	PD	16-APR-1998.
XX	PF	08-OCT-1997; 97WO-US018145.
XX	PR	08-OCT-1996; 96US-0027981P.
XX	PA	(UNIW) UNIV WASHINGTON.
XX	PI	Castillo G, Snow AD;
XX	DR	WPI; 1998-240534/21.
XX	PT	Use of laminin and fragments - for developing products for use in the diagnosis and treatment of amyloid disease, e.g. Alzheimer's disease or CJD.
XX	PS	Claim 15; Page 90-93; 132pp; English.
XX	CC	This is the amino acid sequence of the mouse laminin B1 chain. The primary object of the invention is to use laminin, laminin-derived protein fragments and/or laminin-derived polypeptides as potent inhibitors of amyloid formation, deposition, accumulation and/or persistence in Alzheimer's disease and other amyloidoses. The laminin products (see AAW50888-98) may include mouse or human laminin A or A1 chain, laminin B1 or B2 chain, laminin A2 chain (merosin), laminin G1 chain, the globular repeats of the laminin A1 chain and the beta-amyloid binding domain of the laminin A chain. A claimed method for treating an amyloid disease comprises administering a polypeptide having a conformational similarity to a fragment of a laminin protein. A method for diagnosing an amyloid disease involves determining levels of laminin in a sample. Production of laminin or its fourth globular repeat in vivo provides a method for in vivo inhibition of beta-amyloid amyloidosis. The products and methods can be used for the diagnosis, prognosis, monitoring and treatment of amyloidoses such as Alzheimer's disease, Down's syndrome and hereditary cerebral haemorrhage with amyloidosis of the Dutch type (where the specific amyloid is the beta-amyloid protein), the amyloidosis associated with chronic inflammation, various forms of malignancy and Familial Mediterranean Fever (AA amyloid or inflammation-association amyloidosis), the amyloidosis associated with multiple myeloma and other B-cell abnormalities (AL amyloid), the amyloidosis associated with type II diabetes (amylin or islet amyloid), the amyloidosis associated with prion diseases including Creutzfeldt-Jacob disease, Gertsmann-Straussler syndrome, kuru and animal scrapie (Prp amyloid), the amyloidosis associated with long-term haemodialysis and carpal tunnel syndrome (beta 2-microglobulin amyloid), the amyloidosis associated with senile cardiac amyloid and Familial Amyloidotic Polyneuropathy (prealbumin or transthyretin amyloid), and the amyloidosis associated with endocrine tumours such as medullary carcinoma of the thyroid (variant of procalcitonin)
XX	SQ	Sequence 1776 AA;

Query Match 99.3%; Score 9692; DB 2; Length 1776;

Best Local Similarity 99.8%; Pred. No. 0;					Matches 1776; Conservative 0; Mismatches 0; Indels 0; Gaps 1;				
QY	1	MGLLVAFAGVLALWGTRVCAQPEFSGYCAEGSCYPATGDLIIIGRAQKLSVTSTCGLHK	60						
Db	1	MGLLVAFAGVLALWGTRVCAQPEFSGYCAEGSCYPATGDLIIIGRAQKLSVTSTCGLHK	60						
QY	61	PEPYCIIVSHLQEDKKCFICDSRDPYHETLNPDShLIENVVTFAPNRLKIWQSENGVEN	120						
Db	61	PEPYCIIVSHLQEDKKCFICDSRDPYHETLNPDShLIENVVTFAPNRLKIWQSENGVEN	120						
QY	121	VTIQDLAEAFHFTHLIMTFKTRPAAMLIERSSDFGKTGWVYRYFAYDCESFPFISTG	180						
Db	121	VTIQDLAEAFHFTHLIMTFKTRPAAMLIERSSDFGKTGWVYRYFAYDCESFPFISTG	180						
QY	181	PMKKVDDIICDSRYSIDIEPSTEGEVIFRALDPAFKIEDPYSPRIQNLLKITNLRKIFVKL	240						
Db	181	PMKKVDDIICDSRYSIDIEPSTEGEVIFRALDPAFKIEDPYSPRIQNLLKITNLRKIFVKL	240						
QY	241	HTLGNLLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMC	300						
Db	241	HTLGNLLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMC	300						
QY	301	RHNTKGLNCEL CMDFYHDL PWRPAEGRNSNACKKNCNEHSSSCHFDMAVFLATGNVSGG	360						
Db	301	RHNTKGLNCEL CMDFYHDL PWRPAEGRNSNACKKNCNEHSSSCHFDMAVFLATGNVSGG	360						
QY	361	VCDNCQHNMTGRNCEOCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVG	420						
Db	361	VCDNCQHNMTGRNCEOCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVG	420						
QY	421	LIAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGNPCDSETGYCY	480						
Db	421	LIAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGNPCDSETGYCY	480						
QY	481	CKRLVTGQRCDQCLPOHWGLSNDLDGCRPCDCDLGGALNNSCEDSGQCSCLPHMIGRQC	540						
Db	481	CKRLVTGQRCDQCLPOHWGLSNDLDGCRPCDCDLGGALNNSCEDSGQCSCLPHMIGRQC	540						
QY	541	NEVESGYFTTLDHYIYEAEANLGPVVVVERQYIQDRIPSWTGPGFVRVPEGAYLEFF	600						
Db	541	NEVESGYFTTLDHYIYEAEANLGPVVVVERQYIQDRIPSWTGPGFVRVPEGAYLEFF	600						
QY	601	IDNIPYSMEYEILIRYEPQLPDHWEKAVITVORPGKIPASSRCNGTVPDDDNQVVSLSPG	660						
Db	601	IDNIPYSMEYEILIRYEPQLPDHWEKAVITVORPGKIPASSRCNGTVPDDDNQVVSLSPG	660						
QY	661	SRYVLP RPVCFEKGMYTVRLELPQYTAGSDVESP YTFIDSLVLMPYCKSLDIFTVGG	720						
Db	661	SRYVLP RPVCFEKGMYTVRLELPQYTAGSDVESP YTFIDSLVLMPYCKSLDIFTVGG	720						
QY	721	SGDGEVTNSAWETFORYRCLENSRVVKTPTMTDVCRNIIIFSALIHQTGLACECDPQGS	780						
Db	721	SGDGEVTNSAWETFORYRCLENSRVVKTPTMTDVCRNIIIFSALIHQTGLACECDPQGS	780						
QY	781	LSSVCDPNGGQCQCRPNVVGRTCNRCAPGTFGFGPCKPCDCHLQGSASAFCDAITGQC	840						
Db	781	LSSVCDPNGGQCQCRPNVVGRTCNRCAPGTFGFGPCKPCDCHLQGSASAFCDAITGQC	840						
QY	841	HCFAQIYARQCDRCLPGYWGFPSCQPCQCNHGHALDCDVTGTGECSCQDYTTGHNCECRLA	900						
Db	841	HCFAQIYARQCDRCLPGYWGFPSCQPCQCNHGHALDCDVTGTGECSCQDYTTGHNCECRLA	900						
QY	901	GYGDPPIIGSGDHCRPCPCPDGPDGSDGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCAS	960						
Db	901	GYGDPPIIGSGDHCRPCPCPDGPDGSDGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCAS	960						
QY	961	GFFGNPSDFGGSCQPCQCHNIDTTDPEACDKDTGRCLKCLYHTEGHCQLCQYGYGDA	1020						
Db	961	GFFGNPSDFGGSCQPCQCHNIDTTDPEACDKDTGRCLKCLYHTEGHCQLCQYGYGDA	1020						
QY	1021	LRQDCRKVCNYLGTVKEHCHNGSDCHCDKATGQCSCLPNVIGQNCDCRCApNTWQLASGTG	1080						

Db	1021	LRQDCRKVCNYLGTVKEHCHNGSDCHCDKATGQCSCLPNVIGQNCDCRCApNTWQLASGTG	1080
QY	1081	CGPCNCNAAHSFGPSCNFEFTGQCQCMPPGFGGRTCTSECQELFWGDPDVECRACDCDPRGIE	1140
Db	1081	CGPCNCNAAHSFGPSCNFEFTGQCQCMPPGFGGRTCTSECQELFWGDPDVECRACDCDPRGIE	1140
QY	1141	TPQCDQSTGQCVCVEGVEGPRCDKCTRGYSGVFPDCTPCHQCFCFALWDAIIGELTNRTHKF	1200
Db	1141	TPQCDQSTGQCVCVEGVEGPRCDKCTRGYSGVFPDCTPCHQCFCFALWDAIIGELTNRTHKF	1200
QY	1201	LEKAKALKISGVIGPYRETVDSEVKVNEIKDILAQSPAEPPLKNIIGILFEEAEKLTQDV	1260
Db	1201	LEKAKALKISGVIGPYRETVDSEVKVNEIKDILAQSPAEPPLKNIIGILFEEAEKLTQDV	1260
QY	1261	TEKMAQVEVKLTDTASQSNSTAGELGALQAEAESLDKTVKELAEQLEFIKNSDIOGALDS	1320
Db	1261	TEKMAQVEVKLTDTASQSNSTAGELGALQAEAESLDKTVKELAEQLEFIKNSDIOGALDS	1320
QY	1321	ITKYFQMSLEAEKRVNASITDPNSTVEQSALTRDRVEDLMLERESPFKEQQEEOQARLLDE	1380
Db	1321	ITKYFQMSLEAEKRVNASITDPNSTVEQSALTRDRVEDLMLERESPFKEQQEEOQARLLDE	1380
QY	1381	LAKLQSLDLASAAQMTCTGTPGADCSSECGGPNCRITDEGEKKCGGPGCGGLTVVAHSA	1440
Db	1381	LAKLQSLDLASAAQMTCTGTPGADCSSECGGPNCRITDEGEKKCGGPGCGGLTVVAHSA	1440
QY	1441	WQKAMDFDRDVL SALAEVQLSKMVSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDL	1500
Db	1441	WQKAMDFDRDVL SALAEVQLSKMVSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDL	1500
QY	1501	RNLIKQIRNFLTEDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVI	1560
Db	1501	RNLIKQIRNFLTEDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVI	1560
QY	1561	LQOSAADIARAEALLLEAEKRAKSAATDVKTADVMVKEALEEAEKAQVAAEKAIQADEDI	1620
Db	1561	LQOSAADIARAEALLLEAEKRAKSAATDVKTADVMVKEALEEAEKAQVAAEKAIQADEDI	1620
QY	1621	QGTQNLTSIESETAASEETLTNASQRI SKLERNVEELKRKAQNSGEAEYIEKVYVSVK	1680
Db	1621	QGTQNLTSIESETAASEETLTNASQRI SKLERNVEELKRKAQNSGEAEYIEKVYVSVK	1680
QY	1681	QNADDVKTLDCGELDEKYYKVESLIAQKTEESADARRKAEALLQNEAKTLAQANSKLQLL	1740
Db	1681	---DVKKTLDGELDEKYYKVESLIAQKTEESADARRKAEALLQNEAKTLAQANSKLQLL	1736
QY	1741	EDLERKYEDNOKYLEDKAQELVRLEGEVRSLLKDISEKVA	1780
Db	1737	EDLERKYEDNOKYLEDKAQELVRLEGEVRSLLKDISEKVA	1776

RESULT 5
AAP91672

ID AAP91672 standard; protein; 1764 AA.

XX

AC AAP91672;

XX

DT 25-MAR-2003 (revised)

DT 31-OCT-2002 (revised)

DT 29-JUN-1990 (first entry)

XX

DE Primary amino acid sequence of B1 chain of laminin.

XX

KW Laminin B1 chain fragment; heparin; prosthetic devices;
KW cell culture substrates; cell adhesion promoter; nerve regeneration;
KW wound healing; implant acceptance; cell attachment; metastasis inhibitor.

XX

OS Mus musculus.

OS Synthetic.

XX

PH Location/Qualifiers

FT Peptide

641..660

/note= "designated F9"

FT	Peptide	1171. .1188	/note= "designated F13"
XX	WO8901493-A.		
XX	23-FEB-1989.		
XX	19-AUG-1987;	87US-00087157.	
XX	19-AUG-1987;	87US-00087157.	
XX	(MINU) MINNESOTA UNIVERSITY.		
XX	Charonis A, Furcht LT;		
XX	WPI; 1989-068855/09.		
XX	New laminin B1 chain polypeptide(s) - for promoting heparin binding and cell adhesion.		
XX	Disclosure; Page ?; 42pp; English.		
XX	The new polypeptides have an amino acid sequence corresp. to a laminin B1 chain fragment having specific binding capacity for heparin. Specifically mentioned are the two polypeptides F9 and F13 (see FT). The polypeptides may be used to promote binding of heparin to synthetic substrates and promote cell adhesion, eg endothelial, melanoma, fibrosarcoma, glioma and pheochromocytoma cells. They may be useful for assisting nerve regeneration, promoting wound healing, implant acceptance, cell attachment to culture substrates and inhibiting metastasis of malignant cells. They may be prepd. by conventional Merrifield solid-phase synthesis. Also claimed are prosthetic devices and cell culture substrates coated with the new polypeptides. (Updated on 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PR field.)		
XX	Sequence 1764 AA;		
XX	Query Match	97.5%;	Score 9517.5; DB 1; Length 1764;
XX	Best Local Similarity	98.9%;	Pred. NO. 0;
XX	Matches 1746; Conservative	4;	Mismatches 14; Indels 1; Gaps 1
QY	22 QEPEFSYGCAEGSCYPATGDLIIIGRAQKLSVTSTCGLHKPEPYCIYSHLQEDKKCFICDS	81	
DB	1 QEPEFSYGCAEGSCYPATGDLIIIGRAQKLSVTSTCGLKKPEPYCIYSHLQEDKKCFICDS	60	
QY	82 RDPYHETLNPDSHLIENVVTFAPNRLKIWWQSENGVENVTIQLDLAEFHFTHLIMTFK	141	
DB	61 RDPYHETLNPDSHLIENVVTFAPNRLKIWWQSENGVENVTIQLDLAEFHFTHLIMTFK	120	
QY	142 TFRPAAMLIERSDFGKTGWVYRYFAYDCESFPGISGTPMKKVDDIIICDSRYSDIEPST	201	
DB	121 TFRPAAMLIERSDFGKTGWVYRYFAYDCESFPGISGTPMKKVDDIIICDSRYSDIEPST	180	
QY	202 EGEVIFRALDPAFKIEDPYSPIQNLLKITNLRKIFVKLHTLGDNLDSRMEIREKYYA	261	
DB	181 EGEVIFRALDPAFKIEDPYSPIQNLLKITNLRKIFVKLHTLGDNLDSRMEIREKYYA	240	
QY	262 VYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVGHCMCRHNTKGLNCEL CMDFYHDLFP	321	
DB	241 VYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVGHCMCRHNTKGLNCEL CMDFYHDLFP	300	
QY	322 RPAEGRNSACKKNCNEHSSSCHFDMAVFLATGNVSGVCDNCOHNTMGRNCEQCKPFY	381	
DB	301 RPAEGRNSACKKNCNEHSSSCHFDMAVFLATGNVSGVCDNCOHNTMGRNCEQCKPFY	360	
QY	382 FQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGLIAGQCRCKLHVEGERCDVCK	441	
DB	361 FQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGLIAGQCRCKLHVEGERCDVCK	420	
QY	442 EGFYDLSAEDPYGCKSCACNPLGTIPGGNPCDSETGYCYCKRLVTGORCDQCLPQHWGLS	501	
DB	421 EGFYDLSAEDPYGCKSCACNPLGTIPGGNPCDSETGYCYCKRLVTGORCDQCLPQHWGLS	480	

QY	502	NDLDGCRPCDCLGGALNNSCSDSGQCSCLPHMIGRQCNEVESGYFTILDHYIYEABE	561
Db	481	NDLDGCRPCDCLGGALNNSCSDSGQCSCLPHMIGRQCNEVESGYFTILDHYIYEABE	540
QY	562	ANLPGVVVVERQYIQDRIPSWTGPFGFVRVPEGAYLEFFIDNIPYSMEYEILIRYEPQLP	621
Db	541	ANLPGVVVVERQYIQDRIPSWTGPFGFVRVPEGAYLEFFIDNIPYSMEYEILIRYEPQLP	600
QY	622	DHWEKAVITVQRPCKIPASSRRCGNTVPDDNQVWSLSPGSRYYVVLPRPVCFEKGMNYYTVR	681
Db	601	DHWEKAVITVQRPCKIPASSRRCGNTVPDDNQVWSLSPGSRYYVVLPRPVCFEKGMNYYTVR	660
QY	682	LELPQYTASGSDVESPYTFIDSLVLMPYCKSLDIFTVGGSGDGEVNTSAWETFORYRCLE	741
Db	661	LELPQYTASGSDVESPYTFIDSLVLMPYCKSLDIFTVGGSGDGEVNTSAWETFORYRCLE	720
QY	742	NSRSVVKTPMTDVCRNIIIFSISALIHQTLGLACECDPQGSLSVVCDDPNGGQCQCRPNVVGR	801
Db	721	NSRSVVKTPMTDVCRNIIIFSISALIHQTLGLACECDPQGSLSVVCDDPNGGQCQCRPNVVGR	780
QY	802	TCNRCAPGTFGFGPNCKPCDCHLQGSASAFCDAITGQCHCFQGIYARQCDCRCLPGYWGF	861
Db	781	TCNRCAPGTFGFGPNCKPCDCHLQGSASAFCDAITGQCHCFQGIYARQCDCRCLPGYWGF	840
QY	862	PSCQPCQCNGHALDCDVTGTECLSCQDYITGHNCERCLAGYYGDPPIIGSGDHCRCPCPCPD	921
Db	841	PSCQPCQCNGEALDCDVTGTECLSCQDYITGHNCERCLAGYYGDPPIIGSGDHCRCPCPCPD	900
QY	922	GPDSGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCASGFFGNPSDFGSGCQPCQCHHN	981
Db	901	GPDSGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCASGFFGNPSDFGSGCQPCQCHHN	960
QY	982	IDTTDPEACDKDTRCLKCLYHTEGDHCQLCOGYGYGDALRQDCRKCVCNVLGTVKEHCN	1041
Db	961	IDTTDPEACDKDTRCLKCLYHTEGDHCQLCOGYGYGDALRQDCRKCVCNVLGTVKEHCN	1020
QY	1042	GSDCHDKATGQCSCLPNVIGQNCDCRCAPNTWQLASGTGCGPCNCNAHSGFSPSCNEFTG	1101
Db	1021	GSDCHDKATGQCSCLPNVIGQNCDCRCAPNTWQLASGTGCGPCNCNAHSGFSPSCNEFTG	1080
QY	1102	QCQCMPGFGGRTCECQELFWGDDPVECRACDDPRGIETPQCDQSTGQCVCVEGVEGPR	1161
Db	1081	QCQCMPGFGGRTCECQELFWGDDPVECRACDDPRGIETPQCDQSTGQCVCVEGVEGPR	1140
QY	1162	CDKCTRGYSGVFPDCTPCHQCFAWDIAIIGELTNRTHKFLEKAKALKISGVIGPYRETVD	1221
Db	1141	CDKCTRGYSGVFPDCTPCHQCFAWDIAIIGELTNRTHKFLEKAKALKISGVIGPYRETVD	1200
QY	1222	SVEKKVNEIKDILAQSPAAEPLKNIGILFEBEAELTKDVTEKMAQVEVKLTDTASQSNST	1281
Db	1201	SVKKVKNKIKDILAQIPAAEPLKNIGILFEBEAELTKDVTEKMAQVEVKLTDTASQSNH	1260
QY	1282	AGELGALQAEABSLDKTVKELAEQLEFIKNSDIQGALDLSITKYFQMSLEAEKRVNASTTD	1341
Db	1261	AGELGALQAGABSLDKTVKELAEQLEFIKNSDIQGALDLSITKYFQMSLEAEKRVNASTTD	1320
QY	1342	PNSTVEQSALTDRVEDLMLERESPFKEQCGGPGCGGLVTVHAQKAMDFFDRDVLALAEVEQL	1401
Db	1321	PNSTVEQSALTDRVEDLMLERESPFKEQCGGPGCGGLVTVHAQKAMDFFDRDVLALAEVEQL	1380
QY	1402	PGADCSSECGGPNCRRTDEGEKKCGGPGCGGLVTVHAQKAMDFFDRDVLALAEVEQL	1461
Db	1381	PGADCSSECGGPNCRRTDEGEKKCGGPGCGGLVTVHAQKAMDFFDRDVLALAEVEQL	1440
QY	1462	SKMVSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDLRNLKIQIRNFLTEDSADLDSI	1521
Db	1441	SKMVSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDLRNLKIQIRNFLTEDSADLDSI	1500
QY	1522	EAVANEVLKSGNASTPQQLQNLNLTEDIRERVETLSQVEVILQQSAADIARAEELLEAKRA	1581
Db	1501	EAVANEVLKSGNASTPQQLQNLNLTEDIRERVETLSQVEVILQQSAADIARAEELLEAKRA	1560
QY	1582	SKSATDVKVTVADMVKEALEEAEAKQAAEKAQKQADEDIQGTQNLNLTSEISETAASEETL	1641

Db 1561 SKSATDVKYTADVMVKEALEEAEKAAQVAAEKAIKQADEDIOGTQNLITSIESETAASEBTL 1620
QY 1642 TNASORISKLERNVVELKRKAAQNSGEAEYIEKVYSVKQNAADDVKKTLGDELDEKYKKV 1701
Db 1621 TNASORISKLERNVVELKRKAAQNSGEAEYIEKVYSVKQNAADDVKKTLGDELDEKYKKV 1679
QY 1702 ESLIAOKTESADARRKAELLQNEAKTLLAQANSKIQLEDDLERKYEDNQYLEDKAOEL 1761
Db 1680 ESLIAOKTESADARRKAELLQNEAKTLLAQANSKIQLEDDLERKYEDNQYLEDKAOEL 1739
QY 1762 VRLEGEVRSLLKDISEKVAVYSTCL 1786
Db 1740 VRLEGEVRSLLKDISEKVAVYSTCL 1764

RESULT 6
AAB19800
ID AAB19800 standard; protein; 1725 AA.
XX AC AAB19800;
XX 05-MAR-2001 (first entry)
DT Mouse laminin 2 mature beta-1 chain.
DE
XX Laminin 2; mouse; nerve regeneration; angiogenic; cell adhesion;
KW degenerative muscle disorder; muscular dystrophy; cell therapy.
KW
XX Mus musculus.

OS WO200066730-A2.
XX 09-NOV-2000.
XX 28-APR-2000; 2000WO-US011378.
PF
XX 30-APR-1999; 99US-0131720P.
PR 15-JUN-1999; 99US-0139198P.
PR 12-JUL-1999; 99US-0143289P.
PR 24-SEP-1999; 99US-0155945P.

(UTNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.

Yurchenco P;

WPI; 2000-687537/67.
N-PSDB; AAA88900.

Purified laminin 2 protein, useful for research and therapeutic purposes including peripheral nerve regeneration, treatment of degenerative muscle disorders, angiogenesis regulation, and ex vivo cell therapy.

Claim 5; Page 226-232; 305pp; English.

The present sequence is that of the mouse laminin 2 beta-1 chain mature protein. Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1 (100 kDa) chains. It is thought to be specifically required for stabilizing myotubes during skeletal muscle development, and for preventing apoptosis. Genetic defects in human laminin 2 structure or expression are associated with a major type of congenital muscular dystrophy. Laminin 2 is also thought to be important in Schwann cell/basal lamina interactions. The invention provides laminin 2 alpha-2, beta-1 and gamma-1 chain polypeptides (see AAB19791-806) and the polynucleotides encoding them (see AAA8891-906), methods for making recombinant laminin 2, cells that express recombinant laminin 2, and methods for using purified laminin 2 for research and therapeutic purposes including peripheral nerve regeneration, treatment of degenerative muscle disorders, angiogenesis regulation, promoting cell attachment and migration, ex vivo cell therapy, improving the take of grafts, improving the biocompatibility of medical devices and preparing improved culture devices and media

SQ Sequence 1725 AA;
Query Match 96.6%; Score 9429; DB 3; Length 1725;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 62 EPYCIVSHLQEDKKCFICDSRDPYTHETLNPDShLIENVVTTTAPNRLKIWQSENGVENV 121
Db 1 EPYCIVSHLQEDKKCFICDSRDPYTHETLNPDShLIENVVTTTAPNRLKIWQSENGVENV 60
QY 122 TIQLDLEAEFHFTHLIMTFKTRPAAMLIERSSDFGKTGWVTRPAYDCESSFPGISTGP 181
Db 61 TIQLDLEAEFHFTHLIMTFKTRPAAMLIERSSDFGKTGWVTRPAYDCESSFPGISTGP 120
QY 182 MKKVDDIIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPRIQNLKITNLRKFVKLH 241
Db 121 MKKVDDIIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPRIQNLKITNLRKFVKLH 180
QY 242 TLGDNLLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCHCMCR 301
Db 181 TLGDNLLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCHCMCR 240
QY 302 HNTKGLNCELMDYHDLPRPRAEGNSNACKKNCNEHSSSCHFDMAVFLATGNVSGGV 361
Db 241 HNTKGLNCELMDYHDLPRPRAEGNSNACKKNCNEHSSSCHFDMAVFLATGNVSGGV 300
QY 362 CDNCQHNTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 421
Db 301 CDNCQHNTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 360
QY 422 IAGQCRCKLHVEGERCDVCKEGFYDLSEAEDPYGCKSCACNPLGTIPGGNPCDSETGYCYC 481
Db 361 IAGQCRCKLHVEGERCDVCKEGFYDLSEAEDPYGCKSCACNPLGTIPGGNPCDSETGYCYC 420
QY 482 KRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCLGGALNNSCEDSGQCSCLPHMIGRQCN 541
Db 421 KRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCLGGALNNSCEDSGQCSCLPHMIGRQCN 480
QY 542 EVESGYFTTLDHYIYEAEANLPGVWVVERQYIQDRIPSWTCGPFVRVPEGAYLEFFI 601
Db 481 EVESGYFTTLDHYIYEAEANLPGVWVVERQYIQDRIPSWTCGPFVRVPEGAYLEFFI 540
QY 602 DNIPYSMEYEILIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTPVDDDNQVVSLSPGS 661
Db 541 DNIPYSMEYEILIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTPVDDDNQVVSLSPGS 600
QY 662 RYVWLPRPVCFEKGMNYYTVRLELPQYTAGSDVESPYTFIDSLVLMPYCKSLDIFTVGGG 721
Db 601 RYVWLPRPVCFEKGMNYYTVRLELPQYTAGSDVESPYTFIDSLVLMPYCKSLDIFTVGGG 660
QY 722 GDGEVTNSAWETFORYRCLENSRSVVKTPMTDVCRNIIIFSISALIHQTGLACECDPQGS 781
Db 661 GDGEVTNSAWETFORYRCLENSRSVVKTPMTDVCRNIIIFSISALIHQTGLACECDPQGS 720
QY 782 SSVCDPNGGQCQCRCRPNVVGRTCNRCAPGTFGFGPNCKPCDCHLQGSASAFCDAITGQCH 841
Db 721 SSVCDPNGGQCQCRCRPNVVGRTCNRCAPGTFGFGPNCKPCDCHLQGSASAFCDAITGQCH 780
QY 842 CFQGIYARQCDCRCLPGYWGFPSCQPCQCNHGLDCLDTVTGECCLSCQDYTTGHNCCERCLAG 901
Db 781 CFQGIYARQCDCRCLPGYWGFPSCQPCQCNHGLDCLDTVTGECCLSCQDYTTGHNCCERCLAG 840
QY 902 YYGDPPIIGSGDHCRCPCPCPDGPDGSGRQFARSCYQDPVTTLQACVCDPGYIGSRCDDCASG 961
Db 841 YYGDPPIIGSGDHCRCPCPCPDGPDGSGRQFARSCYQDPVTTLQACVCDPGYIGSRCDDCASG 900
QY 962 FFGNPSDFGGSCQPCQCHNIDTTDPEACDKTGRCLKCLYHTEGDHCLCQYGYGDAL 1021
Db 901 FFGNPSDFGGSCQPCQCHNIDTTDPEACDKTGRCLKCLYHTEGDHCLCQYGYGDAL 960
QY 1022 RQDCRKVCVNYLTGVYKHEHNGSDCHCDKATGCQCSCLPNVIGQNCDCRCAPNTWQLASGTGC 1081
Db 961 RQDCRKVCVNYLTGVYKHEHNGSDCHCDKATGCQCSCLPNVIGQNCDCRCAPNTWQLASGTGC 1020

QY 1082 GPCNCNAAHSGFSCNEFTGQCQCMPGFGGRTCTSECQELFWGDDPDVECRACDCDPRGIET 1141
Db |||||
QY 1021 GPCNCNAAHSGFSCNEFTGQCQCMPGFGGRTCTSECQELFWGDDPDVECRACDCDPRGIET 1080
Db |||||
QY 1142 PQCDQSTGQCVCEGVGPRCDKCTRGYSVGFPPDCTPCHQCQFALWDALIGELTNRTHKFL 1201
Db |||||
QY 1081 PQCDQSTGQCVCEGVGPRCDKCTRGYSVGFPPDCTPCHQCQFALWDALIGELTNRTHKFL 1140
QY 1202 EKAKALKISGVIGPYRETVDVSEKKVNEIKDILAQSPAAPLKNIGILFEEAEKLT KDVT 1261
Db |||||
QY 1141 EKAKALKISGVIGPYRETVDVSEKKVNEIKDILAQSPAAPLKNIGILFEEAEKLT KDVT 1200
QY 1262 EKMAQVEVKLTDTASQSNSTAGELGALQABESLDKTVKELAEQLEFIKNSDIQ GALDSI 1321
Db |||||
QY 1201 EKMAQVEVKLTDTASQSNSTAGELGALQABESLDKTVKELAEQLEFIKNSDIQ GALDSI 1260
QY 1322 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLERESPKEQEEQARLLDEL 1381
Db |||||
QY 1261 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLERESPKEQEEQARLLDEL 1320
QY 1382 AGKLSLDLSAAQMTCTGTPPGADCSSESCGPNCRDTEGEKKCGGPGGLVTVVAHSAW 1441
Db |||||
QY 1321 AGKLSLDLSAAQMTCTGTPPGADCSSESCGPNCRDTEGEKKCGGPGGLVTVVAHSAW 1380
QY 1442 QKAMDFDRDVL SALAEVEQLSKMVSEAKVRADEAKONAQDVLLKTNATKEKVDKSNEDLR 1501
Db |||||
QY 1381 QKAMDFDRDVL SALAEVEQLSKMVSEAKVRADEAKONAQDVLLKTNATKEKVDKSNEDLR 1440
QY 1502 NLIKQIRNFLTEDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVIL 1561
Db |||||
QY 1441 NLIKQIRNFLTEDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVIL 1500
QY 1562 QQSAADIARAELLLEBAKRAKSKSATDVKVTDVMVKEALEEAEKAQVAAEKAQADEDIQ 1621
Db |||||
QY 1501 QQSAADIARAELLLEBAKRAKSKSATDVKVTDVMVKEALEEAEKAQVAAEKAQADEDIQ 1560
QY 1622 GTQNLLTSIESETAASEETLTNASQRIKLERNVEELKRAAQNQSGEAEYIEKVVSVKQ 1681
Db |||||
QY 1561 GTQNLLTSIESETAASEETLTNASQRIKLERNVEELKRAAQNQSGEAEYIEKVVSVKQ 1620
QY 1682 NADDVKKTLTGELDEKYYKVESLIAQKTEESADARRKAELLQNEAKTLLAQANSKLQ LLE 1741
Db |||||
QY 1621 NADDVKKTLTGELDEKYYKVESLIAQKTEESADARRKAELLQNEAKTLLAQANSKLQ LLE 1680
QY 1742 DLERKYEDNQKYLEDKAQELVRLGEVRSLLKDISEKVAVYSTCL 1786
Db |||||
QY 1681 DLERKYEDNQKYLEDKAQELVRLGEVRSLLKDISEKVAVYSTCL 1725

RESULT 7
AAB48451
ID AAB48451 standard; protein; 1725 AA.
XX
AC AAB48451;
XX
DT 02-MAR-2001 (first entry)
XX
DE Mouse laminin 8 polypeptide, SEQ ID NO: 20.
XX
KW Mouse; laminin 8; neuroprotective; angiogenic; osteopathic;
KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;
KW vascular tissue injury; neural injury; angiogenesis regulation.
XX
OS Mus musculus.
XX
PN WO2000066732-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US011543.
XX
PR 30-APR-1999; 99US-0131720P.

PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.
PR 11-FEB-2000; 2000US-0182012P.
XX
PA (BIOS-) BIOSTRATUM INC.
XX
XX Kortessmaa J, Tryggvason K;
PI
XX
DR WPI; 2000-687539/67.
DR N-PSDB; AAC83712.
XX
PT Purified laminin 8 protein, useful for research and therapeutic purposes
PT including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.
XX
PS Claim 5; Page 189-194; 245pp; English.
XX
CC The present sequence is a laminin 8 polypeptide chain. Laminins are a
CC family of heterotrimeric glycoproteins that function via binding
CC interactions with neighbouring cell receptors and by forming laminin
CC networks. They are signalling molecules which influence cellular
CC function. Laminin 8 is useful for treating injuries to tissue of
CC mesenchymal origin, such as bone, cartilage, tendon, and ligament,
CC treating injuries to vascular tissue, promoting cell attachment and
CC migration, ex vivo cell therapy, improving the biocompatibility of
CC medical devices, and preparing improved cell culture devices and media.
CC Laminin 8 is also useful for promoting re-endothelialisation at the site
CC of vascular injuries, improving the take of grafts, improving the
CC biocompatibility of medical devices, treating neural injuries (neural
CC regeneration), regulating angiogenesis, and promoting cell attachment and
CC migration
XX
SQ Sequence 1725 AA;

Query Match 96.6%; Score 9429; DB 3; Length 1725;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 EPYCIVSHLOEDKKCFICDSRDPYHETLNPDSHLIENVVTTFAPNRLKIWQSENGVENV 121
Db |||||
QY 122 TIQLDLEAEFFHFTLIMTKTFERPAAMLIERSDDFGKTGWVRYFAYDCSSFPFGISTGP 181
Db |||||
QY 61 TIQLDLEAEFFHFTLIMTKTFERPAAMLIERSDDFGKTGWVRYFAYDCSSFPFGISTGP 120
QY 182 MKKVDDIICDSRYSIDIEPSTEGEVIFRALDPAPKIEDPYSPIQNLLKITNLRIFVKLH 241
Db |||||
QY 121 MKKVDDIICDSRYSIDIEPSTEGEVIFRALDPAPKIEDPYSPIQNLLKITNLRIFVKLH 180
QY 242 TLGDNLLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGHCRCR 301
Db |||||
QY 181 TLGDNLLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGHCRCR 240
QY 302 HNTKGLNCELMDFFYHDLFWRPAEGRNSNACKKCNNEHSSSCHFFDMVFLATGNVSGGV 361
Db |||||
QY 241 HNTKGLNCELMDFFYHDLFWRPAEGRNSNACKKCNNEHSSSCHFFDMVFLATGNVSGGV 300
QY 362 CDNCQHNTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 421
Db |||||
QY 301 CDNCQHNTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 360
QY 422 IAGQCRCKLHVEGERCDVCKEGFGYDLSEAEDPYGCKSCACNPLGTIPGNPCDSETGYCYC 481
Db |||||
QY 361 IAGQCRCKLHVEGERCDVCKEGFGYDLSEAEDPYGCKSCACNPLGTIPGNPCDSETGYCYC 420
QY 482 KRLVTGQRCDQCLPQHGLSNDLDGCRPCDCLGGALNNSCEDSGQCSCLPHMIGRQCN 541
Db |||||
QY 421 KRLVTGQRCDQCLPQHGLSNDLDGCRPCDCLGGALNNSCEDSGQCSCLPHMIGRQCN 480
QY 542 EVESGYFTTLDHYIEAEAEANLPGVVVVERQYIQDRIPSWTGPFRVPEGAYLEFFI 601
Db |||||
QY 481 EVESGYFTTLDHYIEAEAEANLPGVVVVERQYIQDRIPSWTGPFRVPEGAYLEFFI 540

QY 602 DNIYPSMEYEIILIRYEPQLPDHWEKAVITVORPGKIPASSRCGNTVPDDDNQVVSLSPGS 661
Db 541 DNIYPSMEYEIILIRYEPQLPDHWEKAVITVORPGKIPASSRCGNTVPDDDNQVVSLSPGS 600
QY 662 RYVVLPRPVCFEKGMNYYTVRLELPQYTASGSDVESPYTFIDSLVLMPCYCKSLDIFTVGGS 721
Db 601 RYVVLPRPVCFEKGMNYYTVRLELPQYTASGSDVESPYTFIDSLVLMPCYCKSLDIFTVGGS 660
QY 722 GDGEVINSAWETFORYRCLNSRSVVKTPMTDVCNRIIFSALIHQTLGACEDPQGS 781
Db 661 GDGEVINSAWETFORYRCLNSRSVVKTPMTDVCNRIIFSALIHQTLGACEDPQGS 720
QY 782 SSVCDENGQCQCRPNVVGRTCNRCAPGTFGFGNGCKPCDCHLQGSASAFCDAITGQCH 841
Db 721 SSVCDENGQCQCRPNVVGRTCNRCAPGTFGFGNGCKPCDCHLQGSASAFCDAITGQCH 780
QY 842 CFQGIYARQCDRCLPGYWGFPSCQCCQNGHALDCTVTGECCLSCQDYTTGHNCHERCLAG 901
Db 781 CFQGIYARQCDRCLPGYWGFPSCQCCQNGHALDCTVTGECCLSCQDYTTGHNCHERCLAG 840
QY 902 YGDPPIIGSGDHRPCPCPDGPDGSDGQFARSCYQDPVTILQACVCDPGYIGSRCDDCASG 961
Db 841 YGDPPIIGSGDHRPCPCPDGPDGSDGQFARSCYQDPVTILQACVCDPGYIGSRCDDCASG 900
QY 962 FFGNPSDFGSGCQPCQCHNIDTTDEACDKDTGRCLKCLYHTEGDHCOLCOYGYGDAL 1021
Db 901 FFGNPSDFGSGCQPCQCHNIDTTDEACDKDTGRCLKCLYHTEGDHCOLCOYGYGDAL 960
QY 1022 RQDCRKVCNVLGTVKEHNGSDCHCDKATGQCSCLPNVIGQNCDDRCAPNTWQLASGTGC 1081
Db 961 RQDCRKVCNVLGTVKEHNGSDCHCDKATGQCSCLPNVIGQNCDDRCAPNTWQLASGTGC 1020
QY 1082 GPCNCNAAHSFGPSCNEFTGQCQCMPEFGGRTCECQELFWGDPDVECRACDCDPRGIET 1141
Db 1021 GPCNCNAAHSFGPSCNEFTGQCQCMPEFGGRTCECQELFWGDPDVECRACDCDPRGIET 1080
QY 1142 PQCDQSTGQCVCVEGVEGPRCDKCTRGYSGVFPDCTPCHQCFLWDALIGELTNRTHKFL 1201
Db 1081 PQCDQSTGQCVCVEGVEGPRCDKCTRGYSGVFPDCTPCHQCFLWDALIGELTNRTHKFL 1140
QY 1202 EKAKALKISGVIGPYRETVDVSVEKKVNEIKDILAQSPAAPLKNIGILFEEAEKLT KDVT 1261
Db 1141 EKAKALKISGVIGPYRETVDVSVEKKVNEIKDILAQSPAAPLKNIGILFEEAEKLT KDVT 1200
QY 1262 EKMAQVEVKLTDTASQSNSTAGELGALQAEASLDKTVKELAEQLEFIKNSDIOGALDSI 1321
Db 1201 EKMAQVEVKLTDTASQSNSTAGELGALQAEASLDKTVKELAEQLEFIKNSDIOGALDSI 1260
QY 1322 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRVEDLMLERESPKEQEEQARLLDEL 1381
Db 1261 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRVEDLMLERESPKEQEEQARLLDEL 1320
QY 1382 AGKLOSLDLSAAQMTCTGPPGADCSSECGPNCRCTDEGEKKCGGPGCGGLVTVAHSAW 1441
Db 1321 AGKLOSLDLSAAQMTCTGPPGADCSSECGPNCRCTDEGEKKCGGPGCGGLVTVAHSAW 1380
QY 1442 QKAMDFDRDVL SALAEVEQLSKMVSEAKVRADEAKQNAQDVLLKTNATKEKVDKXSNEDLR 1501
Db 1381 QKAMDFDRDVL SALAEVEQLSKMVSEAKVRADEAKQNAQDVLLKTNATKEKVDKXSNEDLR 1440
QY 1502 NLIKQIRNFLTEDSADLDSIEAVANEVLKSGNASTPQQLQNLNLTEDIRERVETLSQVEVIL 1561
Db 1441 NLIKQIRNFLTEDSADLDSIEAVANEVLKSGNASTPQQLQNLNLTEDIRERVETLSQVEVIL 1500
QY 1562 QQSAADIARAEALLLEAKRASKSATDVKTADVMYKEALEEAEKAQVAEAEKAIKQADEDIQ 1621
Db 1501 QQSAADIARAEALLLEAKRASKSATDVKTADVMYKEALEEAEKAQVAEAEKAIKQADEDIQ 1560
QY 1622 GTQNLTSIESETAASEETLTNASQRIKSLERNVEELKRAAQNQSGEAEVIEKVYSVKQ 1681
Db 1561 GTQNLTSIESETAASEETLTNASQRIKSLERNVEELKRAAQNQSGEAEVIEKVYSVKQ 1620

QY 1682 NADDVKKTLDGELDEKYKVESLIAQKTEESADARRKAEELLQNEAKTLLAQANSKLQLE 1741
Db 1621 NADDVKKTLDGELDEKYKVESLIAQKTEESADARRKAEELLQNEAKTLLAQANSKLQLE 1680
QY 1742 DLERKYEDNQKYLEDKAQLVRLEGEVRSLLKDISEKVAVYSTCL 1786
Db 1681 DLERKYEDNQKYLEDKAQLVRLEGEVRSLLKDISEKVAVYSTCL 1725
RESULT 8
ABB81593
ID ABB81593 standard; protein; 1725 AA.
XX ABB81593;
AC ABB81593;
XX 19-SEP-2002 (first entry)
DT 19-SEP-2002 (first entry)
XX Mouse laminin 10 second chain protein sequence SEQ ID NO:12.
DE Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;
XX Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;
KW tissue repair development; laminin; healing; vascular tissue;
KW re-endothelialisation; vascular injury; cell attachment; cell stasis;
KW proliferation; migration.
XX Mus musculus.
OS Mus musculus.
XX WO200250111-A2.
PN WO200250111-A2.
XX 27-JUN-2002.
PD 27-JUN-2002.
XX 21-DEC-2001; 2001WO-US051035.
PF 21-DEC-2001; 2001WO-US051035.
XX 21-DEC-2000; 2000US-0257449P.
PR 28-MAR-2001; 2001US-0279282P.
PR 13-NOV-2001; 2001US-00279282.
XX (BIOS-) BIOSTRATUM INC.
PA (BIOS-) BIOSTRATUM INC.
XX Tryggvason K, Doi M, Thyboll J;
PI WPI; 2002-557650/59.
XX N-PSDB; ABQ72911.
DR WPI; 2002-557650/59.
XX New human laminin-10 proteins, useful for accelerating the healing of
PT vascular tissue, improving the biocompatibility of grafts, or for
PT promoting re-endothelialization at the site of vascular injuries.
XX Claim 9; Page 153-158; 231pp; English.
PS The present invention describes human laminin alpha 5. Also described is
XX an isolated laminin 10. Laminin 10 has vulnery activity. Laminins are
CC useful in maintaining cell/tissue phenotype as well as promoting cell
CC growth and differentiation in tissue repair development. Specifically,
CC laminin 10 can be used for accelerating the healing injuries of vascular
CC tissue, improving the biocompatibility of grafts useful for treating such
CC injuries, for promoting re-endothelialisation at the site of vascular
CC injuries, and promote cell attachment and subsequent cell stasis,
CC proliferation, differentiation, and/or migration. The present sequence
CC represents a second chain protein of laminin 10, from the present
CC invention.
XX Sequence 1725 AA;
SQ Query Match 96.6%; Score 9429; DB 5; Length 1725;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 62 EPYCIVSHLQEDKKCFICDSRDPYHETLNPDShLIENVTTTFAPNRLKIWQSENGVENV 121
Db 1 EPYCIVSHLQEDKKCFICDSRDPYHETLNPDShLIENVTTTFAPNRLKIWQSENGVENV 60
QY 122 TQLDLEAEFHFTLINTFKTFRPAAMLIERSDFGKTGWVRYFAYDCSSFPGISTGP 181

Db 61 TIQLDLEAEFHFTLIMTKTRPAAMLIERSDFGKTGWVRYRYPAYDCESFPFGISTGP 120
Qy 182 MKKVDDIIICDSRYSDIEPSTEGEVI FRALDPAFKIEDPYSPRIONLLKITNLRIFVKLH 241
Db 121 MKKVDDIIICDSRYSDIEPSTEGEVI FRALDPAFKIEDPYSPRIONLLKITNLRIFVKLH 180
Qy 242 TLGDNLLDSRMEIREKYYAYVDMVVRGNCFYGHASECAPVDGVNEEVEGMVHGCMCR 301
Db 181 TLGDNLLDSRMEIREKYYAYVDMVVRGNCFYGHASECAPVDGVNEEVEGMVHGCMCR 240
Qy 302 HNTKGLNCELMDPFYHDL PWRPAEGRNSNACKKCNNEHSSSCHFDMAVFLATGNVSGV 361
Db 241 HNTKGLNCELMDPFYHDL PWRPAEGRNSNACKKCNNEHSSSCHFDMAVFLATGNVSGV 300
Qy 362 CDNCQHTMGRNCEOCKPFYFQHPERDIRDNLCEPCTCDPAGSENGGICDGYTDFSUGL 421
Db 301 CDNCQHTMGRNCEOCKPFYFQHPERDIRDNLCEPCTCDPAGSENGGICDGYTDFSUGL 360
Qy 422 IAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGNGPCDSETGYCYC 481
Db 361 IAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGNGPCDSETGYCYC 420
Qy 482 KRLVTGORCDQCLPOHWGLSNDLDGCRPCDCDGLGALNNSCEDSGQCSCLPHMIGRQCN 541
Db 421 KRLVTGORCDQCLPOHWGLSNDLDGCRPCDCDGLGALNNSCEDSGQCSCLPHMIGRQCN 480
Qy 542 EVESGYFTTLDHYIYEAEANLPGVWVVERQYIQDRIPSWTGPGRVVRPEGAYLEFFI 601
Db 481 EVESGYFTTLDHYIYEAEANLPGVWVVERQYIQDRIPSWTGPGRVVRPEGAYLEFFI 540
Qy 602 DNIPYSMEYEILIRIEPQLPDHWEKAVITVORPGKIPASSRCGNTVPDDNQVWVSLSPGS 661
Db 541 DNIPYSMEYEILIRIEPQLPDHWEKAVITVORPGKIPASSRCGNTVPDDNQVWVSLSPGS 600
Qy 662 RYVVLPRPVCFEKGMNVTVRLELPQYTASGSDVESPYTFIDSLVLMPYCKSLDIFTVGG 721
Db 601 RYVVLPRPVCFEKGMNVTVRLELPQYTASGSDVESPYTFIDSLVLMPYCKSLDIFTVGG 660
Qy 722 GDGEVNTSAWETFORYLENSRSVVKTPMTDVCRNIIIFSISALIHOTGLACECDPQGS 781
Db 661 GDGEVNTSAWETFORYLENSRSVVKTPMTDVCRNIIIFSISALIHOTGLACECDPQGS 720
Qy 782 SSVCDPNGGQCQCRNVVGRTCNRCAPGTFGFGNGCKPCDCCHLQGSASAFCDAITGQCH 841
Db 721 SSVCDPNGGQCQCRNVVGRTCNRCAPGTFGFGNGCKPCDCCHLQGSASAFCDAITGQCH 780
Qy 842 CFQGIYARQCDRLPGYWGFPSCQPCQCNGHALDCDVTGECCLSCQDYTTGHNCCERCLAG 901
Db 781 CFQGIYARQCDRLPGYWGFPSCQPCQCNGHALDCDVTGECCLSCQDYTTGHNCCERCLAG 840
Qy 902 YYGDPPIIGSGDHCRPCPCDPDPSGRQFARSCYQDPVTLQLACVDPGYIGSRCDDCASG 961
Db 841 YYGDPPIIGSGDHCRPCPCDPDPSGRQFARSCYQDPVTLQLACVDPGYIGSRCDDCASG 900
Qy 962 FFGNPSDFGSGCQPCQCHHNIDTTDPEACDKDTGRCLKLYHTEGHCQLCQGYGGDAL 1021
Db 901 FFGNPSDFGSGCQPCQCHHNIDTTDPEACDKDTGRCLKLYHTEGHCQLCQGYGGDAL 960
Qy 1022 RQDCRKVCNYLGTVKEHCNGSDCHCDKATGQCSCLPNVIGONCDRCAPNTWQLASGTGC 1081
Db 961 RQDCRKVCNYLGTVKEHCNGSDCHCDKATGQCSCLPNVIGONCDRCAPNTWQLASGTGC 1020
Qy 1082 GPCNCAHSAFSPSCNEFTGQCQCMPGFGGRTCECQELFWGDPDVECRACDCDPRGIET 1141
Db 1021 GPCNCAHSAFSPSCNEFTGQCQCMPGFGGRTCECQELFWGDPDVECRACDCDPRGIET 1080
Qy 1142 PQCDQSTGQCVCEGVEGPRCDKCTRGYSGVFPDCTPCHQCFCALWDAIIGELTNRTHKFL 1201
Db 1081 PQCDQSTGQCVCEGVEGPRCDKCTRGYSGVFPDCTPCHQCFCALWDAIIGELTNRTHKFL 1140
Qy 1202 EKAKALKISGVIGPYRETVDVSEKKVNEIKDILAQSPAAEPLKNIGILFEEAEKLTQDVT 1261
Db 1141 EKAKALKISGVIGPYRETVDVSEKKVNEIKDILAQSPAAEPLKNIGILFEEAEKLTQDVT 1200

Qy 1262 EKMAQVEVKLTDTASQSNSTAGELGALQAEASLDKTVKELAEQLEFIKNSDIQGALDSI 1321
Db 1201 EKMAQVEVKLTDTASQSNSTAGELGALQAEASLDKTVKELAEQLEFIKNSDIQGALDSI 1260
Qy 1322 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRDRVEDLMLERESPFKEQEEQARLLDEL 1381
Db 1261 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRDRVEDLMLERESPFKEQEEQARLLDEL 1320
Qy 1382 AGKLQSLDLSAAQMTCTGTPPGADCESECGSPNCRTDEGEKKCGGPGCGGLVTVAHSAW 1441
Db 1321 AGKLQSLDLSAAQMTCTGTPPGADCESECGSPNCRTDEGEKKCGGPGCGGLVTVAHSAW 1380
Qy 1442 OKAMDFDRDVL SALAEVQLSKMVSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDLR 1501
Db 1381 OKAMDFDRDVL SALAEVQLSKMVSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDLR 1440
Qy 1502 NLIKQIRNFLTEDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVIL 1561
Db 1441 NLIKQIRNFLTEDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVIL 1500
Qy 1562 QQSAADIARAELELLEAKRASKSATDVKTADVMVKEALEEAEKAQVAAEKAQKQADEDIQ 1621
Db 1501 QQSAADIARAELELLEAKRASKSATDVKTADVMVKEALEEAEKAQVAAEKAQKQADEDIQ 1560
Qy 1622 GTQNL LTSIESETAASEETLTNASQRI SKLERNVEELKRKAAQNSGEAEYIEKVYYSVKQ 1681
Db 1561 GTQNL LTSIESETAASEETLTNASQRI SKLERNVEELKRKAAQNSGEAEYIEKVYYSVKQ 1620
Qy 1682 NADDVKKTLDGELDEKYKVESLIAQKTESADARRKAELLQNEAKTLLAQANSKLQLE 1741
Db 1621 NADDVKKTLDGELDEKYKVESLIAQKTESADARRKAELLQNEAKTLLAQANSKLQLE 1680
Qy 1742 DLERKYEDNQYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1786
Db 1681 DLERKYEDNQYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1725

RESULT 9
AAW50893

ID AAW50893 standard; protein; 1786 AA.

XX AC AAW50893;

XX DT 07-DEC-1998 (first entry)

XX DE Human laminin B1 chain.

XX KW Laminin; human; beta-amyloid; amyloidosis; Alzheimer's disease;
KW Down's syndrome; hereditary cerebral haemorrhage; inflammation;
KW malignancy; Familial Mediterranean Fever; multiple myeloma;
KW type II diabetes; prion disease; Creutzfeldt-Jacob disease; CJD;
KW Gertsmann-Straussler syndrome; kuru; scrapie; haemodialysis;
KW carpal tunnel syndrome; senile cardiac amyloid polynuropathy;
KW Familial Amyloidotic Polynuropathy; thyroid carcinoma; diagnosis;
therapy.

XX OS Homo sapiens.

XX PN WO9815179-A1.

XX PD 16-APR-1998.

XX PF 08-OCT-1997; 97WO-US018145.

XX PR 08-OCT-1996; 96US-0027981P.

XX PA (UNIW) UNIV WASHINGTON.

XX PI Castillo G, Snow AD;

XX DR WPI; 1998-240534/21.

XX XX

PT Use of laminin and fragments - for developing products for use in the
PT diagnosis and treatment of amyloid disease, e.g. Alzheimer's disease or
PT CJD.
XX
PS Claim 15; Page 86-89; 132pp; English.
XX
CC This is the amino acid sequence of the human laminin B1 chain. The
CC primary object of the invention is to use laminin, laminin-derived
CC protein fragments and/or laminin-derived polypeptides as potent
CC inhibitors of amyloid formation, deposition, accumulation and/or
CC persistence in Alzheimer's disease and other amyloidoses. The laminin
CC products (see AAW50888-98) may include mouse or human laminin A or A1
CC chain, laminin B1 or B2 chain, laminin A2 chain (merosin), laminin G1
CC chain, the globular repeats of the laminin A1 chain and the beta-amyloid
CC binding domain of the laminin A chain. A claimed method for treating an
CC amyloid disease comprises administering a polypeptide having a
CC conformational similarity to a fragment of a laminin protein. A method
CC for diagnosing an amyloid disease involves determining levels of laminin
CC in a sample. Production of laminin or its fourth globular repeat in vivo
CC provides a method for in vivo inhibition of beta-amyloid amyloidosis. The
CC products and methods can be used for the diagnosis, prognosis, monitoring
CC and treatment of amyloidoses such as Alzheimer's disease, Down's syndrome
CC and hereditary cerebral haemorrhage with amyloidosis of the Dutch type
CC (where the specific amyloid is the beta-amyloid protein), the amyloidosis
CC associated with chronic inflammation, various forms of malignancy and
CC Familial Mediterranean Fever (AA amyloid or inflammation-association
CC amyloidosis), the amyloidosis associated with multiple myeloma and other
CC B-cell abnormalities (AL amyloid), the amyloidosis associated with type
CC II diabetes (amylin or islet amyloid), the amyloidosis associated with
CC prion diseases including Creutzfeldt-Jacob disease, Gertsmann-Straussler
CC syndrome, kuru and animal scrapie (PrP amyloid), the amyloidosis
CC associated with long-term haemodialysis and carpal tunnel syndrome (beta
CC 2-microglobulin amyloid), the amyloidosis associated with senile cardiac
CC amyloid and Familial Amyloidotic Polyneuropathy (prealbumin or
CC transthyretin amyloid), and the amyloidosis associated with endocrine
CC tumours such as medullary carcinoma of the thyroid (variant of
CC procalcitonin)
XX
SQ Sequence 1786 AA;
Query Match 93.7%; Score 9144; DB 2; Length 1786;
Best Local Similarity 92.7%; Pred. No. 0;
Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;
QY 1 MGLLQVAFGLVWTRVCAQEPFSGYCAEGSCYPATGDLIGRAQKLSVTSTGLHK 60
DB 1 MGLLQLAFSLCARVRAQEPFSGYCAEGSCYPATGDLIGRAQKLSVTSTGLHK 60
QY 61 PEPYCIYVSHLQEDKCFICDSRDPYHETINPDSHLIENVVTPAPNRLKIWQSENGVEN 120
DB 61 PEPYCIYVSHLQEDKCFICNSQDPYHETINPDSHLIENVVTPAPNRLKIWQSENGVEN 120
QY 121 VTIQLDLEAEFFHETHLIMTFKTRPAAMLIERSDDFGKTGWVYRYFAYDCEASFPGISTG 180
DB 121 VTIQLDLEAEFFHETHLIMTFKTRPAAMLIERSDDFGKTGWVYRYFAYDCEASFPGISTG 180
QY 181 PMKKVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPIQNLLKITNLRIFVKL 240
DB 181 PMKKVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPIQNLLKITNLRIFVKL 240
QY 241 HTLGDNLLDSRMEIREKYYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMC 300
DB 241 HTLGDNLLDSRMEIREKYYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMC 300
QY 301 RHNTKGLNCEL CMDFYHDL PWRPAEGRNSNACKKNCNEHSSSCHFFDMAVFLATGNVSGG 360
DB 301 RHNTKGLNCEL CMDFYHDL PWRPAEGRNSNACKKNCNEHSSSCHFFDMAVFLATGNVSGG 360
QY 361 VCDNCQHTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDESIG 420
DB 361 VCDNCQHTMGRNCEQCKPFYFQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFDSTG 420
QY 421 LIAGQCRCKLHVEGERCDVCKEGFYDLSAEDDPYGCKSCACNPLGTIPGPNPCDSETHCY 480

DB 421 LIAGQCRCKLHVEGERCDVCKEGFYDLSSEDFFGCKSCACNPLGTIPGPNPCDSETHCY 480
QY 481 CKRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCDLGGALNNSCSEDSGQCSCPLHMGRCQ 540
DB 481 CKRLVTGQHCDQCLPEHWGLSNDLDGCRPCDCDLGGALNNSCFAESGQCSCRPHMIGRCQ 540
QY 541 NEVESGYFTTLDHYIYEAEEANLGPVVVVERQYIQDRIPSWTGPGFVRVPEGAYLEFF 600
DB 541 NEVEPGYFATLDHYLYEAEEANLGPVSVIVERQYIQDRIPSWTGPGFVRVPEGAYLEFF 600
QY 601 IDNIPYSMEYEILIRYEPQLPDHWEKAVITVORPGKIPASSRCGNTVPDDDNQVVSLSPG 660
DB 601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVORPGRIPTSSRCGNTIPDDDNQVVSLSPG 660
QY 661 SRYVLPFPVCFEKGMYTVRLLELPQYTAGSDVESPYTFIDSLVMPYCKSLDIFTVGG 720
DB 661 SRYVLPFPVCFEKGTYTVRLLELPQYTTSSDSDVESPYTLIDSLVMPYCKSLDIFTVGG 720
QY 721 SGDEVTNSAWETFORYRCLENSRSVVKTPMTDVCNRIIFSISALIHQTGLACECDPQGS 780
DB 721 SGDVVTNSAWETFORYRCLENSRSVVKTPMTDVCNRIIFSISALLHQTGLACECDPQGS 780
QY 781 LSSVCDPENGCGQCQCRPNVVRTCNRCAPGTGFGFPGNGCKPCDCHLQGSASAFCDAITGQC 840
DB 781 LSSVCDPENGCGQCQCRPNVVRTCNRCAPGTGFGFPGSCKPCBCHLQGSVNAFCNPVTGQC 840
QY 841 HCFQGIYARQCDRCLPGYWGFPSPCQCNGHALDCDTVTGECSCQDYTTGHCNRCERCLA 900
DB 841 HCFQGVYARQCDRCLPGHWGFPSPCQCNGHADDCCDPVTGECNLCQDYTMGHCNRCERCLA 900
QY 901 GYGDPIIGSGDHCRCPCPCPDGPDGSRQFARSCYQDPVTIQLACVCDPGYIGSRCDDCAS 960
DB 901 GYGDPIIGSGDHCRCPCPCPDGPDGSRQFARSCYQDPVTIQLACVCDPGYIGSRCDDCAS 960
QY 961 GFFGNPSDFGSGCQPCQCHNIDITTDPEACDKDTGRCLKCLYHTEGDHCLQCYGYGDA 1020
DB 961 GYFGNPSEVSGSCQPCQCHNIDITTDPEACDKETGRCLKCLYHTEGEHCQCFRFGYGGDA 1020
QY 1021 LRQDCRKVCNVLGTVKEHCNGSDCHCDKATGQCSCLPNVIGQNCDCRCAPNTWQLASGTG 1080
DB 1021 LRQDCRKVCNVLGTVQEHGNGSDCQCDKATGQCCLCPNVIGQNCDCRCAPNTWQLASGTG 1080
QY 1081 CGPCNCNAAHSFGPSCNEFTGQCQCMGFGGRTCTSECQELFWGDPDVECRACDCDPRGIE 1140
DB 1081 CDPNCNAAHSFGPSCNEFTGQCQCMGFGGRTCTSECQELFWGDPDVECRACDCDPRGIE 1140
QY 1141 TPQCDQSTGQCVCEGVEGPRCDKCTRGYSVGFPPDCTPHQCFALWDIAIIGELTNRTHKF 1200
DB 1141 TPQCDQSTGQCVCEGVEGPRCDKCTRGYSVGFPPDCTPHQCFALWDVIIAELTNRTHRF 1200
QY 1201 LEKAKALKISGVIGPYRETVDVSVEKVNKIDILAQSPAAPLKNIGILFEEAEKLTQDV 1260
DB 1201 LEKAKALKISGVIGPYRETVDVSVERKVSEIKDILAQSPAAPLKNIGILFEEAEKLTQDV 1260
QY 1261 TEKMAQVEVKLTDTASQSNSTAGELGALQAEAESLDKTVKELAEQLEFIKNSDIOGALDS 1320
DB 1261 TEMMAQVEVKLSDDTTSQSNSTAKELDSLQTEAESLDNTVKELEAEQLEFIKNSDIRGALDS 1320
QY 1321 ITKYFQMSLEAEKRVNASITDPNSTVEQSALTRDRVEDLMLERESPFKEQEEQARLLDE 1380
DB 1321 ITKYFQMSLEAEKRVNASITTEPNSTVEQSALMRDRVEDVMNERESQFKEQEEQARLLDE 1380
QY 1381 LAGKLSLDLSAAAQMTCTGTPPGADCESECEGPNCRITDEGEKCKGPGCGGLVTVVAHSA 1440
DB 1381 LAGKLSLDLSAAAEMTCTGTPPGASCSETECGGPNCRITDEGERKCGGPGCGGLVTVVAHNA 1440
QY 1441 WQKAMDFDRDVL SALAEVEQLSKMVSSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDL 1500
DB 1441 WQKAMDLDDQVLSALAEVEQLSKMVSSEAKLRADEAKQSAEDILLKTNATKEKMDKSNEL 1500
QY 1501 RNLIKQIRNFLTEDSADLDSIEAVANEVLKSGNASTPQOLQNLITEDIRERVETLSQVEVI 1560

Db 1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLMENPSTPQQLQNLTERVESLSQVEVI 1560

QY 1561 LQSSAADIAAEALLLEAKRASKSATDVKVTADMVKEALEEAEKAQVAEKAQADEDI 1620

Db 1561 LQSSAADIAAEALLLEAKRASKSATDVKVTADMVKEALEEAEKAQVAEKAQADEDI 1620

QY 1621 QGTQNLLTSIESETAASEBTLTNASQRIKSLERNVEELKRKAAQNSGEABYIEKVVSVK 1680

Db 1621 QGTQNLLTSIESETAASEBTLFNASQRISELERNVEELKRKAAQNSGEABYIEKVVTVK 1680

QY 1681 QNADDVKKTLDGELDEKYKKVESLIAQKTESADARRKAEALLQNEAKTLLAQANSKLQLL 1740

Db 1681 QSAEDVKKTLDGELDEKYKKVENLIAKTESADARRKAEMLQNEAKTLLAQANSKLQLL 1740

QY 1741 EDLERKYEDNQYLEDKAQELVRLEGEVRSLLKDISQKAVVYSTCL 1786

Db 1741 KDLERKYEDNQRYLEDKAQELARLEGEVRSLLKDISQKAVVYSTCL 1786

RESULT 10

AAB16522

ID AAB16522 standard; protein; 1786 AA.

XX AAB16522;

AC

XX 27-OCT-2000 (first entry)

DT Human laminin protein sequence.

XX

DE

XX Angiogenesis-inhibiting protein receptor; angiogenesis; angiostatin; endostatin; plasminogen; laminin; treatment; wound healing; solid tumour; psoriasis; scleroderma; myocardial angiogenesis; Crohn's disease; cerebral collateral; arteriovenous malformation; rubeosis; cancer; diabetic retinopathy; arthritis; wound healing; peptic ulcer; Helicobacter related disease; fracture; cat scratch fever.

KW

KW

KW

KW

KW

KW

XX

OS Homo sapiens.

XX

PN WO200032631-A2.

XX

PD 08-JUN-2000.

XX

PF 06-DEC-1999; 99WO-US028897.

XX

PR 04-DEC-1998; 98US-00206059.

XX

PA (ENTR-) ENTREMED INC.

XX

PI Macdonald NJ, Sim KL;

XX

DR WPI; 2000-412290/35.

XX

PT New angiogenesis-inhibiting protein receptors, useful in methods for treating diseases and processes that are mediated by angiogenesis, such as solid tumors, psoriasis, scleroderma and myocardial angiogenesis.

XX

PS Claim 1; Fig 6A; 100pp; English.

XX

CC This invention relates to angiogenesis-inhibiting protein receptors, and the DNA sequences encoding them. Angiogenesis is the generation of new blood vessels into a tissue, and normally occurs in wound healing, foetal and embryonal development and the formation of the corpus luteum, endometrium and placenta. Angiostatin is a protein (see AAB16450 and AAA68202) involved in angiogenesis, and has an amino acid sequence similar to that of a plasminogen fragment (see murine plasminogen AAB16490). Angiostatin has the ability to inhibit angiogenesis.

CC

CC Endostatin is also an angiogenesis inhibiting protein (see AAB16451 and AAA68203). Sequences AAA68242 and AAB16522 represent coding and protein sequences of human laminin. Laminin is an angiostatin binding protein, and some of the peptides of the invention share homology with regions of laminin. Peptides AAB16452-B16521 (excluding AAB16490) are the angiogenesis-inhibiting protein receptor fragments of the invention. The peptides bind either angiostatin or endostatin and can be used in methods

CC for treating diseases and processes that are mediated by angiogenesis, such as solid tumors, psoriasis, scleroderma, myocardial angiogenesis, Crohn's disease, cerebral collaterals, arteriovenous malformations, rubeosis, diabetic retinopathy, arthritis, wound healing, peptic ulcers, Helicobacter related diseases, fractures, placental and cat scratch fever. They are useful for the detection and prognosis of cancer. DNA sequences A628204-A628241 encode the peptides of the invention

XX

SQ Sequence 1786 AA;

Query Match 93.7%; Score 9144; DB 3; Length 1786;

Best Local Similarity 92.7%; Pred. No. 0;

Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;

QY 1 MGLIQVFAFGVLALWGTRVCAQEPFESYGAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60

Db 1 MGLLQLLAFSFLALCARVRVRAQEPFESYGAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60

QY 61 PEPYCIIVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVVTTTFAPNRLKIWQSENGVEN 120

Db 61 PEPYCIIVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVVTTTFAPNRLKIWQSENGVEN 120

QY 121 VTIQLDEAEFHTLIMTFKTRPAAMLIERSDFEKTGWVYRYFAYDCESFPFGISTG 180

Db 121 VTIQLDEAEFHTLIMTFKTRPAAMLIERSDFEKTGWVYRYFAYDCESFPFGISTG 180

QY 181 PMKKVDDIICDSRYSDIEPTEGEVIFRALDPAFKIEDPYSPRIQNLLKITNLRKIFVKL 240

Db 181 PMKKVDDIICDSRYSDIEPTEGEVIFRALDPAFKIEDPYSPRIQNLLKITNLRKIFVKL 240

QY 241 HTLGNLLDSRMEIREKYVYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMC 300

Db 241 HTLGNLLDSRMEIREKYVYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMC 300

QY 301 RHNTKGLNCELCMDFYHDLPRPAEGRNSNACKKCNNEHSSSCHFDMAVFLATGNVSGG 360

Db 301 RHNTKGLNCELCMDFYHDLPRPAEGRNSNACKKCNNEHSSSCHFDMAVFLATGNVSGG 360

QY 361 VCDNCQHTMGRNCEQCKPFYFQHPERDIRDPNLCPECTCDPAGSENGGICDGYTDFSVG 420

Db 361 VCDNCQHTMGRNCEQCKPFYFQHPERDIRDPNLCPECTCDPAGSENGGICDGYTDFSVG 420

QY 421 LIAGQCRCKLHVEGERCDVCKEGFYDLSEDPYGCCKSCACNPLGTIPGPNPCDSETCYCY 480

Db 421 LIAGQCRCKLHVEGERCDVCKEGFYDLSEDPYGCCKSCACNPLGTIPGPNPCDSETCYCY 480

QY 481 CKRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCLGGALNNSCEDSGQCSCPLHMGRCQC 540

Db 481 CKRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCLGGALNNSCEDSGQCSCPLHMGRCQC 540

QY 541 NEVESGYFTTLDHYIYEAEANLGPVGVVVERQYIQDRIPSWTGPGRVVRPEGAYLEFF 600

Db 541 NEVEPGYFATLDHYLYEAEANLGPVGSIVERQYIQDRIPSWTGPGRVVRPEGAYLEFF 600

QY 601 IDNIPYSMEYEILIRYEPQLPDHWEKAVITVQRPCKIPASSRCGNTVPDDDNQVVSLSPG 660

Db 601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPCKIPASSRCGNTVPDDDNQVVSLSPG 660

QY 661 SRYVVLPRPVCPEKGMNVTVRLELPQYTASGSDVESPVTFIDSLVLMPCYCKSLDIFTVGG 720

Db 661 SRYVVLPRPVCPEKGMNVTVRLELPQYTASGSDVESPVTFIDSLVLMPCYCKSLDIFTVGG 720

QY 721 SGDGEVNTSAWETFQYRCLENSRSVVKTPMTDVCRNIFISALIHQTGLACECDPQGS 780

Db 721 SGDGEVNTSAWETFQYRCLENSRSVVKTPMTDVCRNIFISALIHQTGLACECDPQGS 780

QY 781 LSSVCDPNGGQCQCRPNVVGRTCNRCAPGTFGFGPNCKPCDCHLQGSASAFCDAITGQC 840

Db 781 LSSVCDPNGGQCQCRPNVVGRTCNRCAPGTFGFGPNCKPCDCHLQGSASAFCDAITGQC 840

QY 841 HCFQGIYARQCDCRLPGYWGFPSCQPCQCNHGHALDCDVTGTGECCLSCQDYTTGHCNCERCLA 900

Db 841 HCFQGIYARQCDCRLPGYWGFPSCQPCQCNHGHALDCDVTGTGECCLSCQDYTTGHCNCERCLA 900

QY 901 GYGDPIIGSDHCRPCPCPDGPDGSRQFARSCYQDPVTLQACVCDPGYIGSRCDDCAS 960
Db 901 GYGDPIIGSDHCRPCPCPDGPDGSRQFARSCYQDPVTLQACVCDPGYIGSRCDDCAS 960
QY 961 GFGNPSDFGSCQPCQCHNIDITDPEACDKOTGRCLKCLYHTEGDHCLQCYGYGDA 1020
Db 961 GYFNGPSEVGSCQPCQCHNIDITDPEACDKOTGRCLKCLYHTEGDHCLQCYGYGDA 1020
QY 1021 LRQDCRKCVCNLYLGTVEHCNGSDCHCDKATGQSCSCLNVIGQNCDCRCAENTWQLASGTG 1080
Db 1021 LRQDCRKCVCNLYLGTVEHCNGSDCHCDKATGQSCSCLNVIGQNCDCRCAENTWQLASGTG 1080
QY 1081 CGPCNCNAHSGFPGSCNEFTGQCCMPGFGGRTCSCEQLFWGDDPDVECRACDCDPRGIE 1140
Db 1081 CDPNCNAHSGFPGSCNEFTGQCCMPGFGGRTCSCEQLFWGDDPDVECRACDCDPRGIE 1140
QY 1141 TPQCDQSTGQCVCEGVGPRCDKCTRGYSVGFPCDTPCHQCFCALWDAIGELTNRTHKF 1200
Db 1141 TPQCDQSTGQCVCEGVGPRCDKCTRGYSVGFPCDTPCHQCFCALWDAIGELTNRTHKF 1200
QY 1201 LEKAKALKISGVIGPYRETVDSEKKNVEIKDILAQSPAAPLKNIGILFEEAEKLTQDV 1260
Db 1201 LEKAKALKISGVIGPYRETVDSEKKNVEIKDILAQSPAAPLKNIGILFEEAEKLTQDV 1260
QY 1261 TEKMAQVEVKLTDTASQSNSTAGELGALQAEASLDKTVKELAEQLEIFKNSDIQGALDS 1320
Db 1261 TEKMAQVEVKLTDTASQSNSTAGELGALQAEASLDKTVKELAEQLEIFKNSDIQGALDS 1320
QY 1321 ITKYFQMSLEAEKRVNASTTDPNSTVEQSAITRDRVEDLMERESPFKEQOEQARLLDE 1380
Db 1321 ITKYFQMSLEAEKRVNASTTDPNSTVEQSAITRDRVEDLMERESPFKEQOEQARLLDE 1380
QY 1381 LAGKLSLDLSAAQMTCTGTPPGADCSSECGGPGNCRDTEGKKCGGCGGLVTVAHSA 1440
Db 1381 LAGKLSLDLSAAQMTCTGTPPGADCSSECGGPGNCRDTEGKKCGGCGGLVTVAHSA 1440
QY 1441 WQKAMDFDRDVLALAEVEQSLKQVSEAKVRADEAKQADVLKTNATKEKVDKSNEDL 1500
Db 1441 WQKAMDFDRDVLALAEVEQSLKQVSEAKVRADEAKQADVLKTNATKEKVDKSNEDL 1500
QY 1501 RNLIQIRNFLTQDSADLSIEAVANEVLKSGNASTPQQLNLTEDIRERVETLSQVEVI 1560
Db 1501 RNLIQIRNFLTQDSADLSIEAVANEVLKSGNASTPQQLNLTEDIRERVETLSQVEVI 1560
QY 1561 LQSAADIARAELLLLEAKRASKSATDVKVTADMVKEALEEAEKQVAAEKAKQADEDI 1620
Db 1561 LQSAADIARAELLLLEAKRASKSATDVKVTADMVKEALEEAEKQVAAEKAKQADEDI 1620
QY 1621 QGTONLLTSIESETAASEETLNASQRIKSLERNVEELKRAAQNSGEAEYIEKVVSYK 1680
Db 1621 QGTONLLTSIESETAASEETLNASQRIKSLERNVEELKRAAQNSGEAEYIEKVVSYK 1680
QY 1681 QNADDVKTLDGELDEKYYKVESLIAQKTESADARRKAELLQNEAKTLLAQANSKLQLL 1740
Db 1681 QNADDVKTLDGELDEKYYKVESLIAQKTESADARRKAELLQNEAKTLLAQANSKLQLL 1740
QY 1741 EDLERKYEDNQYLEDKQAEQVLRLEGEVRSLLKDISEKAVYSTCL 1786
Db 1741 EDLERKYEDNQYLEDKQAEQVLRLEGEVRSLLKDISEKAVYSTCL 1786

RESULT 11
AAB19797
ID AAB19797 standard; protein; 1786 AA.
XX AAB19797;
AC AAB19797;
XX AAB19797;
DT 05-MAR-2001 (first entry)
XX Human laminin 2 beta-1 chain.
DE Laminin 2; human; nerve regeneration; angiogenic; cell adhesion;
XX Laminin 2; human; nerve regeneration; angiogenic; cell adhesion;
KW

degenerative muscle disorder; muscular dystrophy; cell therapy.

Homo sapiens.

Key Location/Qualifiers
Peptide 1..21
Protein /label= Signal_peptide
22..1786
/label= Mature_protein

WO2000066730-A2.

09-NOV-2000.

28-APR-2000; 2000WO-US011378.

30-APR-1999; 99US-0131720P.

15-JUN-1999; 99US-0139198P.

12-JUL-1999; 99US-0143289P.

24-SEP-1999; 99US-0155945P.

(UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.

Yurchenco P;

WPI; 2000-687537/67.

N-PSDB; AAA88897.

Purified laminin 2 protein, useful for research and therapeutic purposes including peripheral nerve regeneration, treatment of degenerative muscle disorders, angiogenesis regulation, and ex vivo cell therapy.

Claim 5; Page 186-191; 305pp; English.

The present sequence is that of the beta-1 chain of human laminin 2. Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1 (100 kDa) chains. It is thought to be specifically required for stabilizing myotubes during skeletal muscle development, and for preventing apoptosis. Genetic defects in its structure or expression are associated with a major type of congenital muscular dystrophy. Laminin 2 is also thought to be important in Schwann cell/basal lamina interactions. The invention provides laminin 2 alpha-2, beta-1 and gamma-1 chain polypeptides (see AAB19791-806) and the polynucleotides encoding them (see AAA88891-906), methods for making recombinant laminin 2, cells that express recombinant laminin 2, and methods for using purified laminin 2 for research and therapeutic purposes including peripheral nerve regeneration, treatment of degenerative muscle disorders, angiogenesis regulation, promoting cell attachment and migration, ex vivo cell therapy, improving the take of grafts, improving the biocompatibility of medical devices and preparing improved culture devices and media

Sequence 1786 AA;

Query Match 93.7%; Score 9144; DB 3; Length 1786;
Best local Similarity 92.7%; Pred. No. 0;
Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;

QY 1 MGLLQVAFGVLAALWGTRVCAQAEPEFSYGCAGSCYPATGDLIGRAQKLSVTSTCGLHK 60
Db 1 MGLLQVAFGVLAALWGTRVCAQAEPEFSYGCAGSCYPATGDLIGRAQKLSVTSTCGLHK 60
QY 61 PEPCIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVTTFAPNRLKIWQSENGVEN 120
Db 61 PEPCIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVTTFAPNRLKIWQSENGVEN 120
QY 121 VTIOQLLEAEFFHFTLINTFKTERPAAMLIERSDDPKTGWVRYFYAYDCESSFPGISTG 180
Db 121 VTIOQLLEAEFFHFTLINTFKTERPAAMLIERSDDPKTGWVRYFYAYDCESSFPGISTG 180
QY 181 PMKKVDDIICDSRYSIDIEPSTEGEVIIFRALDPAFKIEDPSPRIQNLKITNRIKFVKL 240
Db 181 PMKKVDDIICDSRYSIDIEPSTEGEVIIFRALDPAFKIEDPSPRIQNLKITNRIKFVKL 240

QY 241 HTLGDNLLDSRMEIREKYYAYVDMVVRGNCFYGHASECAPVDGVNEEVEGMVHGHCMC 300
Db HTLGDNLLDSRMEIREKYYAYVDMVVRGNCFYGHASECAPVDGVNEEVEGMVHGHCMC 300
QY 301 RHNTKGLNCELMDPFYHDL PWRPAEGRNSNACKKNCNEHSSSCHFDMAVFLATGNVSGG 360
Db RHNTKGLNCELMDPFYHDL PWRPAEGRNSNACKKNCNEHSSSCHFDMAVFLATGNVSGG 360
QY 361 VCDNCQHNTMGRNCEQCKPFYFQHPERDIRDNLCEPCTCDPAGSENGICDGYTDFSVG 420
Db VCDNCQHNTMGRNCEQCKPFYFQHPERDIRDNLCEPCTCDPAGSENGICDGYTDFSVG 420
QY 421 LIAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGPNPCDSETGYCY 480
Db LIAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGPNPCDSETGYCY 480
QY 481 CKRLVTGQRCDQCLPOHWGLSNDLDGCRPCDCLGGALNNSCEDSGQCSCLPHMIGRQC 540
Db CKRLVTGQRCDQCLPOHWGLSNDLDGCRPCDCLGGALNNSCEDSGQCSCLPHMIGRQC 540
QY 541 NEVESGYFTTLDHYTYEAEANLPGVVVVERQYIQDRIPSWTGPVVRVPEGAYLEFF 600
Db NEVESGYFTTLDHYTYEAEANLPGVVVVERQYIQDRIPSWTGPVVRVPEGAYLEFF 600
QY 601 IDNIPYSMEYILIRYEPQLPDHWEKAVITVORPGKIPASSRCGNTPVDDDNQVWSLSPG 660
Db IDNIPYSMEYILIRYEPQLPDHWEKAVITVORPGKIPASSRCGNTPVDDDNQVWSLSPG 660
QY 661 SRYVVLPRPVCFEKGMNVTVRLELPQYTASGSDVESPYTFIDSLVLMPYCKSLDIFTVGG 720
Db SRYVVLPRPVCFEKGMNVTVRLELPQYTASGSDVESPYTFIDSLVLMPYCKSLDIFTVGG 720
QY 721 SGDGEVNTSAWETFQYRCLENSRSVVKTPMTDVCNRIIFSISALIHOTGLACECDPQGS 780
Db SGDGEVNTSAWETFQYRCLENSRSVVKTPMTDVCNRIIFSISALIHOTGLACECDPQGS 780
QY 781 LSSVCDPNGGQCQCRPNVVGRTCNRCAPGTFGFGPNGCKPCDCHLQGSASAFCAITGQC 840
Db LSSVCDPNGGQCQCRPNVVGRTCNRCAPGTFGFGPNGCKPCDCHLQGSASAFCAITGQC 840
QY 841 HCFQGIYARQCRCPLPGYWGFPSPQCQCQCNHGHALDCDVTVTGECSCQDVTGHCNRCCLA 900
Db HCFQGIYARQCRCPLPGYWGFPSPQCQCQCNHGHALDCDVTVTGECSCQDVTGHCNRCCLA 900
QY 901 GYIGDPIIGSGDHCRPCPCPDGPDGSGRQFARSCYQDPVTLQLACVCDPGYIGSRCDDCAS 960
Db GYIGDPIIGSGDHCRPCPCPDGPDGSGRQFARSCYQDPVTLQLACVCDPGYIGSRCDDCAS 960
QY 961 GFFGNPSDFGSCQPCQCHHNIDTTDPEACDKTGRCLKCLYHTEGHQCLCQYGYGDA 1020
Db GYFGNPSDFGSCQPCQCHHNIDTTDPEACDKTGRCLKCLYHTEGHQCLCQYGYGDA 1020
QY 1021 LRQDCRKVCVNYLGTVKEHNGSGDCHCDKATGQCSCLPNVIGQNCDCRCAPNTWQLASGTG 1080
Db LRQDCRKVCVNYLGTVKEHNGSGDCHCDKATGQCSCLPNVIGQNCDCRCAPNTWQLASGTG 1080
QY 1081 CGPCNCNAAHSFGPSCNFTGQCQCMPGFGGRITCSECQELFWGDDPVECRACDCDPRGIE 1140
Db CGPCNCNAAHSFGPSCNFTGQCQCMPGFGGRITCSECQELFWGDDPVECRACDCDPRGIE 1140
QY 1141 TPQCDQSTGQCVCVEGVEGRCDKCTRGYSGVFPDCTPCHQCFCALWDALIGELTNRTHKF 1200
Db TPQCDQSTGQCVCVEGVEGRCDKCTRGYSGVFPDCTPCHQCFCALWDALIGELTNRTHKF 1200
QY 1201 LEKAKALKISGVIGPYRETVDVSVEKKVNEIKDILAQSPAAEPLKNIGILFEEAEKLTQDV 1260
Db LEKAKALKISGVIGPYRETVDVSVERKVSEIKDILAQSPAAEPLKNIGILFEEAEKLTQDV 1260
QY 1261 TERMAQVEVKLTDTASQSNSTAGELGALQAEASLDKTVKELAEQLEFIKNSDIQGALDS 1320
Db TERMAQVEVKLSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDS 1320

QY 1321 ITKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLERESPFKEQEEQARLLDE 1380
Db ITKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLERESPFKEQEEQARLLDE 1380
QY 1381 LAGKLOSLDLSAAAQMTCGTPPGADCSESECGGPNCRCTDEGEKKCGGPGCGGLVTVAHSA 1440
Db LAGKLOSLDLSAAAQMTCGTPPGASCSETTECGGPNCRCTDEGERKCGGPGCGGLVTVAHNA 1440
QY 1441 WQKAMDFDRDVL SALAEVEQLSKMVSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDL 1500
Db WQKAMDFDRDVL SALAEVEQLSKMVSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDL 1500
QY 1501 RNLIKQIRNFLTEDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVI 1560
Db RNLIKQIRNFLTEDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVI 1560
QY 1561 LQOSAADIARAELLLEAKRASKSATDVKTADMVKEALEEAEKAQVAAEKAIKQADEDI 1620
Db LQOSAADIARAELLLEAKRASKSATDVKTADMVKEALEEAEKAQVAAEKAIKQADEDI 1620
QY 1621 QGTQNLTSIESETAASEETLTNASQRI SKLERNVEELKRKAAQNSGEAEYIEKVYYSVK 1680
Db QGTQNLTSIESETAASEETLTNASQRI SKLERNVEELKRKAAQNSGEAEYIEKVYYSVK 1680
QY 1681 QNADDVVKTLTGELDEKYKKVESLIAQKTEESADARRKAELLQNEAKTLLAQANSKLQLL 1740
Db QNADDVVKTLTGELDEKYKKVESLIAQKTEESADARRKAELLQNEAKTLLAQANSKLQLL 1740
QY 1741 EDLERKYEDNQKYLEDKAQELVRLGEVRSLLKDXISEKVAVYSTCL 1786
Db EDLERKYEDNQKYLEDKAQELVRLGEVRSLLKDXISEKVAVYSTCL 1786
RESULT 12
AAB48448
ID AAB48448 standard; protein; 1786 AA.
XX AAB48448;
AC AAB48448;
XX 02-MAR-2001 (first entry)
XX Human laminin 8 polypeptide, SEQ ID NO: 14.
DE Human; laminin 8; neuroprotective; angiogenic; osteopathic;
KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;
KW vascular tissue injury; neural injury; angiogenesis regulation.
XX Homo sapiens.
XX WO200066732-A2.
PN 09-NOV-2000.
XX 28-APR-2000; 2000WO-US011543.
XX 30-APR-1999; 99US-0131720P.
PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.
PR 11-FEB-2000; 2000US-0182012P.
XX (BIOS-) BIOSTRATUM INC.
XX Kortessmaa J, Tryggvason K;
PI WPI; 2000-687539/67.
XX N-PSDB; AAC83709.
DR Purified laminin 8 protein, useful for research and therapeutic purposes
DR including peripheral nerve regeneration, treatment of degenerative muscle
XX disorders, angiogenesis regulation, and ex vivo cell therapy.
PS Claim 5; Page 150-155; 245pp; English.
XX

CC The present sequence is a laminin 8 polypeptide chain. Laminins are a
CC family of heterotrimeric glycoproteins that function via binding
CC interactions with neighbouring cell receptors and by forming laminin
CC networks. They are signalling molecules which influence cellular
CC function. Laminin 8 is useful for treating injuries to tissue of
CC mesenchymal origin, such as bone, cartilage, tendon, and ligament,
CC treating injuries to vascular tissue, promoting cell attachment and
CC migration, ex vivo cell therapy, improving the biocompatibility of
CC medical devices, and preparing improved cell culture devices and media.
CC Laminin 8 is also useful for promoting re-endothelialisation at the site
CC of vascular injuries, improving the take of grafts, improving the
CC biocompatibility of medical devices, treating neural injuries (neural
CC regeneration), regulating angiogenesis, and promoting cell attachment and
CC migration
XX
SQ Sequence 1786 AA;

Query Match 93.7%; Score 9144; DB 3; Length 1786;
Best Local Similarity 92.7%; Pred. No. 0;
Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;

QY	1	MGLLOVAFGLALWGTRVCAQEPFESYGCAEGSCYPATGDLIGRAQKLSVTSTCGLHK	60
Db	1	MGLLQLAFSLALCARVARAQEPFESYGCAEGSCYPATGDLIGRAQKLSVTSTCGLHK	60
QY	61	PEPYCIVSHLQEDKCKFCICSDRDPYHETLNPDShLIENVTTFAPNRLKIWQSENGVEN	120
Db	61	PEPYCIVSHLQEDKCKFCICNSQDPYHETLNPDShLIENVTTFAPNRLKIWQSENGVEN	120
QY	121	VTIQDLEAEFHFTHLIMTFKTPRPAAMLIERSSDFGKTGWVYRYFAYDCESPPISTG	180
Db	121	VTIQDLEAEFHFTHLIMTFKTPRPAAMLIERSSDFGKTGWVYRYFAYDCESPPISTG	180
QY	181	PMKKVDDIICDSRYSYDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLLKITNLRIFVKL	240
Db	181	PMKKVDDIICDSRYSYDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLLKITNLRIFVKL	240
QY	241	HTLGNLLDSRMEIREKYYIYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMC	300
Db	241	HTLGNLLDSRMEIREKYYIYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMC	300
QY	301	RHNTKGLNCELAMDYHDLPRPABGRNSNACKKNCNNEHSSCHFDMAVFLATGNVSGG	360
Db	301	RHNTKGLNCELAMDYHDLPRPABGRNSNACKKNCNNEHSSCHFDMAVFLATGNVSGG	360
QY	361	VCDNCQHTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVG	420
Db	361	VCDNCQHTMGRNCEQCKPFYFQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTG	420
QY	421	LIAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGPNPCDSETGYCY	480
Db	421	LIAGQCRCKLHVEGERCDVCKEGFYDLSSEDPFYDLSAEDPYGCKSCACNPLGTIPGPNPCDSETGYCY	480
QY	481	CKRLVTGQRCDQCLPQHWGLSNDLDCRPPCDLGGALNNSCEDSDSGQCSCLPHMIGRQC	540
Db	481	CKRLVTGQRCDQCLPEHWGLSNDLDCRPPCDLGGALNNSCFAESGQCSCLPHMIGRQC	540
QY	541	NEVESGYFTTLDHYIYEAEANLGPVWVVERQYIQDRIPSWTGPVVRVPEGAYLEFF	600
Db	541	NEVEPGYFATLDHYLYEAEANLGPVSVIVERQYIQDRIPSWTGPVVRVPEGAYLEFF	600
QY	601	IDNIPYSMEYELIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTVPDDNQVVSLSPG	660
Db	601	IDNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPRIPTSSRCGNTIPDDNQVVSLSPG	660
QY	661	SRYVLPVPVCFEKGMMYTVRLELPQYTAGSDVESPYTFIDSLVLMYPYCKSLDIFTVGG	720
Db	661	SRYVLPVPVCFEKGMMYTVRLELPQYTAGSDVESPYTIDSLVLMYPYCKSLDIFTVGG	720
QY	721	SGDGEVNTSAWETFRYRCLENSRSVVKTPMTDVCRNIIIFSALIHQTLGACEDPQGS	780
Db	721	SGDGVVNTSAWETFRYRCLENSRSVVKTPMTDVCRNIIIFSISALLHQTGLACEDPQGS	780

RESULT 13
AAB90788
ID AAB90788 standard; protein; 1786 AA.
XX

QY	781	LSSVCDPNGGQCCQRENVVGRTCNRCAPGTFGFGPNGCKPCDCHLQGSASAFCDAITGQC	840
Db	781	LSSVCDPNGGQCCQRENVVGRTCNRCAPGTFGFGSGCKPCECHLQGSVNAFCNPVTGQC	840
QY	841	HCFQGIYARQCDRCLPGYWGFPSCQPCQCNHGLDCTVTGECSCQDYTTGHCNRCCLA	900
Db	841	HCFQGIYARQCDRCLPGHGWFPSCQPCQCNHGLDCTVTGECSCQDYTTGHCNRCCLA	900
QY	901	GYGDPPIIGSGDHCRCPCPDGPDGSGRQFARSCVQDPVTLQACVCDPGYIGSRCDDCAS	960
Db	901	GYGDPPIIGSGDHCRCPCPDGPDGSGRQFARSCVQDPVTLQACVCDPGYIGSRCDDCAS	960
QY	961	GFFGNPSDFGGSCQPCQCHNIDTTPDPAECDKDTGRCLKCLYHTEGDHCLQCYGYGDA	1020
Db	961	GYFGNPSEVGGSCQPCQCHNIDTTPDPAECDKETGRCLKCLYHTEGHCQCFRFGYGDA	1020
QY	1021	LRQDCRKCVCNYLGTVKEHNGSDCHCDKATGQCCSLPNVIGQNCDCRCAPNTWQLASGTG	1080
Db	1021	LRQDCRKCVCNYLGTVQEHNGSDCQCDKATGQCCSLPNVIGQNCDCRCAPNTWQLASGTG	1080
QY	1081	CGPCNCAAHSGFSPCNEFTGQCQCMFGFGGRTCEQCELFWDGPDVECRACDCDPRGIE	1140
Db	1081	CDPCNCAAHSGFSPCNEFTGQCQCMFGFGGRTCEQCELFWDGPDVECRACDCDPRGIE	1140
QY	1141	TPQCDOSTGQCVCEGVEGPRCDKCTRGYSVGFDPCTPCHQCFALMDAIIGELTNRTHKF	1200
Db	1141	TPQCDOSTGQCVCEGVEGPRCDKCTRGYSVGFDPCTPCHQCFALMDVIIAELTNRTHRF	1200
QY	1201	LEKAKALKISGVIGPYRETVDSEKKNVEIKDILAQSPAAPLKNIGILFEEAEKLTADV	1260
Db	1201	LEKAKALKISGVIGPYRETVDSEKKNVEIKDILAQSPAAPLKNIGILFEEAEKLIKDV	1260
QY	1261	TEKMAQVEVKLTDTASQSNSTAGELGALQAEAEESLDKTVKELAEQLEFIKNSDIQALDS	1320
Db	1261	TEKMAQVEVKLSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDS	1320
QY	1321	ITKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVMMERESQFKEQEQEARLLDE	1380
Db	1321	ITKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVMMERESQFKEQEQEARLLDE	1380
QY	1381	LAKLQSLDLSAAQMTCTGTPPGADCSSECGGPNCRDTDEGKCKGPGCGGLVTVAHSA	1440
Db	1381	LAKLQSLDLSAAQMTCTGTPPGASCSETECGGPNCRDTDEGKCKGPGCGGLVTVAHNA	1440
QY	1441	WQKAMDEDRDVLALAEVEQLSKMVSEAKVRADEAKQNAQDVLKTNATKEKVDKSNEDL	1500
Db	1441	WQKAMDLDQDVLALAEVEQLSKMVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNEEL	1500
QY	1501	RNLIKQIRNFLTEDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVI	1560
Db	1501	RNLIKQIRNFLTQDSADLDSIEAVANEVLKMEPSTPQQLQNLTEDIRERVESLSQVEVI	1560
QY	1561	LQQAADIAAEALLLEAEKRAKSKSATDVKTADVMVKEALBEAEKAQVAAEKAIQADEDI	1620
Db	1561	LQHAADIAAEALLLEAEKRAKSKSATDVKTADVMVKEALBEAEKAQVAAEKAIQADEDI	1620
QY	1621	QGTQNLTSISETAASEETLTNASQRIKSLERNVEELKRAAQNSGEAEYIEKVVSVK	1680
Db	1621	QGTQNLTSISETAASEETLFNASQRISELERNVEELKRAAQNSGEAEYIEKVVTVK	1680
QY	1681	QNAEDVKKTLDDGELDEKYYKVESLIAQKTEESADARRKAEILLQNEAKTLQAQNSKLQLL	1740
Db	1681	QSAEDVKKTLDDGELDEKYYKVENLIAKTEESADARRKAEILLQNEAKTLQAQNSKLQLL	1740
QY	1741	EDLERKYEDNQKYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL	1786
Db	1741	KDLERKYEDNQRYLEDKAQELARLEGEVRSLLKDISQKVAVYSTCL	1786

AC AAB90788;
XX
DT 15-JUN-2001 (first entry)
XX
DE Human shear stress-response protein SEQ ID NO: 76.
XX
KW Human; shear stress-response protein; vascular disease; arteriosclerosis.
XX
OS Homo sapiens.
XX
PN WO200125427-A1.
XX
PD 12-APR-2001.
XX
PF 02-OCT-2000; 2000WO-JP006840.
XX
PR 01-OCT-1999; 99JP-00280976.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PA (NOJI/) NOJIMA H.
XX
PI Nojima H, Yoshisue H, Obayashi M, Ota T, Kawabata A, Sakurada K;
PI Kuga T, Sekine S, Nakamura Y, Sugano S;
XX
DR WPI; 2001-266308/27.
DR N-PSDB; AAH02911.
XX
PT DNA sequences, proteins encoded by them and antibodies against them
PT useful in diagnosis and treatment of vascular disease caused by
PT arteriosclerosis.
XX
PS Claim 60; Page 440-449; 678pp; Japanese.
XX
CC The present invention provides the protein and coding sequences of a
CC number of human shear stress response proteins. These are useful in the
CC diagnosis, treatment and screening of vascular diseases caused by
CC arteriosclerosis, including heart failure, post-PTCA restenosis and
CC hypertension
XX
SQ Sequence 1786 AA;

Query Match 93.7%; Score 9144; DB 4; Length 1786;
Best Local Similarity 92.7%; Pred. No. 0;
Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;

QY 1 MGLLQVAFGLVWTRVCAQEPFESYGCAGSCYPATGDLILIGRAQLSVTSTCGLHK 60
Db
QY 61 PEPYCIIVSHLQEDKKCFICDSRDPYHETLNPDHSHLIENVVTFAPNRLKIWWQSENGVEN 120
Db 61 PEPYCIIVSHLQEDKKCFICNSQDPYHETLNPDHSHLIENVVTFAPNRLKIWWQSENGVEN 120
QY 121 VTIQLDLEAEFHFTHLINTFKTFRPAAMLIERSSDFGKTGWVYRYPAYDCEASFPGISG 180
Db 121 VTIQLDLEAEFHFTHLINTFKTFRPAAMLIERSSDFGKTGWVYRYPAYDCEASFPGISG 180
QY 181 PMKKVDDIIICDSRYSYDIEPSTEGEVIFRALDPAFKIEDPYSPRIQNLLKITNLRIFVKL 240
Db 181 PMKKVDDIIICDSRYSYDIEPSTEGEVIFRALDPAFKIEDPYSPRIQNLLKITNLRIFVKL 240
QY 241 HTLGDNLLDSRMEIREKYIYAVYDMVVRGNCFCYGHASECAPVDGVNVEEVMVHGCMC 300
Db 241 HTLGDNLLDSRMEIREKYIYAVYDMVVRGNCFCYGHASECAPVDGVNVEEVMVHGCMC 300
QY 301 RHNTKGLNCELAMDYFHDLPWRPAEGRNSNACKKNCNEHSSSCHFDMAVELATGNVSGG 360
Db 301 RHNTKGLNCELAMDYFHDLPWRPAEGRNSNACKKNCNEHSISCHFDMAVELATGNVSGG 360
QY 361 VCDNCQHNTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVG 420
Db 361 VCDNCQHNTMGRNCEQCKPFYFQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSG 420

QY 421 LIAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGGNPCDSETGYCY 480
Db
QY 481 CKRLVTGQRCDQCLPQHWGLSNDLDCRCPCDCLGGALNNSCEDSGCCSCLPHMIGRQC 540
Db
QY 541 NEVESGYFTTLDHYIYEAEANLPGVVVVERQYIQDRIPSWTGTGPFVRVPEGAYLEFF 600
Db
QY 601 IDNIPYSMEYILIRYEPQLPDHWEKAVITVORPGKIPASSRCNGTVPDNDNQVLSLSPG 660
Db
QY 661 SRYVWLPRPVCFEKGMNYTVRLELPQYTAGSDVESPYTFIDSLVLMPYCKSLDIFTVGG 720
Db
QY 721 SGDGEVNTSAWETFQYRCLENSRSVVKTMTDVCRNIIIFSISALIHQTGLACECDPQGS 780
Db
QY 781 LSSVCDPNGGQCQCRPNVVGRTCNRCAPGTGFGPNGCKPCDCHLOGSASAFCDAITGQC 840
Db
QY 841 HCFQGIYARQCDCRLPGYMGFPSCQPCQCNHGLDCTVTGECSCQDYTTGHCERCLA 900
Db
QY 901 GYGDPIIGSGDHCRCPCPDGPDGSGRQFARSCYQDPVTLOLACVCDPGYIGSRCDCCAS 960
Db
QY 961 GFFGNPSDFGSGCQPCQCHNIDTTDPEACDKDTGRCLKCLYHTEGDHCOLQYGYGDA 1020
Db
QY 1021 LRQDCRKVCVNYLGTVEHCNGSDCHCDKATGCQSCCLPNVIGQNCDCRCAPNTWQLASGTG 1080
Db
QY 1081 CGPCNCAAHSGFSPSCNEFTGCQCMFPGFGRGTCECQELFWGDPDVECRACDCCDPRGIE 1140
Db
QY 1141 TPQCDQSTGQCVCVEGVEGPRCDKCTRGYSGVFPDCTPCHQCFALWDAIIGELTNRTHKF 1200
Db
QY 1201 LEKAKALKISGIVIGPYRETVDVSEKVNKNEIKDILAQSPAAEPLKNIGILFEEAEKLTQDV 1260
Db
QY 1261 TEKMAQVEVKLTDTASQSNSTAGELGALQAEASLDKTVKELAEQLEFIKNSDIQGALDS 1320
Db
QY 1321 ITKYFQMSLEAEKRVNASTTDPNSTVEQSALTFRDVEDLMLERESPFKEQEEQARLLDE 1380
Db
QY 1381 LAGKIQSLDLSAAQMTGCTPPGADCSSECGGPNCRDTEGEKKCGGPGCGGLVTVVAHSA 1440
Db
QY 1441 WQKAMDFFDRDVLALAEVEQLSKMVSEAKVRADEAKQNAQDVLTKTNATKEKVDKSNEDL 1500
Db
QY 1501 RNLKIQIRNFLTEDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVERTLSQVEVI 1560

Db 1501 RNLKQIRNFLTQDSADLDSIEAVANEVLKMPSTPQQLQNLTDIRERVESLSQVEVI 1560
QY 1561 LQSAADIAARAELLLLEAKRASKSATDVKVTADMVKEALEEAEKAQVAAEKAIKQADEDI 1620
Db 1561 LQSAADIAARAELLLLEAKRASKSATDVKVTADMVKEALEEAEKAQVAAEKAIKQADEDI 1620
QY 1621 QGTQNLTSIESETAASEETLTNASQRIKSLERNVEELKRAAQNSGEAEYIEKVYYSVK 1680
Db 1621 QGTQNLTSIESETAASEETLTNASQRISELERNVEELKRAAQNSGEAEYIEKVYVTVK 1680
QY 1681 QNADDVKKTLDGELDEKYYKKVESLIAQKTEESADARRKAEMLQNEAKTLQAQANSKLQLL 1740
Db 1681 QSAEDVKKTLDGELDEKYYKKVENLIAKTEESADARRKAEMLQNEAKTLQAQANSKLQLL 1740
QY 1741 EDLERKYEDNQYLEDKAOELVRLEGEVRSLLKDISEKVAVYSTCL 1786
Db 1741 KDLERKYEDNQYLEDKAOELARLEGEVRSLLKDISQKVAVYSTCL 1786

RESULT 14
ABB81590
ID ABB81590 standard; protein; 1786 AA.
XX ABB81590;
AC ABB81590;
XX 19-SEP-2002 (first entry)
XX Human laminin 10 second chain protein sequence SEQ ID NO:6.
DE Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;
KW tissue repair development; laminin; healing; vascular tissue;
KW re-endothelialisation; vascular injury; cell attachment; cell stasis;
KW proliferation; migration.
XX Homo sapiens.

Key Location/Qualifiers
FT Peptide 1..21
FT /label= signal
FT Protein 22..1786
FT /label= laminin_10_second_chain

XX WO200250111-A2.
PN 27-JUN-2002.
XX 21-DEC-2001; 2001WO-US051035.
XX 21-DEC-2000; 2000US-0257449P.
PR 28-MAR-2001; 2001US-0279282P.
PR 13-NOV-2001; 2001US-00279282.
XX (BIOS-) BIOSTRATUM INC.
XX Tryggvason K, Doi M, Thyboll J;
PI WPI; 2002-557650/59.
XX N-PSDB; ABQ72908.
DR New human laminin-10 proteins, useful for accelerating the healing of
XX vascular tissue, improving the biocompatibility of grafts, or for
PT promoting re-endothelialization at the site of vascular injuries.
XX Claim 9; Page 113-119; 231pp; English.

XX The present invention describes human laminin alpha 5. Also described is
CC an isolated laminin 10. Laminin 10 has vulnerary activity. Laminins are
CC useful in maintaining cell/tissue phenotype as well as promoting cell
CC growth and differentiation in tissue repair development. Specifically,
CC laminin 10 can be used for accelerating the healing injuries of vascular
CC tissue, improving the biocompatibility of grafts useful for treating such
CC injuries, for promoting re-endothelialisation at the site of vascular

CC injuries, and promote cell attachment and subsequent cell stasis,
CC proliferation, differentiation, and/or migration. The present sequence
CC represents a second chain protein of laminin 10, from the present
CC invention
XX
SQ Sequence 1786 AA;

Query Match 93.7%; Score 9144; DB 5; Length 1786;
Best Local Similarity 92.7%; Pred. No. 0;
Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;

QY 1 MGLLQVFAFGVLALWGTRVCAQBEPEFSYGAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60
Db 1 MGLLQLLAFSFLALCRARVRAQEPFESYGAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60
QY 61 PEPYCIIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVVTTFAPNRLKIWWQSENGVEN 120
Db 61 PEPYCIIVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVVTTFAPNRLKIWWQSENGVEN 120
QY 121 VTIQLDLAEAFHFTLIMTFKTPFAAMLIERSDDFGKTGWVYRYFAYDCESFPFGISTG 180
Db 121 VTIQLDLAEAFHFTLIMTFKTPFAAMLIERSDDFGKTGWVYRYFAYDCESFPFGISTG 180
QY 181 PMKKVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPRIQNLLKITNLRKIFVKL 240
Db 181 PMKKVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPRIQNLLKITNLRKIFVKL 240
QY 241 HTLGDNLDSRMEIREKYYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMC 300
Db 241 HTLGDNLDSRMEIREKYYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMC 300
QY 301 RHNTKGLNCEL CMDFYHDLWPRAEGRNSNACKKCNNEHSSSCHFDMAVFLATGNVSGG 360
Db 301 RHNTKGLNCEL CMDFYHDLWPRAEGRNSNACKKCNNEHSSSCHFDMAVFLATGNVSGG 360
QY 361 VCDNCQHNMTGRNCEQCKPFYFQHPERDIRDNLCEPCTCDPAGSENGGICDGYTDFSVG 420
Db 361 VCDNCQHNMTGRNCEQCKPFYFQHPERDIRDNLCEPCTCDPAGSENGGICDGYTDFSVG 420
QY 421 LIAGQCRCKLHVEGERCDVCKEGFYDLSEAEDPYGCKSCACNPLGTIPGPNPCDSETGYCY 480
Db 421 LIAGQCRCKLHVEGERCDVCKEGFYDLSEAEDPYGCKSCACNPLGTIPGPNPCDSETGYCY 480
QY 481 CKRLVTGQRCDQCLPQHGLSNDLDCGRPCDCDLGGLNNSCSESDSGQCSCLPHMIGRQC 540
Db 481 CKRLVTGQRCDQCLPQHGLSNDLDCGRPCDCDLGGLNNSCSESDSGQCSCLPHMIGRQC 540
QY 541 NEVESGYFTTLDHYIYEAEANLCPGVVVERQYIQDRIPSWTGPVVRVPEGAYLEFF 600
Db 541 NEVESGYFTTLDHYIYEAEANLCPGVVVERQYIQDRIPSWTGPVVRVPEGAYLEFF 600
QY 601 IDNIPYSMEYEILIRYEPQLPDHWEKAVITVQRPCKIPASSRCGNTVPDDDNQVVSLSPG 660
Db 601 IDNIPYSMEYEILIRYEPQLPDHWEKAVITVQRPCKIPASSRCGNTVPDDDNQVVSLSPG 660
QY 661 SRYVVLPRPVCPEKGMNYYTVRLELPQYTAGSDVESPYTFIDSLVLMYPYCKSLDIFTVGG 720
Db 661 SRYVVLPRPVCPEKGMNYYTVRLELPQYTAGSDVESPYTFIDSLVLMYPYCKSLDIFTVGG 720
QY 721 SGDEVTNSAWETFORYRCLNSRSVVKTPMTDVCNIIIFSALIHQTGLACECDPQGS 780
Db 721 SGDEVTNSAWETFORYRCLNSRSVVKTPMTDVCNIIIFSALIHQTGLACECDPQGS 780
QY 781 LSSVCDPNNGGQCQCRPNVVGRTCNRCAPGTGFGPNCKPCDCHLQGSASAFCDAITGQC 840
Db 781 LSSVCDPNNGGQCQCRPNVVGRTCNRCAPGTGFGPNCKPCDCHLQGSASAFCDAITGQC 840
QY 841 HCFQGIYARQCDRLPGYWGFPSCQPCQCNHGLDCTVTGECISQDYYTTGHCNRCCLA 900
Db 841 HCFQGIYARQCDRLPGYWGFPSCQPCQCNHGLDCTVTGECISQDYYTTGHCNRCCLA 900
QY 901 GYGDPIIGSGDHCRPCPCPDGPDGSGRQFARSCYQDPVTLOLACVCDPGYIGSRCDDCAS 960
Db 901 GYGDPIIGSGDHCRPCPCPDGPDGSGRQFARSCYQDPVTLOLACVCDPGYIGSRCDDCAS 960

Db 901 GYGDPILIGSDHCRPCPCPDGPDGSRQFARSCYQDPVTLQLACVCDPVGIGSRCDDCAS 960

Qy 961 GFFGNPSDFGSCQPCQCHHNIDITDPEACDKOTGRCLKCLYHTEGDHCQLCQYGYVGDA 1020

Db 961 GYFGNPSEVGSCQPCQCHHNIDITDPEACDKOTGRCLKCLYHTEGEHCQFCRFGYVGDA 1020

Qy 1021 LRQDCRKVCNVLGTVKEHCHNGSDCHCDKATGCSCCLPNVIGQNCDCRCAPNTWQLASGTG 1080

Db 1021 LRQDCRKVCNVLGTVQEHCHNGSDCQCDKATGCCLCLPNVIGQNCDCRCAPNTWQLASGTG 1080

Qy 1081 CGPCNCNAAHSPGSCNEFTGCQCMPPGFGGRTCECQELFWGDPDVECRACDCDPRGIE 1140

Db 1081 CDPNCNAAHSPGSCNEFTGCQCMPPGFGGRTCECQELFWGDPDVECRACDCDPRGIE 1140

Qy 1141 TPQCDQSTGQCVCEGVGPRCDKCTRGYSVFPDCTPCHQCFCALWDVIAELTNRTHKF 1200

Db 1141 TPQCDQSTGQCVCEGVGPRCDKCTRGYSVFPDCTPCHQCFCALWDVIAELTNRTHRF 1200

Qy 1201 LEKAKALKISGIVGYPYRETVDVSEKKNVNEIKDILAQSPAAEPLKNIGILFEEAEKLTQDV 1260

Db 1201 LEKAKALKISGIVGYPYRETVDVSEKKNVNEIKDILAQSPAAEPLKNIGILFEEAEKLTQDV 1260

Qy 1261 TEKMAQVEVKLTDTASQSNSTAGELGALQAEBSLDKTVKELABOLEFIKNSDIOGALDS 1320

Db 1261 TEMMAQVEVKLSDTTSQSNSTAKELDSLQTEABSLDNTVKELABOLEFIKNSDIRGALDS 1320

Qy 1321 ITKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLERESPFEQEEQARLLDE 1380

Db 1321 ITKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDVMMERESQFEKEQEEQARLLDE 1380

Qy 1381 LAGKLSLDLSAAAMTCGTPPGADCSEECGPNCRCTDEGEKKCGGPGCGGLVTVAHSA 1440

Db 1381 LAGKLSLDLSAAAMTCGTPPGASCSETECGGPNCRCTDEGERKCGGPGCGGLVTVAHNA 1440

Qy 1441 WQKAMDFDRDVLASALAEVQLSKWSEAKVRADEAKQNAQDVLKTNATKEKVDKSNEDL 1500

Db 1441 WQKAMDLQDVLASALAEVQLSKWSEAKLRADAQSAEDILLKTNATKEKMDKSNEL 1500

Qy 1501 RNLIKQIRNFLTSDSADLDSIEAVANEVLKSGNASTPQQLQNLNLTEDIRERVETLSQVEVI 1560

Db 1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKNEMPSTPQQLQNLNLTEDIRERVESLSQVEVI 1560

Qy 1561 LQQSAADIARAEILLLEAKRASKSATDVKTADVMVKEALEEAEKAAQVAAEKAIKQADEDI 1620

Db 1561 LQHSAAADIARAEMLLEAKRASKSATDVKTADVMVKEALEEAEKAAQVAAEKAIKQADEDI 1620

Qy 1621 QGTQNLNLTISSETAASEETLTNASQRISKLERNVEELKRKAQNSGEAEYIEKVYYSVK 1680

Db 1621 QGTQNLNLTISSETAASEETLFNASQRISSELERNVEELKRKAQNSGEAEYIEKVYTVK 1680

Qy 1681 QNADDVKTLTGELDEKYKKVESLIAQKTESADARRKAEALLQNEAKTLLAQANSKLQLL 1740

Db 1681 QSAEDVKTLTGELDEKYKKVENLIAKTESADARRKAEMLQNEAKTLLAQANSKLQLL 1740

Qy 1741 EDLERKYEDNQKLEDKAQELVRLGEVRSLLKDISQKAVVYSTCL 1786

Db 1741 KDLERKYEDNORYLEDKAQELARLEGEVRSLLKDISQKAVVYSTCL 1786

RESULT 15

AAM48896

ID AAM48896 standard; protein; 1786 AA.

XX AC AAM48896;

XX DT 04-APR-2002 (first entry)

XX DE Laminin protein.

XX KW Human; angiostatin; endostatin; angiogenesis; cancer; metastasis;

KW psoriasis; scleroderma; Crohn's disease; corneal disease; retinopathy;

KW arthritis; wound healing; Helicobacter pylori; peptic ulcer;

KW gene therapy; angiostatin antagonist; endostatin antagonist;

KW antiangiogenic; cytostatic; antiarthritic; antiinflammatory;

KW cerebroprotective; antidiabetic; virucide; antipyretic; vulnerary;

XX gynaecological; cat scratch fever.

OS Unidentified.

XX WO200193897-A2.

XX PN 13-DEC-2001.

XX PD 04-JUN-2001; 2001WO-US017947.

XX PF 02-JUN-2000; 2000US-0209065P.

XX PR 08-MAY-2001; 2001US-0289387P.

XX PA (ENTR-) ENTREMED INC.

XX XX Sim KL, Macdonald NJ;

XX WPI; 2002-130569/17.

XX DR N-PSDB; ABA97525.

XX PT Regulating angiogenesis and treatment of angiogenesis-mediated diseases,

XX PT e.g. hemangioma, tumors or cancer, by administering a tropomyosin binding

XX PT compound or actin disrupting compound.

XX PS Example 11; Fig 6A; 95pp; English.

XX XX The present invention relates to methods of regulating angiogenesis in an

CC individual by administering an angiogenesis regulating composition

CC comprising a tropomyosin binding compound or an actin disrupting

CC compound. The compositions are useful for treating diseases and processes

CC mediated by angiogenesis including haemangioma, solid tumours, blood

CC bourne tumours, leukaemia, metastasis, Crohn's disease, coronary or

CC cerebral collaterals, arthritis, diabetic neovascularisation, macular

CC degeneration, wound healing, Helicobacter related diseases, ovulation,

CC menstruation, and cat scratch fever. The present sequence is a protein

CC described in the exemplification of the invention

XX SQ Sequence 1786 AA;

Query Match 93.6%; Score 9131; DB 5; Length 1786;

Best Local Similarity 92.6%; Pred. No. 0;

Matches 1654; Conservative 71; Mismatches 61; Indels 0; Gaps 0;

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Db 1 MGLLQLLAFSLALCRARVRAQEPEFSYGAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60

Qy 61 PEPYCIIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVEN 120

Db 61 PEPYCIIVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVEN 120

Qy 121 VTQLDLEAEFHFTHLIMTFKTRPAAMLIERSSDFGKTGWVYRYFAYDCESSFPGISTG 180

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Qy 181 PMKKVDDIIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPRIQNLKITNLRIKFVKL 240

Db 181 PMKKVDDIIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPRIQNLKITNLRIKFVKL 240

Qy 241 HTLGDNLNLDLSRMEIREKYVYAVYDMVVRGNCFCYGHASECAPVDGVNNEVEGMVHGCMC 300

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Db 301 RHNTKGLNCELCMDYHDLWPWPAEGRNSNACKKNCNEHSISCHFDMAVFLATGNVSGG 360

Qy 361 VCDNCQHNTMGRNCEQCKPFYFQHPERDIRDPNLCPECTCDPAGSENGGICDGYTDFSVG 420

Db 361 VCDDCQHNTMGRNCEQCKPFYFQHPERDIRDPNLCPECTCDPAGSQNEGICDGYTDFSTG 420

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Db 421 LIAGQCRKLVHEGERCDVCKEGFYDLSSEDPPFGCKSCACNPLGTIPGNGPCDSETHGYC 480
QY 481 CKRLVTGQRCDQCLPQHGLSNDLDGCRPCDCLGGALNNKSCSEDSGQCSCLPHMIGRQC 540
Db 481 CKRLVTGQHCDQCLPEHGLSNDLDGCRPCDCLGGALNNKSCFAESGQCSCRPHMIGRQC 540
QY 541 NEVESGYFTTLDHYIYEAEBANLPGVWVVERQYIQDRIPSWTGPGFVRVPEGAYLEFF 600
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QY 841 HCFQGIYARQCDRCLPGYWGFPSPCQPCQNGHALDCDVTVTGELSCQDYTTGHNCRCLA 900
Db 841 HCFQGVYARQCDRCLPGHWGFPSPCQPCQNGHADDCDPTVTEGCLNCQDYTMGHNCRCLA 900
QY 901 GYGDPIIGSDHCRPCPCPDGPDGSRQFARSCYQDPVTLQACVCDPGYIGSRCDDCAS 960
Db 901 GYGDPIIGSDHCRPCPCPDGPDGSRQFARSCYQDPVTLQACVCDPGYIGSRCDDCAS 960
QY 961 GFFGNPSDFGSGCQPCQCHHNIDTTDPEACDKDTGRCLKCLYHTEGDHCOLCQYGYTGA 1020
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Db 1021 LRQDCRKVCNYLGTIVQEHNGSDCQCDKATGQCCLPNVIGONCDRCAPNTWQLASGTG 1080
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QY 1141 TPQCDQSTGQCVCEGVGPRCDKCTRGYSGVFPDCTPCHQCPCALWDALIGELTNRTHKF 1200
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QY 1321 ITKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLERESPFKEQEEQARLLDE 1380
Db 1321 ITKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVMMERESQFKEQEEQARLLDE 1380
QY 1381 LAGKLOSLDLSAAQMTCTGTPPGADCSSECGGNPCRTDEGEKKCGGPGCGGLVTVAHSA 1440
Db 1381 LAGKLOSLDLSAAEMTCGTPPGASCSETECGGNPCRTDEGERKCGGPGCGGLVTVAHNA 1440
QY 1441 WQKAMDFDRDVLALAEVEQLSKMVSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDL 1500
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Db 1501 RNLIKQIRNFELTQDSADLDSIEAVANEVLKXMPSTPQQLQNLTEDIRERVESLSQVEVI 1560
QY 1561 LQOSAADIARAELLLEEAKRASKSATDVKVTADMVKEALEEAEKAQVAAEKAIKQADEDI 1620
Db 1561 LQSAADIARAEMLLLEEAKRASKSATDVKVTADMVKEALEEAEKAQVAAEKAIKQADEDI 1620
QY 1621 QGTQNLTSIESETAASEETLTNASQRIKSLERNVEELKRAAQNNGEAEYIEKVVSVK 1680
Db 1621 QGTQNLTSIESETAASEETLFNASQRISELERNVVEELKRAAQNNGEAEYIEKVVTVK 1680
QY 1681 QNADDVKKTLDGELDEKYYKKVESLIAQKTEESADARRKAEELLQNEAKTLLAQANSKLQLL 1740
Db 1681 QSAEDVKKTLDGELDEKYYKKVENLIAKTEESADARRKAEMLQNEAKTLLAQANSKLQLL 1740
QY 1741 EDLERKYEDNQKYLEDKAQELVLEGEVRSLLKDISQKVAVYSTCL 1786
Db 1741 KDLERKYEDNQRYLEDKAQELARLEGEVRSLLKDISQKVAVYSTCL 1786

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Job time : 55.5494 secs

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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:30:58 ; Search time 13.5107 Seconds
(without alignments)
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Title: US-10-037-182-10
Perfect score: 9758
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Scoring table: BLOSUM62
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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9758	100.0	1786	4 US-09-562-702A-18	Sequence 18, Appl
2	9758	100.0	1786	4 US-09-561-818A-18	Sequence 18, Appl
3	9429	96.6	1725	4 US-09-562-702A-20	Sequence 20, Appl
4	9429	96.6	1725	4 US-09-561-818A-20	Sequence 20, Appl
5	9144	93.7	1786	4 US-09-562-702A-14	Sequence 14, Appl
6	9144	93.7	1786	4 US-09-561-818A-14	Sequence 14, Appl
7	9144	93.7	1786	4 US-09-561-709B-9	Sequence 9, Appl
8	9092	93.2	1765	4 US-09-562-702A-16	Sequence 16, Appl
9	9092	93.2	1765	4 US-09-561-818A-16	Sequence 16, Appl
10	5697.5	58.4	1196	1 US-08-144-121-4	Sequence 4, Appl
11	5697.5	58.4	1196	2 US-08-735-893-4	Sequence 4, Appl
12	5066.5	51.9	1799	4 US-09-845-583A-6	Sequence 6, Appl
13	4907	50.3	1798	4 US-09-561-709B-11	Sequence 11, Appl
14	4902	50.2	1798	4 US-09-845-583A-8	Sequence 8, Appl
15	3813.5	39.1	1761	4 US-09-561-709B-1	Sequence 1, Appl
16	3068.5	31.4	1101	4 US-09-561-709B-5	Sequence 5, Appl
17	2880.5	29.5	1342	4 US-09-561-709B-13	Sequence 13, Appl
18	1661.5	17.0	1572	4 US-09-562-702A-32	Sequence 32, Appl
19	1661.5	17.0	1572	4 US-09-561-818A-28	Sequence 28, Appl
20	1661.5	17.0	1605	4 US-09-562-702A-30	Sequence 30, Appl
21	1661.5	17.0	1605	4 US-09-561-818A-26	Sequence 26, Appl
22	1651	16.9	1609	4 US-09-562-702A-22	Sequence 22, Appl
23	1651	16.9	1609	4 US-09-561-818A-22	Sequence 22, Appl
24	1651	16.9	1617	4 US-09-562-702A-26	Sequence 26, Appl
25	1643	16.8	1576	4 US-09-562-702A-24	Sequence 24, Appl
26	1643	16.8	1576	4 US-09-561-818A-24	Sequence 24, Appl
27	1643	16.8	1584	4 US-09-562-702A-28	Sequence 28, Appl

28	1619	16.6	271	1 US-08-152-019A-28	Sequence 28, Appl
29	1584	16.2	3635	4 US-09-845-583A-2	Sequence 2, Appl
30	1572.5	16.1	3075	2 US-08-460-309-5	Sequence 5, Appl
31	1572.5	16.1	3075	2 US-08-125-077-5	Sequence 5, Appl
32	1560.5	16.0	3111	2 US-08-460-309-4	Sequence 4, Appl
33	1560.5	16.0	3111	2 US-08-125-077-4	Sequence 4, Appl
34	1555	15.9	3110	4 US-09-562-702A-2	Sequence 2, Appl
35	1555	15.9	3110	4 US-09-562-702A-6	Sequence 6, Appl
36	1555	15.9	3110	4 US-09-561-709B-7	Sequence 7, Appl
37	1553.5	15.9	3088	4 US-09-562-702A-8	Sequence 8, Appl
38	1553.5	15.9	3089	4 US-09-562-702A-4	Sequence 4, Appl
39	1550.5	15.9	1172	4 US-09-919-172-16	Sequence 16, Appl
40	1548	15.9	279	1 US-08-152-019A-29	Sequence 29, Appl
41	1542	15.8	278	2 US-08-460-309-13	Sequence 13, Appl
42	1542	15.8	278	2 US-08-125-077-13	Sequence 13, Appl
43	1541.5	15.8	1170	4 US-09-561-709B-12	Sequence 12, Appl
44	1524	15.6	3106	4 US-09-562-702A-10	Sequence 10, Appl
45	1522.5	15.6	3084	4 US-09-562-702A-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-562-702A-18
; Sequence 18, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-562-702A-18

Query Match 100.0%; Score 9758; DB 4; Length 1786;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGLLQVFAFGVLALWGTRVCAQAEPEFSYGC	AEGSCYPATGDL	LLIGRAQKLSVTSTCGLHK	60	
Db	1	MGLLQVFAFGVLALWGTRVCAQAEPEFSYGC	AEGSCYPATGDL	LLIGRAQKLSVTSTCGLHK	60	
Qy	61	PEPYCIVSHLQEDKKCFICDSRDPYHETLNPD	SHLIENVVTTFAPNRLKIWQSENGVEN	120		
Db	61	PEPYCIVSHLQEDKKCFICDSRDPYHETLNPD	SHLIENVVTTFAPNRLKIWQSENGVEN	120		
Qy	121	VTIQDLAEAEFFHFLIMTFKTRPAAMLIERSSD	FGKTGWVYRYFAYDC	ESSFPGISTG	180	
Db	121	VTIQDLAEAEFFHFLIMTFKTRPAAMLIERSSD	FGKTGWVYRYFAYDC	ESSFPGISTG	180	
Qy	181	PMKKVDDIIICDSRYS	DI	EPSTEGEVI	FRLDPAPFKIEDPYSPRIQNLLKITNRIKFVKL	240
Db	181	PMKKVDDIIICDSRYS	DI	EPSTEGEVI	FRLDPAPFKIEDPYSPRIQNLLKITNRIKFVKL	240
Qy	241	HTLGDNLLDSRMEIREKYYYAVYDMVVRGNC	FCYGHASECAPVDGVNEE	VEGMVGHCHMC	300	
Db	241	HTLGDNLLDSRMEIREKYYYAVYDMVVRGNC	FCYGHASECAPVDGVNEE	VEGMVGHCHMC	300	

QY 301 RHNTKGINCELMDFYHDLWPRPAEGRNSNACKKCNNEHSSSCHDFMAVFLATGNVSGG 360
DB 301 RHNTKGINCELMDFYHDLWPRPAEGRNSNACKKCNNEHSSSCHDFMAVFLATGNVSGG 360
QY 361 VCDNCOHNTMGRNCEQCKPFYFOHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVG 420
DB 361 VCDNCOHNTMGRNCEQCKPFYFOHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVG 420
QY 421 LIAGQCRCKLHVEGERCDVCKEGFYDLAEDPYGCKSCACNPLGTIPGPNPCDSETGYCY 480
DB 421 LIAGQCRCKLHVEGERCDVCKEGFYDLAEDPYGCKSCACNPLGTIPGPNPCDSETGYCY 480
QY 481 CKRLVTGORCDQCLPOHWGLSNDLDGCRPCDCLGGALNNSCSEDSGQCSCLPHMIGRQC 540
DB 481 CKRLVTGORCDQCLPOHWGLSNDLDGCRPCDCLGGALNNSCSEDSGQCSCLPHMIGRQC 540
QY 541 NEVESGYFTTLDHYIYEAEEANLPGVWVVERQYIQDRIPSWTGPGFVRVPEGAYLEFF 600
DB 541 NEVESGYFTTLDHYIYEAEEANLPGVWVVERQYIQDRIPSWTGPGFVRVPEGAYLEFF 600
QY 601 IDNIPYSMEYEILIRYEPQLPDHWEKAVITVORPGKIPASSRCGNTVPDDDNQVVSLSPG 660
DB 601 IDNIPYSMEYEILIRYEPQLPDHWEKAVITVORPGKIPASSRCGNTVPDDDNQVVSLSPG 660
QY 661 SRYVVLPRPVCFEKGMYTVRLELPQYTASGSDVESPYTFIDSLVLMYPYCKSLDIFTVGG 720
DB 661 SRYVVLPRPVCFEKGMYTVRLELPQYTASGSDVESPYTFIDSLVLMYPYCKSLDIFTVGG 720
QY 721 SGDGEVNTSAWETFQYRCLENSRSVVKTPMTDVCNIIIPISALIHQTGLACECDPQGS 780
DB 721 SGDGEVNTSAWETFQYRCLENSRSVVKTPMTDVCNIIIPISALIHQTGLACECDPQGS 780
QY 781 LSSVCDPENGQQCRPNVVGRTCNRCAPGTFGFGPNCKPCDCHLQGSASAFCDAITGQC 840
DB 781 LSSVCDPENGQQCRPNVVGRTCNRCAPGTFGFGPNCKPCDCHLQGSASAFCDAITGQC 840
QY 841 HCFQGIYARQDRCLPGYWGFPSCQPCQNGHALDCDVTGECCLSCQDYTTGHNCRCLA 900
DB 841 HCFQGIYARQDRCLPGYWGFPSCQPCQNGHALDCDVTGECCLSCQDYTTGHNCRCLA 900
QY 901 GYGDPIIGSGDHCRPCPCPDGSDGRQFARSCYQDPVTQLACVCDPGYIGSRCDDCAS 960
DB 901 GYGDPIIGSGDHCRPCPCPDGSDGRQFARSCYQDPVTQLACVCDPGYIGSRCDDCAS 960
QY 961 GFFGNPSDFGSGCQPCQCHNIDTTPDPAECDKDTGRCLCKLYHTEGDHCLCQGYGYGDA 1020
DB 961 GFFGNPSDFGSGCQPCQCHNIDTTPDPAECDKDTGRCLCKLYHTEGDHCLCQGYGYGDA 1020
QY 1021 LRQDCRKVCNVLGTVKEHCHGSDCHCDKATGQCCLPNVIGONCDRCAPNTWOLASGTG 1080
DB 1021 LRQDCRKVCNVLGTVKEHCHGSDCHCDKATGQCCLPNVIGONCDRCAPNTWOLASGTG 1080
QY 1081 CGPCNCNAAHSFGPSCNEFTGQCQCMPFGGRTCECQELFWGDPDVECRACDCDPRGIE 1140
DB 1081 CGPCNCNAAHSFGPSCNEFTGQCQCMPFGGRTCECQELFWGDPDVECRACDCDPRGIE 1140
QY 1141 TPQCDQSTGQCVCEGVEGPRCDKCTRYSYSGVFPDCTPCHQCFAWDAIIGELTNRTHKF 1200
DB 1141 TPQCDQSTGQCVCEGVEGPRCDKCTRYSYSGVFPDCTPCHQCFAWDAIIGELTNRTHKF 1200
QY 1201 LEKAKALKISGVIQPYRETVDVSEKKVNEIKDILAQSPAAPLKNIGILFEEAEKLTADV 1260
DB 1201 LEKAKALKISGVIQPYRETVDVSEKKVNEIKDILAQSPAAPLKNIGILFEEAEKLTADV 1260
QY 1261 TEKMAQVEVKLTDTASQSNSTAGELGALQABAEASLDKTVKELAEQLEFIKNSDIQCALDS 1320
DB 1261 TEKMAQVEVKLTDTASQSNSTAGELGALQABAEASLDKTVKELAEQLEFIKNSDIQCALDS 1320
QY 1321 ITKYFQMSLEAEKRVNASTTDPNSTVEQALTRDRVEDLMLERESPFKEQOEQARLLDE 1380
DB 1321 ITKYFQMSLEAEKRVNASTTDPNSTVEQALTRDRVEDLMLERESPFKEQOEQARLLDE 1380
QY 1381 LAGKLQSLDLSAAQMTCTGTPPGADCSSECGGNCRCTDEGEKKCGGPGGLVTVHAHA 1440

DB 1381 LAGKLQSLDLSAAQMTCTGTPPGADCSSECGGNCRCTDEGEKKCGGPGGLVTVHAHA 1440
QY 1441 WQKAMDFDRDVLALAEVEQISKMVSEAKVRADEAKQNAQDVLLKTNAATKEKVDKSNEDL 1500
DB 1441 WQKAMDFDRDVLALAEVEQISKMVSEAKVRADEAKQNAQDVLLKTNAATKEKVDKSNEDL 1500
QY 1501 RNLIKQIRNFLTSDSADLDSIEAVANEVLKSGNASTPQOLQNLTEDIRERVETLSQVEVI 1560
DB 1501 RNLIKQIRNFLTSDSADLDSIEAVANEVLKSGNASTPQOLQNLTEDIRERVETLSQVEVI 1560
QY 1561 LQOSAADIARAELLLEEAERASKSATDVKVTADVMKEALEEAEKAQVAEKAQKQADEDI 1620
DB 1561 LQOSAADIARAELLLEEAERASKSATDVKVTADVMKEALEEAEKAQVAEKAQKQADEDI 1620
QY 1621 QGTQNLTSIESETAASEETLTNASORISKLEARNVEELKRAAQNAGEAEYIEKVVSVK 1680
DB 1621 QGTQNLTSIESETAASEETLTNASORISKLEARNVEELKRAAQNAGEAEYIEKVVSVK 1680
QY 1681 QNADDVKKTLDGELDEKYYKKVESLIAQKTESADARRKAEELLQNEAKTLAQANSKLQLL 1740
DB 1681 QNADDVKKTLDGELDEKYYKKVESLIAQKTESADARRKAEELLQNEAKTLAQANSKLQLL 1740
QY 1741 EDLERKYEDNQKYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1786
DB 1741 EDLERKYEDNQKYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1786

RESULT 2
US-09-561-818A-18
; Sequence 18, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortessmaa, Jarrko
; APPLICANT: Tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 18
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-561-818A-18

Query Match 100.0%; Score 9758; DB 4; Length 1786;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLLQVFAFGVLALWGRVCAQEPESYGCAGSCYPATGDLIGRAQKLSVTSTCGLHK 60
DB 1 MGLLQVFAFGVLALWGRVCAQEPESYGCAGSCYPATGDLIGRAQKLSVTSTCGLHK 60
QY 61 PEPYCIVSHLQEDKKCFICDSRDPVHETLNPDSHLIENVVTFAPNRLKIWWQSENGVEN 120
DB 61 PEPYCIVSHLQEDKKCFICDSRDPVHETLNPDSHLIENVVTFAPNRLKIWWQSENGVEN 120
QY 121 VTIQLDLEAEFHTHLIMTFKTFRPAAMLIERSSDFGKTGWVYRFPAYDCESFPFGISTG 180
DB 121 VTIQLDLEAEFHTHLIMTFKTFRPAAMLIERSSDFGKTGWVYRFPAYDCESFPFGISTG 180
QY 181 PMKKVDDIIICDSRYSYSDIEPSTEGETIFRALDPAFKIEDPYSPIQNLLKITNLRKFKVL 240
DB 181 PMKKVDDIIICDSRYSYSDIEPSTEGETIFRALDPAFKIEDPYSPIQNLLKITNLRKFKVL 240
QY 241 HTLGDNLLDSRMEIREKYYYAVYDMVVRGNCFCYGHASECAPVDGVNVEEVEGMVHGCMC 300
DB 241 HTLGDNLLDSRMEIREKYYYAVYDMVVRGNCFCYGHASECAPVDGVNVEEVEGMVHGCMC 300
QY 301 RHNTKGLNCELMDFYHDLWPRPAEGRNSNACKKCNNEHSSSCHDFMAVFLATGNVSGG 360

Db 301 RHNTKGLNCELMDFYHDLPRWPAEGRNSNACKKCNKCNHSSSCHFDMAVFLATGNVSGG 360
QY 361 VCDNCQHNMTMGRNCEQCKPFYFQHPERDIRDNLCEPCTCDPAGSENGGICDGYTDFSVG 420
Db 361 VCDNCQHNMTMGRNCEQCKPFYFQHPERDIRDNLCEPCTCDPAGSENGGICDGYTDFSVG 420
QY 421 LIAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGGNCPDSETGYCY 480
Db 421 LIAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGGNCPDSETGYCY 480
QY 481 CKRLVTGORCDQCLPOHWGLSNDLDGCRPCDCLGGALNNSCSBDSGQCSCLPHMIGROC 540
Db 481 CKRLVTGORCDQCLPOHWGLSNDLDGCRPCDCLGGALNNSCSBDSGQCSCLPHMIGROC 540
QY 541 NEVESGYFTTLDHYIYEAEANLPGVVVVERQYIQRIPSWTGPFGFVRVPEGAYLEFF 600
Db 541 NEVESGYFTTLDHYIYEAEANLPGVVVVERQYIQRIPSWTGPFGFVRVPEGAYLEFF 600
QY 601 IDNIPYSMEYEILIRYEPOLPDHWEKAVITVORPGKIPASSRCNGNTVPDDDNQVVSLSPG 660
Db 601 IDNIPYSMEYEILIRYEPOLPDHWEKAVITVORPGKIPASSRCNGNTVPDDDNQVVSLSPG 660
QY 661 SRYVLP RPVPCFEKGMNVTVRLELPQYTAGSDVESPYTFIDSLVLMPYCKSLDIFTVGG 720
Db 661 SRYVLP RPVPCFEKGMNVTVRLELPQYTAGSDVESPYTFIDSLVLMPYCKSLDIFTVGG 720
QY 721 SGDGEVNTSAWETFQRYRCLENSRSVVKTPTMTDVCNRIIFSISALIHQTGLACECDPQGS 780
Db 721 SGDGEVNTSAWETFQRYRCLENSRSVVKTPTMTDVCNRIIFSISALIHQTGLACECDPQGS 780
QY 781 LSSVCDPNGGQCQCRPNVVGRTCNRCAPGTGFGPGNGCKPCDCHLOGSASAFCAITGQC 840
Db 781 LSSVCDPNGGQCQCRPNVVGRTCNRCAPGTGFGPGNGCKPCDCHLOGSASAFCAITGQC 840
QY 841 HCFQGIYARQCRLPGYWGFPSCQPCQCNHGHALDCTVTGECCLSCQDYTTGHCNRCCLA 900
Db 841 HCFQGIYARQCRLPGYWGFPSCQPCQCNHGHALDCTVTGECCLSCQDYTTGHCNRCCLA 900
QY 901 GYGDPIIGSGDHCRPCPCPDGPDGSRQRFARSCYQDPVTLQLACVCDPFGYIGSRCDDCAS 960
Db 901 GYGDPIIGSGDHCRPCPCPDGPDGSRQRFARSCYQDPVTLQLACVCDPFGYIGSRCDDCAS 960
QY 961 GFFGNPSDFGGSCQPCQCHNIDTTDPEACDKDTGRCLKCLYHTEGDHCQLCQYGYGDA 1020
Db 961 GFFGNPSDFGGSCQPCQCHNIDTTDPEACDKDTGRCLKCLYHTEGDHCQLCQYGYGDA 1020
QY 1021 LRQDCRKVCNLYGTVKEHCNCGSDCHCDKATGCSCLPNVIGQNCDCRCAPNTWQLASGTG 1080
Db 1021 LRQDCRKVCNLYGTVKEHCNCGSDCHCDKATGCSCLPNVIGQNCDCRCAPNTWQLASGTG 1080
QY 1081 CGPCNCAAHSGFPCSCNEFTGCQCMFGGRTCECQELFWGDPDVECRACDCDPRGIE 1140
Db 1081 CGPCNCAAHSGFPCSCNEFTGCQCMFGGRTCECQELFWGDPDVECRACDCDPRGIE 1140
QY 1141 TPQCDQSTGQCVCVEGVEGPRCDKCTRGYSGVFPDCTPCHQCFCALWDALIGELTNRTHKF 1200
Db 1141 TPQCDQSTGQCVCVEGVEGPRCDKCTRGYSGVFPDCTPCHQCFCALWDALIGELTNRTHKF 1200
QY 1201 LEKAKALKISGVIGPYRETVDVSVEKKVNEIKDILAQSPAAEPLKNIGILFEEAEKLTQDV 1260
Db 1201 LEKAKALKISGVIGPYRETVDVSVEKKVNEIKDILAQSPAAEPLKNIGILFEEAEKLTQDV 1260
QY 1261 TEKMAQVEVKLTDTASQSNSTAGELGALQAEAESLDKTVKELAEQLEFINKNSDIOGALDS 1320
Db 1261 TEKMAQVEVKLTDTASQSNSTAGELGALQAEAESLDKTVKELAEQLEFINKNSDIOGALDS 1320
QY 1321 ITKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRVEDLMLERESPFEKQEQEEQARLLDE 1380
Db 1321 ITKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRVEDLMLERESPFEKQEQEEQARLLDE 1380
QY 1381 LAGKLOSLDLSAAQAOMTCGTPPGADCSESECGGPNCRDTDEGEKKCGGCGGLVTVAHSA 1440
Db 1381 LAGKLOSLDLSAAQAOMTCGTPPGADCSESECGGPNCRDTDEGEKKCGGCGGGLVTVAHSA 1440

QY 1441 WQKAMDFDRDVL SALAEVEQLSKMVSEAKVRADEAKONAQDVLTKTNATKEKVDKSNEDL 1500
Db 1441 WQKAMDFDRDVL SALAEVEQLSKMVSEAKVRADEAKONAQDVLTKTNATKEKVDKSNEDL 1500
QY 1501 RNLIKQIRNFLTSDSADLDSIEAVANEVLKSGNASTPQQLQNLNLTEDIRERVETLSQVEVI 1560
Db 1501 RNLIKQIRNFLTSDSADLDSIEAVANEVLKSGNASTPQQLQNLNLTEDIRERVETLSQVEVI 1560
QY 1561 LQOASAADIARAEILLLEAKRASKSATDVKVTADMVKEALEEAEKAQVAAEKAQKQADEDI 1620
Db 1561 LQOASAADIARAEILLLEAKRASKSATDVKVTADMVKEALEEAEKAQVAAEKAQKQADEDI 1620
QY 1621 QGTQNLTSIESETAASEETLTNASQRIKSLERNVEELKRKAAQNSGEAEYIEKVVSVK 1680
Db 1621 QGTQNLTSIESETAASEETLTNASQRIKSLERNVEELKRKAAQNSGEAEYIEKVVSVK 1680
QY 1681 QNADDVKKTLDGELDEKYYKKVESLIAQKTEESADARRKAEELLQNEAKTLQAQANSKLQLL 1740
Db 1681 QNADDVKKTLDGELDEKYYKKVESLIAQKTEESADARRKAEELLQNEAKTLQAQANSKLQLL 1740
QY 1741 EDLERKYEDNQKYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1786
Db 1741 EDLERKYEDNQKYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1786

RESULT 3

US-09-562-702A-20
; Sequence 20, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 1725
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-562-702A-20

Query Match 96.6%; Score 9429; DB 4; Length 1725;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 EPYCIIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVVTTFAPNRLKIWWQSENGVENV 121
Db 1 EPYCIIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVVTTFAPNRLKIWWQSENGVENV 60
QY 122 TIQLDLEAEFHFTHLIMTFKTRPAAMLIERSDDFGKTGWVRYFYAYDCSSFPFGISTGP 181
Db 61 TIQLDLEAEFHFTHLIMTFKTRPAAMLIERSDDFGKTGWVRYFYAYDCSSFPFGISTGP 120
QY 182 MKKVDDIICDSRYSIDIEPSTEGEVI FRALDPAPFKIEDPYSRIONLLKTNRIKFKVLH 241
Db 121 MKKVDDIICDSRYSIDIEPSTEGEVI FRALDPAPFKIEDPYSRIONLLKTNRIKFKVLH 180
QY 242 TLGDNLLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNNEEVEGMVGHCMCR 301
Db 181 TLGDNLLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNNEEVEGMVGHCMCR 240
QY 302 HNTKGLNCELMDFYHDLPRWPAEGRNSNACKKCNKCNHSSSCHFDMAVFLATGNVSGV 361

Db 241 HNTKGLNCELMDFYHDLWPAEGRNSNACKKCNCHSSCHFDMAVFLATGNVSGGV 300
QY 362 CDNCQHNTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 421
Db 301 CDNCQHNTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 360
QY 422 IAGQCRCKLHVGERCDVCKEGFYDLAEDPYGCKSCACNPLGTIPGPNPCDSETGYCYC 481
Db 361 IAGQCRCKLHVGERCDVCKEGFYDLAEDPYGCKSCACNPLGTIPGPNPCDSETGYCYC 420
QY 482 KRLVTGQRCDQCLPQHGLSLNDLDCRPPCDLGGALNNCSSEDSGQCSCLPHMIGRQCN 541
Db 421 KRLVTGQRCDQCLPQHGLSLNDLDCRPPCDLGGALNNCSSEDSGQCSCLPHMIGRQCN 480
QY 542 EVESGYFTTLDHYIYEAEEANLPGVWVVERQYIQDRIPSWTGPFGFVRVPEGAYLEFFI 601
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QY 602 DNIPYSMEYELIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTVPDDNQVSLSPGS 661
Db 541 DNIPYSMEYELIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTVPDDNQVSLSPGS 600
QY 662 RYVVLPRPVCFEKGMNYYTVRLELPQYTAGSDVESPYTFIDSLVMPYCKSLDIFTVGS 721
Db 601 RYVVLPRPVCFEKGMNYYTVRLELPQYTAGSDVESPYTFIDSLVMPYCKSLDIFTVGS 660
QY 722 GDGEVTSNAWETFORYRCLENSRVSVMTPMTDVCNIIIFSISALIHOTGLACECDPQGS 781
Db 661 GDGEVTSNAWETFORYRCLENSRVSVMTPMTDVCNIIIFSISALIHOTGLACECDPQGS 720
QY 782 SSVCDPNGGQCCRPNVVGRITCNRCAPGTFGFGPNCKPCDCHLQGSASAFCAITGOCH 841
Db 721 SSVCDPNGGQCCRPNVVGRITCNRCAPGTFGFGPNCKPCDCHLQGSASAFCAITGOCH 780
QY 842 CFQGIYARQDRCLPGYWGFPSCQPCQCNHALDCDVTGECCLSCQDYTTGHNCRCLAG 901
Db 781 CFQGIYARQDRCLPGYWGFPSCQPCQCNHALDCDVTGECCLSCQDYTTGHNCRCLAG 840
QY 902 YGDPITIGSGDHCRPCPCPDGSDSGRQFARSCYQDPVTLQACVCPGYSRCDCCASG 961
Db 841 YGDPITIGSGDHCRPCPCPDGSDSGRQFARSCYQDPVTLQACVCPGYSRCDCCASG 900
QY 962 FFGNPSDFGSGCQPCQCHNIDTDPDPEACDKOTGRCLKCLYHTEGHCQLCYGYGDAL 1021
Db 901 FFGNPSDFGSGCQPCQCHNIDTDPDPEACDKOTGRCLKCLYHTEGHCQLCYGYGDAL 960
QY 1022 RQDCRKVCNYLGTVKEHNGSDCHCDKATGQCSCLPNVIGQNCDCRACAPNTWQLASGTGC 1081
Db 961 RQDCRKVCNYLGTVKEHNGSDCHCDKATGQCSCLPNVIGQNCDCRACAPNTWQLASGTGC 1020
QY 1082 GPCNCAHSGFSPSCNEFTGQCCMPFGGRTCSQELFWGDPDVECRACDCDPRGIET 1141
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QY 1202 EKAKALKISGVIGPYRETVDVSVEKKVNEIKDILAQSPAAEPLKNIGILFEEAEKLTJTDVT 1261
Db 1141 EKAKALKISGVIGPYRETVDVSVEKKVNEIKDILAQSPAAEPLKNIGILFEEAEKLTJTDVT 1200
QY 1262 EKMAQVEVKLTDTASQSNSTAGELGALQAEESLDKTVKELAEQLEFIKNSDIQGALDSI 1321
Db 1201 EKMAQVEVKLTDTASQSNSTAGELGALQAEESLDKTVKELAEQLEFIKNSDIQGALDSI 1260
QY 1322 TKYFQMSLEAEKRVNASITDPNSTVEQSALTRDRVEDLMLERESPKEQEQEQLLDEL 1381
Db 1261 TKYFQMSLEAEKRVNASITDPNSTVEQSALTRDRVEDLMLERESPKEQEQEQLLDEL 1320
QY 1382 AGKLQSLDLSAAQMTCTGTPPGADCSSECGGNCRCTDEGEKKCGGPGGLVTVHAHSAW 1441

Db 1321 AGKLQSLDLSAAQMTCTGTPPGADCSSECGGNCRCTDEGEKKCGGPGGLVTVHAHSAW 1380
QY 1442 QKAMDFDRDVLALAEVEQLSKMSEAKVRADAEAKQNAQDVLTKTNATKEKVKDSNEDLR 1501
Db 1381 QKAMDFDRDVLALAEVEQLSKMSEAKVRADAEAKQNAQDVLTKTNATKEKVKDSNEDLR 1440
QY 1502 NLIKQIRNFLTEDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVIL 1561
Db 1441 NLIKQIRNFLTEDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVIL 1500
QY 1562 QQSAADIARAEELLEEAKRASKSATDVKTADVMVKEALEEAEKAAKQADEDIQ 1621
Db 1501 QQSAADIARAEELLEEAKRASKSATDVKTADVMVKEALEEAEKAAKQADEDIQ 1560
QY 1622 GTQNLTSIESETAASEETLTNASORISKLERNEVELKRAAQNAGEAYIEKVVSQVKQ 1681
Db 1561 GTQNLTSIESETAASEETLTNASORISKLERNEVELKRAAQNAGEAYIEKVVSQVKQ 1620
QY 1682 NADDVKKTLDGELDEKYYKKVESLIAQKTEESADARRKAEELLQNEAKTLLAQANSKIQLLE 1741
Db 1621 NADDVKKTLDGELDEKYYKKVESLIAQKTEESADARRKAEELLQNEAKTLLAQANSKIQLLE 1680
QY 1742 DLERKYEDNQKYLEDKAQELVRLGEVRSLLKIDISEKVAVYSTCL 1786
Db 1681 DLERKYEDNQKYLEDKAQELVRLGEVRSLLKIDISEKVAVYSTCL 1725

RESULT 4

US-09-561-818A-20
; Sequence 20, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortessmaa, Jarrko
; APPLICANT: Tyyggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 1725
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-561-818A-20

Query Match 96.6%; Score 9429; DB 4; Length 1725;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 EPYCIVSHLOEDKKCFICDSRDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENV 121
Db 1 EPYCIVSHLOEDKKCFICDSRDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENV 60
QY 122 TIQDLLEAEFFHETHLIMTFKTRPAAMLIERSDDFGKTGWYRYFAYDCESFPFGISTGP 181
Db 61 TIQDLLEAEFFHETHLIMTFKTRPAAMLIERSDDFGKTGWYRYFAYDCESFPFGISTGP 120
QY 182 MKKVDDIICDSRYSIDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLKITNLRIKFKVLH 241
Db 121 MKKVDDIICDSRYSIDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLKITNLRIKFKVLH 180
QY 242 TLGDNLLDSRMEIREKYYIAYVDMVVRGNCFCYGHASECAPVDGVNEEVGVMVGHCMCR 301
Db 181 TLGDNLLDSRMEIREKYYIAYVDMVVRGNCFCYGHASECAPVDGVNEEVGVMVGHCMCR 240
QY 302 HNTKGLNCELMDFYHDLWPAEGRNSNACKKCNCHSSCHFDMAVFLATGNVSGGV 361
Db 241 HNTKGLNCELMDFYHDLWPAEGRNSNACKKCNCHSSCHFDMAVFLATGNVSGGV 300
QY 362 CDNCQHNTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 421
Db 301 CDNCQHNTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 360

QY 422 IAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGPNPCDSEIGCYC 481
Db 361 IAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGPNPCDSEIGCYC 420
QY 482 KRLVTGORCDQCLPQHGLSLNDLDCGRPCDCLGGALNNSCSDSGQCSCPLMHIGRCN 541
Db 421 KRLVTGORCDQCLPQHGLSLNDLDCGRPCDCLGGALNNSCSDSGQCSCPLMHIGRCN 480
QY 542 EVESGYFTTLDHYIYEAEANLPGVWVVERQYIQDRIPSWTGPFGFVRVPEGAYLEFFI 601
Db 481 EVESGYFTTLDHYIYEAEANLPGVWVVERQYIQDRIPSWTGPFGFVRVPEGAYLEFFI 540
QY 602 DNIPYSMEYEILIRYEPQLPDHWEKAVITVQRPKIPASSRCNGTVPDDDDNQVVSLSPGS 661
Db 541 DNIPYSMEYEILIRYEPQLPDHWEKAVITVQRPKIPASSRCNGTVPDDDDNQVVSLSPGS 600
QY 662 RYVVLPRPVCFEKGMMYTVRLELPQYTAGSDVESPYTFIDSLVLMYPYCKSLDIFTVGGS 721
Db 601 RYVVLPRPVCFEKGMMYTVRLELPQYTAGSDVESPYTFIDSLVLMYPYCKSLDIFTVGGS 660
QY 722 GDGEVNTSAWETFQRYRCLENSRSVVKTPMTDVCRNIIIFSALIHQTGLACEDPQGS 781
Db 661 GDGEVNTSAWETFQRYRCLENSRSVVKTPMTDVCRNIIIFSALIHQTGLACEDPQGS 720
QY 782 SSVCDPNGGQCQCRPNVWGRTCNRCAPGTFGFGPNCKPCDCHLQGSASAFCDAITGOCH 841
Db 721 SSVCDPNGGQCQCRPNVWGRTCNRCAPGTFGFGPNCKPCDCHLQGSASAFCDAITGOCH 780
QY 842 CFQGIYARQCDCRCLPGYWGFFSPCQPCQCNHGDCTVTGECISQDYTTGHNCCERCLAG 901
Db 781 CFQGIYARQCDCRCLPGYWGFFSPCQPCQCNHGDCTVTGECISQDYTTGHNCCERCLAG 840
QY 902 YGDPPIIGSGDHCRPCPCPDGPDGSDGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCASG 961
Db 841 YGDPPIIGSGDHCRPCPCPDGPDGSDGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCASG 900
QY 962 FFGNPSDFGGSCQPCQCHNHIDTTDPEACDKTGRCLKCLYHTEGHCQLCQYGYGDAL 1021
Db 901 FFGNPSDFGGSCQPCQCHNHIDTTDPEACDKTGRCLKCLYHTEGHCQLCQYGYGDAL 960
QY 1022 RODCRKVCNYLGTVKEHCNGSDCHCDKATGQSCSCLPNVIGQNCRCAPNTWQLASGTGC 1081
Db 961 RODCRKVCNYLGTVKEHCNGSDCHCDKATGQSCSCLPNVIGQNCRCAPNTWQLASGTGC 1020
QY 1082 GPCNCNAAHSFGPSCNEFTGQCQCMPFGGRTCEQELFWGDPDVECRACDCDPRGIET 1141
Db 1021 GPCNCNAAHSFGPSCNEFTGQCQCMPFGGRTCEQELFWGDPDVECRACDCDPRGIET 1080
QY 1142 PQCDQSTGQCVCEGVEGPRCDKCTRGYSGVFPDCTPCHQCQFALWDIAIIGELTNRTHKFL 1201
Db 1081 PQCDQSTGQCVCEGVEGPRCDKCTRGYSGVFPDCTPCHQCQFALWDIAIIGELTNRTHKFL 1140
QY 1202 EKAKALKISGIVGPIRETVDSEKKNVNEIKDILAQSPAAEPLKNIGILFEEAEKLTKDVT 1261
Db 1141 EKAKALKISGIVGPIRETVDSEKKNVNEIKDILAQSPAAEPLKNIGILFEEAEKLTKDVT 1200
QY 1262 ERMAQVEVKLTDTASQSNSTAGELGALQAEAESLDKTVKELAEQLEFIKNSDIOGALDSI 1321
Db 1201 ERMAQVEVKLTDTASQSNSTAGELGALQAEAESLDKTVKELAEQLEFIKNSDIOGALDSI 1260
QY 1322 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLERESPKEQOEQARLLDEL 1381
Db 1261 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLERESPKEQOEQARLLDEL 1320
QY 1382 AGKLQSLDLSAAQMTCGTPPGADCSESECGPNCRTEGEKCKGCGGLVTVHAHSAW 1441
Db 1321 AGKLQSLDLSAAQMTCGTPPGADCSESECGPNCRTEGEKCKGCGGLVTVHAHSAW 1380
QY 1442 QKAMDFDRDVLALABVEQLSKMVSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDLR 1501
Db 1381 QKAMDFDRDVLALABVEQLSKMVSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDLR 1440

QY 1502 NLIKQIRNFELTSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVIL 1561
Db 1441 NLIKQIRNFELTSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVIL 1500
QY 1562 QQSAADIAAEALLLEBEAKRASKSATDVKVTADMVKEALEEAEKAQVAEKAIKQADEDIQ 1621
Db 1501 QQSAADIAAEALLLEBEAKRASKSATDVKVTADMVKEALEEAEKAQVAEKAIKQADEDIQ 1560
QY 1622 GTQNLTSIETSETAASEETLTNASQRIKSLERNVEELKRKAAQNSGEAEYIEKVVSVKQ 1681
Db 1561 GTQNLTSIETSETAASEETLTNASQRIKSLERNVEELKRKAAQNSGEAEYIEKVVSVKQ 1620
QY 1682 NADDVKKTLGDGELDEKYYKVESLIAQKTEESADARRKAELLQNEAKTLLAQANSKLQLE 1741
Db 1621 NADDVKKTLGDGELDEKYYKVESLIAQKTEESADARRKAELLQNEAKTLLAQANSKLQLE 1680
QY 1742 DLERKYEDNQYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1786
Db 1681 DLERKYEDNQYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1725

RESULT 5
US-09-562-702A-14
; Sequence 14, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-14

Query Match 93.7%; Score 9144; DB 4; Length 1786;
Best Local Similarity 92.7%; Pred. No. 0;
Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;

QY 1 MGLLQVFAFGVLAWGTRVCAQEPESYGCABGSCYPATGDLIGRAQKLSVTSTCGLHK 60
Db 1 MGLLQLLAFSFLALCRARVRAQEPESYGCABGSCYPATGDLIGRAQKLSVTSTCGLHK 60
QY 61 PEPYCIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVVTTTAPNRLKIWWQSENGVEN 120
Db 61 PEPYCIVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVVTTTAPNRLKIWWQSENGVEN 120
QY 121 VTIQDLLEAEFHFHLMFTKTFRPAAMLIERSSDFGKTGWVRYFYAYDCESSFPGISTG 180
Db 121 VTIQDLLEAEFHFHLMFTKTFRPAAMLIERSSDFGKTGWVRYFYAYDCEASFPGISTG 180
QY 181 PMKKVDDIIICDSRYSIDIEPSTEGEVI FRALDPAFKIEDPSPRIQNLKITNLIKFKVKL 240
Db 181 PMKKVDDIIICDSRYSIDIEPSTEGEVI FRALDPAFKIEDPSPRIQNLKITNLIKFKVKL 240
QY 241 HTLGDNLLDSRMEIREKYYIYAVYDMVVRGNCFCYGHASECAPVDGVNVEEGVWGHCMC 300
Db 241 HTLGDNLLDSRMEIREKYYIYAVYDMVVRGNCFCYGHASECAPVDGVNVEEGVWGHCMC 300
QY 301 RHNTKGLNCEL CMDFYHDL PWRPAEGRNSNACKNCNEHSSSCHDFMAVFLATGNVSGG 360
Db 301 RHNTKGLNCEL CMDFYHDL PWRPAEGRNSNACKNCNEHSSSCHDFMAVFLATGNVSGG 360

Db 301 RHNTKGLNCEL CMDFYHDL PWRPAEGRNSNACKKCNCHSISCHFDMAVYLATGNVSGG 360
Qy 361 VCDNCQHNTMGRNCEQCKPFYFQHPERDIRDPNLCEPTCDPAGSENGGICDGYTDFSVG 420
Db 361 VCDNCQHNTMGRNCEQCKPFYFQHPERDIRDPNFCERCTCDPAGSQNEGICDSTDFSTG 420
Qy 421 LIAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGGNPCDSETGYCY 480
Db 421 LIAGQCRCKLHVEGERCDVCKEGFYDLSSEDPFYGCKSCACNPLGTIPGGNPCDSETGHY 480
Qy 481 CKRLVTGQRCDQCLPQHGLSNDLDGCRPCDCLGGALNNSCSEDSGQCSCLPHMIGRQC 540
Db 481 CKRLVTGQRCDQCLPEHWGLSNDLDGCRPCDCLGGALNNSCFAESGQCSCLPHMIGRQC 540
Qy 541 NEVESGYFTTLDHYIYEAEEANLPGVWVVERQYIQDRIPSWTGPFGFVRVPEGAYLEFF 600
Db 541 NEVEPGYFATLDHYLYEAEEANLPGVSVIVERQYIQDRIPSWTGAFFVRVPEGAYLEFF 600
Qy 601 IDNIPYSMEYEILIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTVPDDNQVVSLSPG 660
Db 601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPSTSSRCGNTIPDDNQVVSLSPG 660
Qy 661 SRYVVLPRPVCFEKGMNVTYRLBELPQYTAGSDVESPYTFIDSLVLMYPYCKSLDIFTVGG 720
Db 661 SRYVVLPRPVCFEKGTNYTYRLBELPQYTAGSDVESPYTLIDSLVLMYPYCKSLDIFTVGG 720
Qy 721 SGDEVTNSAWETFORYRCLENSRSVVKTPMTDVCNRIIFSISALIHQTLGACEDPPQGS 780
Db 721 SGDGVTNSAWETFORYRCLENSRSVVKTPMTDVCNRIIFSISALLHQTGLACEDPPQGS 780
Qy 781 LSSVCDPNQSGQCRPNVVGRTCNRCAPGTGFGPNCKPCDCHLQGSASAFCDAITGQC 840
Db 781 LSSVCDPNQSGQCRPNVVGRTCNRCAPGTGFGPSGCKPCCECHLQGSVNAFCNPVTGQC 840
Qy 841 HCFQGIYARQCDRCLPGYWGFPSCQPCQNGHALDCDVTGTECLSCQDYTTGHNCERCLA 900
Db 841 HCFQGVYARQCDRCLPGHWGFPSCQPCQNGHADDCDPTGTECLNCQDYTMGHNCERCLA 900
Qy 901 GYGDPIITGSDHCRPCPCPDGSDSGRQFARSCYQDPVTQLACVCDPQGYIGSRDCCAS 960
Db 901 GYGDPIITGSDHCRPCPCPDGSDSGRQFARSCYQDPVTQLACVCDPQGYIGSRDCCAS 960
Qy 961 GFFGNPSPDFGSGCQPCQCHNIDITDPEACDKDTGRCLKCLYHTEGDHQCQLCQGYYGDA 1020
Db 961 GYFGNPSEVGGSCQPCQCHNIDITDPEACDKETGRCLKCLYHTEGEHCQCFRFGYYGDA 1020
Qy 1021 LRQDCRKVCNLYGTVKEHCNGSDCHCDKATGQCSCLPNVIGQNCDCRCAPNTWQLASGTG 1080
Db 1021 LRQDCRKVCNLYGTVQEHNCNGSDCQCDKATGQCLCLPNVIGQNCDCRCAPNTWQLASGTG 1080
Qy 1081 CGPCNCNAHSFGPSCNEFTGQCQCMFPGFGGRTCSCEQELFWGDPDVECRACDCDPRGIE 1140
Db 1081 CDPNCNAHSFGPSCNEFTGQCQCMFPGFGGRTCSCEQELFWGDPDVECRACDCDPRGIE 1140
Qy 1141 TPQCDDQSTGQCVCEGVEGPRCDKCTRGYSGVFPDCTPCHQCFALWDIAIIGELTNRTHKF 1200
Db 1141 TPQCDDQSTGQCVCEGVEGPRCDKCTRGYSGVFPDCTPCHQCFALWDVIIAELTNRTHRF 1200
Qy 1201 LEKAKALKISGVIGPYRETVDVSVEKKVNEIKDILAQSPAAEPLKNIGILFEEAEKLTADV 1260
Db 1201 LEKAKALKISGVIGPYRETVDVSVERKVSEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDV 1260
Qy 1261 TEKMAQVEVKLTDTASQSNSTAGELGALQAEASLDKTVKELAEQLEFIKNSDIOGALDS 1320
Db 1261 TEMMAQVEVKLSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDS 1320
Qy 1321 ITKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLERESPFFKEQQEQEARLLDE 1380
Db 1321 ITKYFQMSLEAEFERNVASTTEPNSTVEQSALMRDRVEDVNMRESQFKEKQEQEARLLDE 1380
Qy 1381 LAGKLQSLDLSAAQMTCTGTPPGADCSSECGGPNCRCTDEGERKCGGPGCGGLVTVAHSA 1440
Db 1381 LAGKLQSLDLSAAEWTCTGTPPGASCSETECGGPNCRCTDEGERKCGGPGCGGLVTVAHNA 1440

Qy 1441 WQKAMDFDRDVL SALAEVEQLSKMVSEAKVRADAEAKQNAQDVL LKTNATKEKVDKSNEDL 1500
Db 1441 WQKAMDLDDQDVL SALAEVEQLSKMVSEAKLRADAEAKQSAEDILLKTNATKEKMDKSNEL 1500
Qy 1501 RNLIKQIRNFLTSDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVI 1560
Db 1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKMEMPSTPQQLQNLTEDIRERVESLSQVEVI 1560
Qy 1561 LQSAADIAARAE LLEAEKASKSATDVKVTADVMVKEALEEAEKAQVAAEKAIKQADEDI 1620
Db 1561 LQSAADIAARAE LLEAEKASKSATDVKVTADVMVKEALEEAEKAQVAAEKAIKQADEDI 1620
Qy 1621 QGTQNLTSISETAASEETLTNASQRISKLRNVEELKRAAQNSEAEYIEKVYISVK 1680
Db 1621 QGTQNLTSISETAASEETLTNASQRISSELRNVEELKRAAQNSEAEYIEKVYISVK 1680
Qy 1681 QNADDVKKTLDGELDEKYKVESLIAQKTESADARRKAE LLLQNEAKTLLAQANSKLQLL 1740
Db 1681 QSAEDVKKTLDGELDEKYKVENLIAKTESADARRKAE LLLQNEAKTLLAQANSKLQLL 1740
Qy 1741 EDLERKYEDNQKYLEDKAQELVRLEGEVRSLLKDISSEKVAVYSTCL 1786
Db 1741 KDLERKYEDNQRYLEDKAQELARLEGEVRSLLKDISQKVAVYSTCL 1786

RESULT 6
US-09-561-818A-14
; Sequence 14, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortessmaa, Jarrko
; APPLICANT: Tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-818A-14

Query Match 93.7%; Score 9144; DB 4; Length 1786;
Best Local Similarity 92.7%; Pred. No. 0;
Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;

Qy 1 MGLLQVFAPGV LALWGRVCAQEPFESYGCABGSCYPATGDLIGRAQKLSVTSTCGLHK 60
Db 1 MGLLQLLAFSFLALCRARVRAQEPFESYGCABGSCYPATGDLIGRAQKLSVTSTCGLHK 60
Qy 61 PEPYCIVSHLQEDKKCFICDSRDPYHETLNPD SHLIENVVTFAPNRLKIWWQSENGVEN 120
Db 61 PEPYCIVSHLQEDKKCFICNSQDPYHETLNPD SHLIENVVTFAPNRLKIWWQSENGVEN 120
Qy 121 VTIQDLAEAFHFTHLIMTFKTFEPAAMLIERSSDFGKTWGVYRYFAYDCESFPFGISTG 180
Db 121 VTIQDLAEAFHFTHLIMTFKTFEPAAMLIERSSDFGKTWGVYRYFAYDCESFPFGISTG 180
Qy 181 PMKKVDDIIICDSRYSYDIEPSTEGEVIFRALDP AFKIEDPYSPRIQNLLKITNLRIFVKL 240
Db 181 PMKKVDDIIICDSRYSYDIEPSTEGEVIFRALDP AFKIEDPYSPRIQNLLKITNLRIFVKL 240
Qy 241 HTLGDNLDSRMEIREKYYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCHMC 300
Db 241 HTLGDNLDSRMEIREKYYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCHMC 300
Qy 301 RHNTKGLNCEL CMDFYHDL PWRPAEGRNSNACKKCNCHSISCHFDMAVYLATGNVSGG 360
Db 301 RHNTKGLNCEL CMDFYHDL PWRPAEGRNSNACKKCNCHSISCHFDMAVYLATGNVSGG 360

QY 301 RHNTKGLNCEL CMDFYHDL PWRPAEGRNSNACKKCNONEHSSSCHFDMAVFLATGNVSGG 360
Db RHNTKGLNCEL CMDFYHDL PWRPAEGRNSNACKKCNONEHSSSCHFDMAVFLATGNVSGG 360
QY 361 VCDNCOHNTMGRNCEQCKPFYFOHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVG 420
Db VCDNCOHNTMGRNCEQCKPFYFOHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVG 420
QY 421 LIAGQCRCKLHVEGERCDVCKEGFYDLSEADPYGCKSCACNPLGTIPGNGPCDSETGYCY 480
Db LIAGQCRCKLHVEGERCDVCKEGFYDLSEADPYGCKSCACNPLGTIPGNGPCDSETGYCY 480
QY 481 CKRLVTGQRCDQCLPQHGLSNDLDGCRPCDCLGGLNNSCSEDSGQCSCPLPHMIGRQC 540
Db CKRLVTGQRCDQCLPQHGLSNDLDGCRPCDCLGGLNNSCSEDSGQCSCPLPHMIGRQC 540
QY 541 NEVESGYFTTLDHYIYEAEEANLPGVWVVERQYIQDRIPSWTGPGFVRVPEGAYLEFF 600
Db NEVESGYFTTLDHYIYEAEEANLPGVWVVERQYIQDRIPSWTGPGFVRVPEGAYLEFF 600
QY 601 IDNIPYSMEYILIRYEPQLPDHWEKAVITVORPGKIPASSRCNGTVPDDDNQVVSLSPG 660
Db IDNIPYSMEYILIRYEPQLPDHWEKAVITVORPGKIPASSRCNGTVPDDDNQVVSLSPG 660
QY 661 SRYVVLPRPVCFEKGMYTVRLLELPQYTAGSDVESPYTFIDSLVLMYPYCKSLDIFTVGG 720
Db SRYVVLPRPVCFEKGMYTVRLLELPQYTAGSDVESPYTFIDSLVLMYPYCKSLDIFTVGG 720
QY 721 SGDEVTNSAWETFORYRCLENSRSVVKTPMTDVCNRNIFPSISALIHOTGLACECDPQGS 780
Db SGDEVTNSAWETFORYRCLENSRSVVKTPMTDVCNRNIFPSISALIHOTGLACECDPQGS 780
QY 781 LSSVCDPNNGCQCRCRPNVVGRTNRCAPGTFGFGPNCGKPCDCHLQGSASAFCDAITGQC 840
Db LSSVCDPNNGCQCRCRPNVVGRTNRCAPGTFGFGPNCGKPCDCHLQGSASAFCDAITGQC 840
QY 841 HCFQGIYARQCRCRCLPGYWGFPSPCQCNGHALDCDVTGTECLSCDQYTTGHCNRCCLA 900
Db HCFQGIYARQCRCRCLPGYWGFPSPCQCNGHALDCDVTGTECLSCDQYTTGHCNRCCLA 900
QY 901 GYGDPITIGSGDHCRPCPCPDGPDGSRQFARSCYQDPVTIQLACVCDPGYIGSRCDDCAS 960
Db GYGDPITIGSGDHCRPCPCPDGPDGSRQFARSCYQDPVTIQLACVCDPGYIGSRCDDCAS 960
QY 961 GFFGNPSPDFGSGCPCQCCHNIDTTDPEACDKOTGRCLKCLYHTEGDHQCQLCYGYGDA 1020
Db GFFGNPSPDFGSGCPCQCCHNIDTTDPEACDKOTGRCLKCLYHTEGDHQCQLCYGYGDA 1020
QY 1021 LRQDCRKVCNYLGTVEHNGSDCHCDKATGQCCLPNVIGQNCDCRCAPNTWQLASGTG 1080
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QY 1081 CGPCNCNAAHSFGPSCNEFTGQCQCMPGFGGRTCECQELFWGDPDVECRACDCDPRGIE 1140
Db CGPCNCNAAHSFGPSCNEFTGQCQCMPGFGGRTCECQELFWGDPDVECRACDCDPRGIE 1140
QY 1141 TPQCDQSTGQCVCEGVGPRCDKCTRGYSVGFPPDCTPCHQCFALWDIAIIGELTNRTHKF 1200
Db TPQCDQSTGQCVCEGVGPRCDKCTRGYSVGFPPDCTPCHQCFALWDIAIIGELTNRTHKF 1200
QY 1201 LEKAKALKISGVI GPYRETVDVSVEKKVNEIKDILAQS PAAEPLKNIGILFEEAEKLT KD V 1260
Db LEKAKALKISGVI GPYRETVDVSVEKKVNEIKDILAQS PAAEPLKNIGILFEEAEKLT KD V 1260
QY 1261 TEKMAQVEVKLTDTASQSNSTAGELGALQAEAESLDKTVKELAEQLEFIKNSDIOGALDS 1320
Db TEKMAQVEVKLTDTASQSNSTAGELGALQAEAESLDKTVKELAEQLEFIKNSDIOGALDS 1320
QY 1321 ITKYFQMSLEAEKRVNASTTDPNSTVQSALTRDRVEDLMLERESPFEKEQEEQARLLDE 1380
Db ITKYFQMSLEAEKRVNASTTDPNSTVQSALTRDRVEDLMLERESPFEKEQEEQARLLDE 1380

QY 1381 LAGKLOSLDLSAAQMTCTGTPPGADCESECGGPNCRCTDEGEKKCGGPGCGGLVTVAHSA 1440
Db LAGKLOSLDLSAAQMTCTGTPPGADCESECGGPNCRCTDEGEKKCGGPGCGGLVTVAHSA 1440
QY 1441 WQKAMDFDRDVL SALAEVEQLSKMVSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEEDL 1500
Db WQKAMDFDRDVL SALAEVEQLSKMVSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEEDL 1500
QY 1501 RNLIQIRNFLTEDSADLDSIEAVANEVLKSGNASTPOOLQNLTEDIRERVETLSQVEVI 1560
Db RNLIQIRNFLTEDSADLDSIEAVANEVLKSGNASTPOOLQNLTEDIRERVETLSQVEVI 1560
QY 1561 LQQAADIARAELLLLEAEKRAKSKSATDVKVTADMVKEALEEAEKAQVAAEKAIKQADEDI 1620
Db LQQAADIARAELLLLEAEKRAKSKSATDVKVTADMVKEALEEAEKAQVAAEKAIKQADEDI 1620
QY 1621 QGTQNLTSIESETAASEETLTNASQRI SKLERNVEELKRAAQNSEGEAEYIEKVVSVK 1680
Db QGTQNLTSIESETAASEETLTNASQRI SKLERNVEELKRAAQNSEGEAEYIEKVVSVK 1680
QY 1681 QNADDVKKTLDGELDEKYEKKVYESLIAQKTEESADARRKAEELLQNEAKTLLAQANSKLQLL 1740
Db QNADDVKKTLDGELDEKYEKKVYESLIAQKTEESADARRKAEELLQNEAKTLLAQANSKLQLL 1740
QY 1741 EDLERKYEDNQKYLEDKAQELVRLGEVRSLLKDISQKVAVYSTCL 1786
Db EDLERKYEDNQKYLEDKAQELVRLGEVRSLLKDISQKVAVYSTCL 1786

RESULT 8
US-09-562-702A-16
; Sequence 16, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 16
; LENGTH: 1765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-16

Query Match 93.2%; Score 9092; DB 4; Length 1765;
Best Local Similarity 93.0%; Pred. No. 0;
Matches 1642; Conservative 71; Mismatches 52; Indels 0; Gaps 0;
QY 22 QEPFSGYGAEGSCYPATGDL LIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICDS 81
Db QEPFSGYGAEGSCYPATGDL LIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICDS 60
QY 82 RDPYHETLNPDSHLIENVVTTAFAPNLKIWQSENGVENVTIQDLLEAEFHTHLIMTFK 141
Db RDPYHETLNPDSHLIENVVTTAFAPNLKIWQSENGVENVTIQDLLEAEFHTHLIMTFK 120
QY 142 TFRPAAMLIERSSDFGKTGWVRYFAYDCESFPFGISTGPMKKVDDIICDSRYSIDIEPST 201
Db TFRPAAMLIERSSDFGKTGWVRYFAYDCESFPFGISTGPMKKVDDIICDSRYSIDIEPST 180
QY 202 EGEVIFRALDPAFKIEDPSPRIQNLKITNLRIKLVKLTGLDNLDSRMEIREKYIYA 261
Db EGEVIFRALDPAFKIEDPSPRIQNLKITNLRIKLVKLTGLDNLDSRMEIREKYIYA 261

Db 181 EGEVIFRALDPAFKIEDPSPRIQNLLKLTNLRKFKVHLHTLGLDNLDSRMEIREKYYVA 240
Qy 262 VYDMVVRGNCFCYGHASECAPVDGVNNEEVGMVGHGCMCRHNTKGLNCELAMDYFHDLPW 321
Db 241 VYDMVVRGNCFCYGHASECAPVDGFNEEVGMVGHGCMCRHNTKGLNCELAMDYFHDLPW 300
Qy 322 RPAEGRNSNACKKNCNEHSSSCHFDMAVFLATGNVSGVCDNCQHNTMGRNCEQCKPFY 381
Db 301 RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGVCDNCQHNTMGRNCEQCKPFY 360
Qy 382 FOHPERDIRDPNLCEBCTCDPAGSENGGICDGYTDFSVGLIAGQCRCKLHVEGERCDVCK 441
Db 361 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSTGLIAGQCRCKLNVEGEHCDVCK 420
Qy 442 EGFYDLSAEDPYGCKSCACNPLGTIPGGNPCDSETGYCYCKRLVTGQRCDQCLPQHWGLS 501
Db 421 EGFYDLSSEDPFGCKSCACNPLGTIPGGNPCDSETGHCHYCKRLVTGQHCDQCLPEHWGLS 480
Qy 502 NDLGCRPCDCLGGALNNSCSEDSGQCSCLPHMIGRQCNEVESGYFTTLDHYIYEAE 561
Db 481 NDLGCRPCDCLGGALNNSCFAESGQCSRPHMIGRQCNEVEPGYYPATLDHYLYEAE 540
Qy 562 ANLPGVWVVERQYIQDRIPSWTGPGFVRVPEGAYLEFFIDNIPYSMEYEILIRYEQLP 621
Db 541 ANLPGVSIVERQYIQDRIPSWTGPGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEQLP 600
Qy 622 DHWEKAVITVQRPKIPASSRCNGTVPDDNQVVSLSPGSRYVVLPRPVCFEKGMNYYTVR 681
Db 601 DHWEKAVITVQRPRIPTSSRCNGTIPDDNQVVSLSPGSRYVVLPRPVCFEKGTNYTVR 660
Qy 682 LELPQYTAGSDVESPYTFIDSLVLMYPYCKSLDIFTVGGSGDGEVNTSAWETFQRYRCLE 741
Db 661 LELPQYTSSDVESPYTLIDSLVLMYPYCKSLDIFTVGGSGDGVVNTSAWETFQRYRCLE 720
Qy 742 NSRSVVKTPMTDVCNRIIFSISALIHQTLACEDDPQGSLSVCDPNPGGQCQCRPNVUGR 801
Db 721 NSRSVVKTPMTDVCNRIIFSISALLHQTLACEDDPQGSLSVCDPNPGGQCQCRPNVUGR 780
Qy 802 TCNRCAPGTFGFGPNCKPCDCHLQGSASAFCDAITGQCHCFQGIYARQCDRCLPGYWG 861
Db 781 TCNRCAPGTFGFGSPGCKPCCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDRCLPGHW 840
Qy 862 PSCQPCQNGHALDCDVTGTECLSCQDYTTGHCNRCERLAGYGDPIIGSGDHCRCPCPCPD 921
Db 841 PSCQPCQNGHADDCDPVTGTECLNCQDYTMGHCNRCERLAGYGDPIIGSGDHCRCPCPCPD 900
Qy 922 GPDSGRQFARSCYQDPVTLOLACVCDPGYIGSRCDDCASGFFGNPSPDFGSSCQPCQCHN 981
Db 901 GPDSGRQFARSCYQDPVTLOLACVCDPGYIGSRCDDCASGYFGNPNSEVGSCQPCQCHN 960
Qy 982 IDTTDPEACDKDTGRCLKLYHTEGDHCOLCOYGYGDALRODCRCKVCNLYLGTVKEHCN 1041
Db 961 IDTTDPEACDKETGRCLKLYHTEGEHCQCFRFGYGDALRODCRCKVCNLYLGTVQEHCN 1020
Qy 1042 GSDCHCDKATGQCSCLPNVIGQNCDCRCAPNTWQLASGTGCGPCNCNAAHSFGPSCNEFTG 1101
Db 1021 GSDCQCDKATGQCLCLPNVIGQNCDCRCAPNTWQLASGTGCDPCNCNAAHSFGPSCNEFTG 1080
Qy 1102 QCQCMFGGRTCSQCELFWGDPPDVECRACDPRGIETPQCDQSTGQCVCEGVEGPR 1161
Db 1081 QCQCMFGGRTCSQCELFWGDPPDVECRACDPRGIETPQCDQSTGQCVCEGVEGPR 1140
Qy 1162 CDKCTRGYSGVFPDCTPCHQCQFALWDIAIIGELTNRTHKFLEKAKALKISGVIGPYRETVD 1221
Db 1141 CDKCTRGYSGVFPDCTPCHQCQFALWDVIIAELTNRTHRFLEKAKALKISGVIGPYRETVD 1200
Qy 1222 SVEKKVNEIKOILAQSPAAPLKNIGILFEEAEKLTQDVTEKMAQVEVKLTDTASQSNST 1281
Db 1201 SVERKVSEIKDILAQSPAAPLKNIGNLFEEAEKLIKDVTEMMAQVEVKLSDTTSQSNST 1260
Qy 1282 AGELGALQAEAESLDKTVKELAEQLEFIKNSDIOGALDSITKYFQMSLEAEKRVNASTTD 1341
Db 1261 AKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTTE 1320

Qy 1342 PNSTVEQSALTRDRVEDLMLERESPFKEQEQEQARLLDELAKLQSLDLSAAQMTCTGTP 1401
Db 1321 PNSTVEQSALMRDRVEDVMMERESQFKEKEQEQARLLDELAKLQSLDLSAAAEMTCTGTP 1380
Qy 1402 PGADCSESECGGPNCRDTDEGEKKCGGPGCGGLVTVHAQWQKAMDFFDRDVL SALAEVEQL 1461
Db 1381 PGASCSETECGGPNCRDTDEGERKCGGPGCGGLVTVAHNAQWQKAMDLDQDVL SALAEVEQL 1440
Qy 1462 SKWVSEAKVRADAEAKQNAQDVLLKTNATKKEKVDKSNEDLRNLKIQIRNFLTEDSADLDSI 1521
Db 1441 SKWVSEAKLRADAEAKQSAEDILLKTNATKKEKMDKSNELRNLIKQIRNFLTQDSADLDSI 1500
Qy 1522 EAVANEVLKSGNASTPOOLQNLTEDIRERVETLSQVEVILQQAADIAPAELLLIEEAKRA 1581
Db 1501 EAVANEVLKMEMPSTPOOLQNLTEDIRERVESLSQVEVILQHSAAADIAPAELMLIEEAKRA 1560
Qy 1582 SKSATDVKVTDVMVKEALEEAEAKAQAQAAEKAIKQADEDIQGTQNL LTSIESETAASEETL 1641
Db 1561 SKSATDVKVTDVMVKEALEEAEAKAQAQAAEKAIKQADEDIQGTQNL LTSIESETAASEETL 1620
Qy 1642 TNASQRISKLERNVVEELKRAAQNQSGEAEYIEKVYVSVKQNAADVVKTL DGELEDKEYKKV 1701
Db 1621 FNASQRISELERNVVEELKRAAQNQSGEAEYIEKVYVTVKQSAEDVVKTL DGELEDKEYKKV 1680
Qy 1702 ESLIAQKTEESADARRKAEALLQNEAKTLLAQANSKLQLEDLERKYEDNQYLEDKAQEL 1761
Db 1681 ENLIAKTEESADARRKAEMLQNEAKTLLAQANSKLQLLKDLERKYEDNQRYLEDKAQEL 1740
Qy 1762 VRLEGEVRSLLKDISEKVAVYSTCL 1786
Db 1741 ARLEGEVRSLLKDISQKVAVYSTCL 1765

RESULT 9
US-09-561-818A-16
; Sequence 16, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortessmaa, Jarrko
; APPLICANT: Tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 1765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-818A-16

Query Match 93.2%; Score 9092; DB 4; Length 1765;
Best Local Similarity 93.0%; Pred. No. 0;
Matches 1642; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

Qy 22 QEPFSGCAEGSCYPATGDL LIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICDS 81
Db 1 QEPFSGCAEGSCYPATGDL LIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICNS 60
Qy 82 RDPYHETLNPDSHLIENVVTFAPNRLKIWWQSENGVENVTIQLDLEAEFHTHIMTFK 141
Db 61 QDPYHETLNPDSHLIENVVTFAPNRLKIWWQSENGVENVTIQLDLEAEFHTHIMTFK 120
Qy 142 TFRPAAMLIERSSDFGKTGWVYRYFAYDCESFPGISTGPMKKVDDIIICDSRYSDIEPST 201
Db 121 TFRPAAMLIERSSDFGKTGWVYRYFAYDCEASFPGISTGPMKKVDDIIICDSRYSDIEPST 180
Qy 202 EGEVIFRALDPAFKIEDPSPRIQNLLKITNLRKFKVHLHTLGLDNLDSRMEIREKYYVA 261
Db 181 EGEVIFRALDPAFKIEDPSPRIQNLLKITNLRKFKVHLHTLGLDNLDSRMEIREKYYVA 240

QY 262 VYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGHCMCRHNTKGLNCELMDPFYHDLPW 321
DB 241 VYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGHCMCRHNTKGLNCELMDPFYHDLPW 300
QY 322 RPAEGRNSNACKKCNNEHSSCHFDMAVFLATGNVSGVCDNCQHNTMGRNCEQCKPFY 381
DB 301 RPAEGRNSNACKKCNNEHSSCHFDMAVFLATGNVSGVCDNCQHNTMGRNCEQCKPFY 360
QY 382 FQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGLIAGQCRCKLHVGERCDVCK 441
DB 361 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFSTGLIAGQCRCKLNVGEHCDVCK 420
QY 442 EGFYDLSAEDPYGCKSCACNPLGTIPGGNPPCDSETGYCYCKRLVTGQRCDQCLPOHWGLS 501
DB 421 EGFYDLSSEDPPFGCKSCACNPLGTIPGGNPPCDSETGHYCKRLVTGQHCDCQCLPEHWGLS 480
QY 502 NDLGCRPCDCLGGALNNSCEDSGQSCSLPHMIGRCNEVESGYFTTLDHYIYEAEE 561
DB 481 NDLGCRPCDCLGGALNNSCFAESGQSCSRPHMIGRCNEVEPGYFATLDHYIYEAEE 540
QY 562 ANLPGVVVERQYIQDRIPSWTGPFRVVRPEGAYLEFFIDNIPYSMEYEILIRYEPQLP 621
DB 541 ANLPGVSIIVERQYIQDRIPSWTGAFFVRVVRPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 600
QY 622 DHWEKAVITVORPGKIPASSRCNTVPDDNQVWSLSPGSRVVLPRPVCFEKGMNVTVR 681
DB 601 DHWEKAVITVORPGRIPTSSRCNTIPDDNQVWSLSPGSRVVLPRPVCFEKGINVTVR 660
QY 682 LELPOYTASGSDVESPYTFIDSLVLMPCYCKSLDIFTVGGSGDGEVNTNSAWETFORYRCLE 741
DB 661 LELPOYTSSSDVESPYTLIDSLVLMPCYCKSLDIFTVGGSGDGVNTNSAWETFORYRCLE 720
QY 742 NSRSVVKTPMTDVCNIIIFSISALIHQTLGLACECDPQGLSSVCDPNGGQCQCRPNVVR 801
DB 721 NSRSVVKTPMTDVCNIIIFSISALLHQTLGLACECDPQGLSSVCDPNGGQCQCRPNVVR 780
QY 802 TCNRCAPGTFEGFPNGCKPCDCHLQGSASAFCDAITGQCHCFQGIYARQCDRLPGYWG 861
DB 781 TCNRCAPGTFEGFPNGCKPCDCHLQGSVNAFCNPVTGQCHCFQGIYARQCDRLPGH 840
QY 862 PSCQPCQCNHGLDCTVTGECCLSCQDYTTGHCNRCERCLAGYVGPDIIGSGDHCRPC 921
DB 841 PSCQPCQCNHGLDCTVTGECCLSCQDYTTGHCNRCERCLAGYVGPDIIGSGDHCR 900
QY 922 GPDSGRQFARSCYQDPVTLOLACVCDPVGYSRCDCCASGFFGNPSPDFGSGCQPC 981
DB 901 GPDSGRQFARSCYQDPVTLOLACVCDPVGYSRCDCCASGYFGNPSVGGSCQPC 960
QY 982 IDTTDPEACDKTGRCLKCLYHTEGDCQYGYGDLALRQDCRCKVCNVLGTVKEHCN 1041
DB 961 IDTTDPEACDKTGRCLKCLYHTEGDCQYGYGDLALRQDCRCKVCNVLGTVQEH 1020
QY 1042 GSDCHCDKATGQCSCLPNVIGQNCDCRCAPNWTQALASGTGCGPCNCAHSPGSCNEFTG 1101
DB 1021 GSDCQCDKATGQCLCLPNVIGQNCDCRCAPNWTQALASGTGCDPCNCAHSPGSCNEFTG 1080
QY 1102 QCQCMFGGRTCSQCELFWGDPPDVECRACDPRGIETPQCDQSTGQCVCEGVEGPR 1161
DB 1081 QCQCMFGGRTCSQCELFWGDPPDVECRACDPRGIETPQCDQSTGQCVCEGVEGPR 1140
QY 1162 CDKCTRGYSGVFPDCTPCHQCFALWDIAIIGELTNRTHKFLKAKALKISGVIGPYRETVD 1221
DB 1141 CDKCTRGYSGVFPDCTPCHQCFALWDVIAELTNRTHRFLKAKALKISGVIGPYRETVD 1200
QY 1222 SVEKKVNEIKDILAQSPAAPLKNIGILFEAEKLTQDTEKMAQVEVKLTDTSQSNST 1281
DB 1201 SVERKVSEIKDILAQSPAAPLKNIGILFEAEKLTQDTEKMAQVEVKLTDTSQSNST 1260
QY 1282 AGEKGALQAEASLDKTVKELAEQLEFIKNSDIQCALDSDITKYFQMSLEAEKRVNASTTD 1341
DB 1261 AKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSDITKYFQMSLEAEKRVNASTTE 1320
QY 1342 PNSTVEQSALTRDRVEDLMLERESPFKEQEQEQARLLDELAKGLQSLDLSAAQMTCTGP 1401

DB 1321 PNSTVEQSALMRDRVEDVMMERESQFKEQEQEQARLLDELAKGLQSLDLSAAQMTCTGP 1380
QY 1402 PGADCESECEGPNCRRTDEGEKKGCGPGCGGLVTVHAHSAWQKAMDFDRDVLASAEVEQL 1461
DB 1381 PGASCSETECGPNCRRTDEGERKCGPGCGGLVTVHAHNAWQKAMDLDQDVLASAEVEQL 1440
QY 1462 SKMVSEAKVRADEAKQNAQDVLKTNATKEKVDKSNEDLRLNIKQIRNFLTSDSADLDSI 1521
DB 1441 SKMVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNEDLRLNIKQIRNFLTQDSADLDSI 1500
QY 1522 EAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVILQQAADIAAEALLLEBAKRA 1581
DB 1501 EAVANEVLKMEMPTPQQLQNLTEDIRERVESLSQVEVILQQAADIAAEALLLEBAKRA 1560
QY 1582 SKSATDVKVTADVMKEALEEAEKAAQAAEKAIAKQADEDIQGTQNLTSIESETAASEETL 1641
DB 1561 SKSATDVKVTADVMKEALEEAEKAAQAAEKAIAKQADEDIQGTQNLTSIESETAASEETL 1620
QY 1642 TNASQRIKSLERNVEELKRKAQNSGEAEYIEKVVSVKQNAADDVKTLDGELDEKVKV 1701
DB 1621 FNASQRISELERNVVEELKRKAQNSGEAEYIEKVVTVKQSAEDVKTLDGELDEKVKV 1680
QY 1702 ESLIAQKTESADARRKAELLQNEAKTLLAQANSKLQLEDELERKYEDNOKYLEDKAQEL 1761
DB 1681 ENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLEDELERKYEDNOKYLEDKAQEL 1740
QY 1762 VRLEGEVRSLLKDISEKVAVYSTCL 1786
DB 1741 ARLEGEVRSLLKDISQKVAVYSTCL 1765

RESULT 10

US-08-144-121-4
; Sequence 4, Application US/08144121
; Patent No. 5610031
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert E.
; APPLICANT: Wagman, David W.
; TITLE OF INVENTION: B1k CHAIN OF LAMININ AND METHODS OF USE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: United States
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/144,121
; FILING DATE: 27-OCT-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: (MGH-0780.0) MGP-021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1196 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Domain

LOCATION: 1..250
FEATURE: Domain
NAME/KEY: 251..437
LOCATION: 251..437
FEATURE: Domain
NAME/KEY: 438..807
LOCATION: 438..807
FEATURE: Domain
NAME/KEY: 808..840
LOCATION: 808..840
FEATURE: Domain
NAME/KEY: 841..1196
LOCATION: 841..1196
US-08-144-121-4
Query Match 58.4%; Score 5697.5; DB 1; Length 1196;
Best Local Similarity 63.3%; Pred. No. 0;
Matches 1117; Conservative 46; Mismatches 32; Indels 571; Gaps 2;
QY 22 QEPEFSYGCAEGSCYPATGDLIGRAQKLSVTS-TGGLHKPEPYCIVSHLOEDKKCFICD 80
Db 1 QEPEFSYGCAEGSCYPATGDLIGRAQKLSVTS-TGGLHKPEPYCIVSHLOEDKKCFICN 60
QY 81 SRDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENVTIQLDLAEAFHFTLIMTF 140
Db 61 SQDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENVTIQLDLAEAFHFTLIMTF 120
QY 141 KTFRPAAMLIERSDFGKTGWVYRYFAYDCESFPFGISTGPMKKVDDIICDSRYSDIEPS 200
Db 121 KTFRPAAMLIERSDFGKTGWVYRYFAYDCESFPFGISTGPMKKVDDIICDSRYSDIEPS 180
QY 201 TEGEVIFRALDPAFKIEDPYSPRIQNLLKITNLRKFKVHLTLGDNLLDSRMEIREKYYY 260
Db 181 TEGEVIFRALDPAFKIEDPYSPRIQNLLKITNLRKFKVHLTLGDNLLDSRMEIREKYYY 240
QY 261 AVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGHCRCRHTKGLNCELMDFFYHDLDP 320
Db 241 AVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGHCRCRHTKGLNCELMDFFYHDLDP 300
QY 321 WRPAEGRNSNACKKNCNEHSSCHFDMAVFLATGNVSGGVCDNCQHNMTGRNCEQCKPF 380
Db 301 WRPAEGRNSNACKKNCNEHSSCHFDMAVFLATGNVSGGVCDNCQHNMTGRNCEQCKPF 360
QY 381 YFOHPERDIRDNLCEPCTDPAAGSENGGICDGYTDFSVGLIAGQCRCRKLHVEGERCDVC 440
Db 361 YVQHPERDIRDNLCEPCTDPAAGSENGGICDGYTDFSVGLIAGQCRCRKLHVEGERCDVC 420
QY 441 KEGFYDLSEADPYGCKSCACNPLGTIPGGNPNCDSETGYCYCKRLVTGQRCDCLPQHWGL 500
Db 421 KEGFYDLSEADPYGCKSCACNPLGTIPGGNPNCDSETGYCYCKRLVTGQRCDCLPQHWGL 437
QY 501 SNLDLDCRCPDCDLGALNNSCSESDSGQCSCLPHMIGRQCNEVESGYFTTLDHYIYEA 560
Db 438 SNLDLDCRCPDCDLGALNNSCSESDSGQCSCLPHMIGRQCNEVESGYFTTLDHYIYEA 437
QY 561 EANLPGVVVVERQYIQDRIPSWTGPFGFVRVPEGAYLEFFIDNIPYSMEYEILIRYEPQL 620
Db 438 EANLPGVVVVERQYIQDRIPSWTGPFGFVRVPEGAYLEFFIDNIPYSMEYEILIRYEPQL 437
QY 621 PDHWEKAVITVQRPKIPASSRCGNTVPDDDNQVVSLSPGSRVYVLPVPVCFEKGMYTV 680
Db 438 PDHWEKAVITVQRPKIPASSRCGNTVPDDDNQVVSLSPGSRVYVLPVPVCFEKGMYTV 437
QY 681 RLELPQYTAGSDVESPYTFIDSLVLMPCYKSLDIFTVGGSGDGEVTNSAWETFORYRCL 740
Db 438 RLELPQYTAGSDVESPYTFIDSLVLMPCYKSLDIFTVGGSGDGEVTNSAWETFORYRCL 437
QY 741 ENSRSVVKTPMTDVCNRIIFSISALIHQTGLACECDPQSSLSVCDPNGGQCQCRPNVVG 800
Db 438 ENSRSVVKTPMTDVCNRIIFSISALIHQTGLACECDPQSSLSVCDPNGGQCQCRPNVVG 437
QY 801 RTCNRCAPGTGFGPNCKPCDCHLQGSASAFCDALTGQCHCFQGIYARQCDRCLPGYWG 860
Db 438 RTCNRCAPGTGFGPNCKPCDCHLQGSASAFCDALTGQCHCFQGIYARQCDRCLPGYWG 437

Db 438 ----- 437
QY 861 FPSCQPCQCNHGLDCDVTGECCLSCQDYTTGHNCECLAGYYGDPICSGDHRPCPCP 920
Db 438 ----- 437
QY 921 DGPDSGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCASGFFGNPSDFGSCQPCQCHH 980
Db 438 ----- 437
QY 981 NIDTTDPEACDKDTRCLKLYHTEGDHQCLCOYGYGDALRQDCRKCVCNVLGTVKEHC 1040
Db 438 -----CVCNVLGTVQEHK 450
QY 1041 NGSDCHCDKATGQCSCLPNVIGONCDRCAPNTWQLASGTGCGPCNCAHSGFSPSCNEFT 1100
Db 451 NGSDCQCDKATGQCLCLPNVIGONCDRCAPNTWQLASGTGCDPCNCAHSGFSPSCNEFT 510
QY 1101 GQCQMPGFGGRTCECOELFWGDDPVECRACDPRGIETPQCQDOSTGQCVCEGVEGP 1160
Db 511 GQCQMPGFGGRTCECOELFWGDDPVECRACDPRGIETPQCQDOSTGQCVCEGVEGP 570
QY 1161 RCDKTRGYSGVFPDCTPCHQCFALWDALIGELTNRTHKFLKAKALKISGVIOPYRET 1220
Db 571 RCDKTRGYSGVFPDCTPCHQCFALWDALIGELTNRTHKFLKAKALKISGVIOPYRET 630
QY 1221 DSVEKKVNEIKDILAQSPAAEPLKNIGILFEEAEKLTQVTEKMAQVEVKLTDTASQNS 1280
Db 631 DSVERKVSEIKDILAQSPAAEPLKNIGILFEEAEKLTQVTEKMAQVEVKLTDTASQNS 690
QY 1281 TAGELGALQAEASLDKTVKELAEQLEFIRKNSDIQCALDSITKYFQMSLEAEKRVNASTT 1340
Db 691 TAKELDSLQTEAESLDNTVKELAEQLEFIRKNSDIQCALDSITKYFQMSLEAEKRVNASTT 750
QY 1341 DPNSTVEQSALTRDRVEDIMLERESPFKEQEEQARLLDELAKQLQSLDLSAAQMTCTG 1400
Db 751 EPNSTVEQSALTRDRVEDIMLERESPFKEQEEQARLLDELAKQLQSLDLSAAQMTCTG 810
QY 1401 PPGADCESECGGPNCRDTEGEKKCGGPGGGLVTVVAHSAWQKAMDFDRVLSALAEVEQ 1460
Db 811 PPGADCESECGGPNCRDTEGEKKCGGPGGGLVTVVAHSAWQKAMDFDRVLSALAEVEQ 870
QY 1461 LSKMVSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDLRNLKQIRNFLETDSADLDS 1520
Db 871 LSKMVSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDLRNLKQIRNFLETDSADLDS 930
QY 1521 IEAVANEVLKSGNASTPQOLQNLTEDIRERVETLSQVEVILQQAADIAAEMLLEEAKR 1580
Db 931 IEAVANEVLKSGNASTPQOLQNLTEDIRERVETLSQVEVILQQAADIAAEMLLEEAKR 990
QY 1581 ASKSATDVKVTADVMVKEALEEAEKAQVAAEKAQVAAEKAQVAAEKAQVAAEKAQVAAE 1640
Db 991 ASKSATDVKVTADVMVKEALEEAEKAQVAAEKAQVAAEKAQVAAEKAQVAAEKAQVAAE 1050
QY 1641 LTNASQRISELERNEVEELKRAAQNAGEAEYIEKVYVSVKQADDDVKTLDGELDEKYYK 1700
Db 1051 LTNASQRISELERNEVEELKRAAQNAGEAEYIEKVYVSVKQADDDVKTLDGELDEKYYK 1110
QY 1701 VESLIAQKTEESADARRKAEMLQNEAKTLLAQANSKLOLLEDLERYEDNQYLEDKAE 1760
Db 1111 VESLIAQKTEESADARRKAEMLQNEAKTLLAQANSKLOLLEDLERYEDNQYLEDKAE 1170
QY 1761 LVRLEGEVRSLLKQISEKAVYSTCL 1786
Db 1171 LVRLEGEVRSLLKQISEKAVYSTCL 1196

RESULT 11
US-08-735-893-4
; Sequence 4, Application US/08735893
; Patent No. 5914317
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert E.

APPLICANT: Wagman, David W.
TITLE OF INVENTION: BIK CHAIN OF LAMININ AND METHODS OF USE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: BOSTON
STATE: Massachusetts
COUNTRY: United States
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/735,893
FILING DATE: 18-OCT-1996
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/144,121
FILING DATE: 27-OCT-1993

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: (MGH-0780.1) MGP-021DV
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 1196 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
FEATURE:

NAME/KEY: Domain
LOCATION: 1..250

NAME/KEY: Domain
LOCATION: 251..437

NAME/KEY: Domain
LOCATION: 438..807

NAME/KEY: Domain
LOCATION: 808..840

NAME/KEY: Domain
LOCATION: 841..1196

US-08-735-893-4

Query Match 58.4%; Score 5697.5; DB 2; Length 1196;
Best Local Similarity 63.3%; Pred. No. 0;
Matches 1117; Conservative 46; Mismatches 32; Indels 571; Gaps 2;

QY	22	QEPEFSYGCAGSCYPATGDLILIGRAQKLSVTS-TCGLHKPEPYCIIVSHLQEDKKCFICD	80
Db	1	QEPEFSYGCAGSCYPATGDLILIGRAQKLSVTS-TCGLHKPEPYCIIVSHLQEDKKCFICN	60
QY	81	SRDPYHEINLPDASHLIENVTTFAPNRLKIWWQSENGVENVTIQLDLEAEFFHFLIMTF	140
Db	61	SQDPYHEINLPDASHLIENVTTFAPNRLKIWWQSENGVENVTIQLDLEAEFFHFLIMTF	120
QY	141	KTFRPAAMLIERSSDFGKTGWVRYFYAYDCESSFPGISTGPMKKVDDIICDSRYSIDIEPS	200
Db	121	KTFRPAAMLIERSSDFGKTGWVRYFYAYDCEASFPGISTGPMKKVDDIICDSRYSIDIEPS	180
QY	201	TEGEVIFRALDPAPFKIEDPSPRIQNLLKITNLRKIFVKLHTIGDNLDDSRMEIREKYYY	260
Db	181	TEGEVIFRALDPAPFKIEDPSPRIQNLLKITNLRKIFVKLHTIGDNLDDSRMEIREKYYY	240

QY	261	AVYDMVVRGNCFCYGHASECAPVDGVNEEVEGVHGHCMCRHNTKGLNCELMDFYHDLDP	320
Db	241	AVYDMVVRGNCFCYGHASECAPVDGVNEEVEGVHGHCMCRHNTKGLNCELMDFYHDLDP	300
QY	321	WPAEGRNSNACKKCNCHSSCHFDMAVFLATGNVSGVCDNCQHNTMGRNCEQCKPF	380
Db	301	WPAEGRNSNACKKCNCHSSCHFDMAVFLATGNVSGVCDNCQHNTMGRNCEQCKPF	360
QY	381	YFQHPERDIRPNLCEPCTCDPAGSENGGICDGYTDFSVGLIAGQCRCRKLHVEGERCDVC	440
Db	361	YFQHPERDIRPNLCEPCTCDPAGSENGGICDGYTDFSVGLIAGQCRCRKLHVEGERCDVC	420
QY	441	KEGFYDLSEAEDPYGCKSCACNPLGTIPGGNPNCDSETGYCYCKRLVTGQRCDQCLPQHWGL	500
Db	421	KEGFYDLSEAEDPYGCKSCACNPLGTIPGGNPNCDSETGYCYCKRLVTGQRCDQCLPQHWGL	480
QY	501	SNLDGCRPCDCDLGGALNNSCSEDSGQCSCLPHMIGRCNEVESGYFTTLDHYIYEA	560
Db	481	SNLDGCRPCDCDLGGALNNSCSEDSGQCSCLPHMIGRCNEVESGYFTTLDHYIYEA	540
QY	561	EANLPGVVVVERQYIQDRIPSWTGPFRVPEGAYLEFFIDNIPYSMEYEILLIRYEPQL	620
Db	541	EANLPGVVVVERQYIQDRIPSWTGPFRVPEGAYLEFFIDNIPYSMEYEILLIRYEPQL	600
QY	621	PDHWEKAVITVQRPKIPASSRCGNTVPDDDNQVVSLSPGSRVYVLPFPRVCFEKGMYTV	680
Db	601	PDHWEKAVITVQRPKIPASSRCGNTVPDDDNQVVSLSPGSRVYVLPFPRVCFEKGMYTV	660
QY	681	RLELPQYTAGSDVESPYTFIDSLVLMPCYSKSLDIFTVGGSGDGEVTSNAWETFQRYRCL	740
Db	661	RLELPQYTAGSDVESPYTFIDSLVLMPCYSKSLDIFTVGGSGDGEVTSNAWETFQRYRCL	720
QY	741	ENSRVVKTPMTDVCNRIIFSISALIHQTGLACECDPQSSVCDPNGGQCCQCRPNVVG	800
Db	721	ENSRVVKTPMTDVCNRIIFSISALIHQTGLACECDPQSSVCDPNGGQCCQCRPNVVG	780
QY	801	RTCNRCAPGTFGFGPNGCKBCDCHLQGSASAFCDALTGQCHCFQGIYARQCDRLPGYWG	860
Db	781	RTCNRCAPGTFGFGPNGCKBCDCHLQGSASAFCDALTGQCHCFQGIYARQCDRLPGYWG	840
QY	861	FPSCQPCQNGHALDCDTVTGECSCQDYTTGHNCRCLAGYGDPIIGSGDHCRPCPCP	920
Db	841	FPSCQPCQNGHALDCDTVTGECSCQDYTTGHNCRCLAGYGDPIIGSGDHCRPCPCP	900
QY	921	DGPDGRQFARSCYQDPVTILQACVCDPGYIGSRCDDCAGFFGNPSDFGSGCQPCQCHH	980
Db	901	DGPDGRQFARSCYQDPVTILQACVCDPGYIGSRCDDCAGFFGNPSDFGSGCQPCQCHH	960
QY	981	NIDTTPACDKDTGRCLKLYHTEGDHCLCQYGYGDALRQDCKKVCNVLGTVEHC	1040
Db	961	NIDTTPACDKDTGRCLKLYHTEGDHCLCQYGYGDALRQDCKKVCNVLGTVEHC	1020
QY	1041	NGSDCHCDKATGQCSCLPNVIGONCDRCAPNTWQLASGTGCGPCNCAHSGFSPSCNEFT	1100
Db	1021	NGSDCHCDKATGQCSCLPNVIGONCDRCAPNTWQLASGTGCGPCNCAHSGFSPSCNEFT	1080
QY	1101	GQCQCMFPGGRTCSECCQELFWGDDVECRACDCDPRGIETPQCDQSTGQCVCVEGVEGP	1160
Db	1081	GQCQCMFPGGRTCSECCQELFWGDDVECRACDCDPRGIETPQCDQSTGQCVCVEGVEGP	1140
QY	1161	RCDKCTRGYSGVFPDCTPCHQCFALWDALIGELTNRTHKFLKAKALKISGVIQYRET	1220
Db	1141	RCDKCTRGYSGVFPDCTPCHQCFALWDALIGELTNRTHKFLKAKALKISGVIQYRET	1200
QY	1221	DSVEKKVNEIKDILAQSPAAEPLKNIGILFEEAEKLTQDVTQMAQVEVKLTDTASQNS	1280
Db	1201	DSVEKKVNEIKDILAQSPAAEPLKNIGILFEEAEKLTQDVTQMAQVEVKLTDTASQNS	1260
QY	1281	TAGELGALQAEASLDKTVKELAEQLEFIKNDSIQGALDSITKYFQMSLEAEKRVNAST	1340
Db	1261	TAGELGALQAEASLDKTVKELAEQLEFIKNDSIQGALDSITKYFQMSLEAEKRVNAST	1320
QY	1341	TAKELDSLQTEAESLDNTVKELAEQLEFIKNDSIRGALDSITKYFQMSLEAEKRVNAST	1400
Db	1321	TAKELDSLQTEAESLDNTVKELAEQLEFIKNDSIRGALDSITKYFQMSLEAEKRVNAST	1380

Dd 1265 GLRHEIGKTERLTQLEAELTAVODENFNANHALSGLERDGFALNLTLRQLDOHLEILKH 1324
Qy 1312 SDIOGALDSITKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRVEDLMLERESPFEKQQ 1371
Dd 1325 SNFLGAYDSIRHAHSQSTEAEERRANASTFAVPSVNSADTTRRTTEVLMGACKENFNROH 1384
Qy 1372 EEQARLLDELAKGLQSLDLASAAQMTCTGTPPGADCSESEGGPNCRTEGEKKCGGPGCG 1431
Dd 1385 LANQOALGRLSAHAHTLSLTGINELVCGAPGDAPCATSPCGAGCRDEQPRCGLGCS 1444
Qy 1432 GLTVVAHSANQKAMDFDRDVLASALAEVEQLSKMVSEAKVRADEAKQNAQDVLLKTNATKE 1491
Dd 1445 GAAAPADLALGRARHSQAEQLRALVEGGILSRVSETRRQAEAAQRAQAALDKANASRG 1504
Qy 1492 KVDKSNEDLRNLIKQIRNFLTEDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERV 1551
Dd 1505 QVEQANQELRELIONVKDFLSQEGADPDSIEMVATRVLDISIPASPEQIORLASEIAERV 1564
Qy 1552 ETLQSEVEVILQOQSAADIARAELLLEBEAKRASKSATDVKVTDADMVKEALEEAEKAQVAAEK 1611
Dd 1565 RSLADVDTTILAHMGDVRRAEQQLQDAHRPARSRAEGEROKAETVQAALAEAAQRAQAAG 1624
Qy 1612 AIKQADEDIQGTQNLITSIESETAASEETLTNASQIRSKLERNVEELKRKAQNSGEAEY 1671
Dd 1625 AIRGAVVDTQNTQTLQRVQERMAGREKSLNSAGERAROLDALLEALKLRAGNSLAAST 1684
Qy 1672 IEKVVSVKQNAADVKKTLGDELDEKXKVESLIAQKTEESADARRKAELLQNEAKTLA 1731
Dd 1685 AEETAGSAQSRAREAEKOLREOVGDQYQTVRALAERKAEGVLAQAARAEQLRDEARDLQ 1744
Qy 1732 QANSKLQLEDLERKVEDNQKYLEDKAQELVRLEGEVRSLLKDISSEKVAVYSTC 1785
Dd 1745 AAQDKLQRLQLEGTYEENERALEGKAAQLDGLAARMRSVLQAINLQVQIYNTC 1798

RESULT 13
US-09-561-709B-11
; Sequence 11, Application US/09561709B
; Patent No. 6682911
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Champliand, Marie-France
; APPLICANT: Olson, Pamela
; APPLICANT: Koch, Manuel
; APPLICANT: Brunken, William
; TITLE OF INVENTION: LAMININS AND USES THEREOF
; FILE REFERENCE: 10287-060001
; CURRENT APPLICATION NUMBER: US/09/561,709B
; CURRENT FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 09/168,949
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: US 60/061,609
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1798
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-709B-11

Query Match 50.3%; Score 4907; DB 4; Length 1798;
Best Local Similarity 49.6%; Pred. NO. 2.7e-281;
Matches 888; Conservative 308; Mismatches 573; Indels 20; Gaps 8;
Qy 3 LLQVFAFGVLALWGTRVCAQEPEFSYGCAGSCYPATGDLILIGRAQKLSVTSTCGLHKPE 62
Dd 23 LLSVLA-----ATLAQAPADVP-GCSRGSCYPATADLLVGRADRLTASSTCGLNGRQ 74
Qy 63 PYCIVSHLOEDKKCFICDSRDPYHETLNPDSHLIENVVTTFAPNRLKIWWQSENGVENVT 122
Dd 75 PYCIVSHLOEDKKCFICDSRRRPFSSARDNPNPHTRIQNVVTSFAPQRRAAWWSQNGIPAVT 134

Qy 123 IQDLLEAEFHTLIMTFKTRPAAMLIERSDFGKTGWVYRYPAYDCESSEFFGISTGPM 182
Dd 135 IQDLLEAEFHTLIMTFKTRPAAMLVERSADFGRTWHVYRYFSYDCGADFPGVPLAPP 194
Qy 183 KKVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPRIQNLKLTNLRIFKVLKHT 242
Dd 195 RHWDVVVCESTRYSEIEPSTEGEVIYRVLDPAIPIDPYSSRIQNLKLTNLRVNLTLHT 254
Qy 243 LGDNLDSRMEIREKYYYAVYDMVVRGNCFYGHASECAPVDGVNBEVEGMVHGHNCMRH 302
Dd 255 LGDNLDPREIREKYYYALVELVVRGNCFYGHASECAPAPGAPAHAEVMVHGACICKH 314
Qy 303 NTKGLNCELCMDFYHDLWPWPAEGRNSNACKKCNENHSSSCHDFMAVFLATGNVSGGVC 362
Dd 315 NTRGLNCEQCQDFYRDLWPWPAEDGHSHACKKCDRHGTHSCHDFMAVYLGSGNVSGGVC 374
Qy 363 DNCQHTMGRNCEQCKPFYFQHPERDIRDNLCEPCTCDPAGSENGGICDGYTDFSVGLI 422
Dd 375 DGCQHTAYRHCELCRPFYRDPDKDLRDPAVCRSCDCDPMGSDQGGRCDSHDDPALGLV 434
Qy 423 AGQCRCKLHVEGERCDVCKEGFYDLSEADPYGCKSCACNPLGTIPGPNPCDSETGYCYCK 482
Dd 435 SGQCRCKEHVVGTRCQCRDGFGLSISDPSGRRCCQCNARGTVPGSTPCDPNSGSCYCK 494
Qy 483 RLVTGQRCDQLPQHGLNSLDGCRPCDCDLGGALNNSCEDSGQCSCLPHMIGRQCNE 542
Dd 495 RLVTGRGCDRCLPGHWGLSLDLLGCRPCDCDVGGALDPQDEGTGQCHCRQHMVGRRCBQ 554
Qy 543 VESGYFTTLDHYIYEAEANLPGVYVVERQYIQDRIPSWTGPFGVVRVPEGAYLEFFID 602
Dd 555 VQPGYFRPFLDHLIWEAENTR-GQVLDVVERLVTGPETPSWTGSGFVRVLEGGTLEFLVA 613
Qy 603 NIPYSMEYEILIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTVDDDNQVVSLSGSR 662
Dd 614 SVPNAMDYDLLRLLEPQVPEQWAELELIVQRPQVPAHSLGHLVPRDDRIGQTLQPHAR 673
Qy 663 YVVLPRPVCPEKGMNYTVRLELPQYTAGSDVESPYT---FIDSLVLMYPCKSLDIFTV 718
Dd 674 YLIFPNPVCLEPGISYKHLHLKLV- TGSSAQETPYSGPGLLIDSLVLLPRVLVLEMF-- 730
Qy 719 GSGDGEVTNSAWETFORYRCLENSRSVVKTPTMTDVCNRIIFSISALIHQTGLACECDPQ 778
Dd 731 --SGDDAAALERQATFERYQCHEEGLVPSKTSPEACAPLLISLSTLIYNGALPCQCNPQ 788
Qy 779 GSLSSVCDPNCGCQCRPNVVGRTCNRCAPGTGFGPNGCKPCDCHLQGSASAFCDAITG 838
Dd 789 GSLSSSECNPHGGQCLCKPGVVGRRCDTCAPGYVGFPTGCQACQCSPRGALSSLCERTSG 848
Qy 839 QCHCFQGIYARQCDRCLPGYWGFPSCQPCQCNHGHALDCDTVTGECCLSCQDYTTGHCNCR 898
Dd 849 QCLCRTGAFGLRCDACQRGQWGFPSRCPVCNCGHADECNTHTGACLCGRDHTGGEHCERC 908
Qy 899 LAGYGDPIIGSGDHCRCPCPDGPDGSGRQFARSCYQDPVTLQACVCDPQYIGSRCDDC 958
Dd 909 IAGFHGDPRLPYGAQCRPCPCPEGPGSQRHAFATSCHQDEYSQIVCHCRAGYTGLRCEAC 968
Qy 959 ASGFFGNPSPDFGSCQPCQCHNIDTTDPEACDKDTGRCLKLYHTEGDHCOLCQYGYG 1018
Dd 969 APQFGDPSRPGRCQLCECSGNIDPMDPDACDPHPGQCLRLUHHTEGPHCAHSKPGFHG 1028
Qy 1019 DALRQDCRKVCVNYLGTVKEHNCNSD-CHCDKATGQCSCLPNVIGQNCDCRCAPNTWQLAS 1077
Dd 1029 QAAARQSCHRCTCNLLGTNPQQCPSPDQCHCDPSSGQCPCLPNVQALAVDRCAPNFWNLTS 1088
Qy 1078 GTGCGPCNCNAAHSFGPSCNEFTGQCQCMFGGRTCSECQELFWGDDVECRACDCDPR 1137
Dd 1089 GHGQCPACALPSPBEGPTCNEFTGQCHCLCGFGGRTCSECQELHWGDFGLQCHACDCDSR 1148
Qy 1138 GIETPQCDQSTGQVCVEGVEGPRCDKCTRGYSGVFPDCTPCHQCFAWDALIGELTNRT 1197
Dd 1149 GIDTPQCHRTGHCTCRPGVSGVRCDQCARGFSGIFPACHPCHACFGDWDVVDLAART 1208
Qy 1198 HKFLEKAKALKISGVIQPYRETVDVSEKVKNEIKDIL-AQSPAAEPLKVNIGILFEEAEKL 1256

QY 1198 HKFLEKAKALISGVIQYRETVDSVEKKVNEIKDIL-AQSPAAEPLKNIGILFEEAEKL 1256
Db 1209 QRLEQRAQELQOQTGVLGAFESSFWHMQEKLGIVQGIVGARNTSAASTAQLVEATEELRRE 1268
QY 1257 TKDVTAKMAQVEVKLTDTASQSNSTAGELGALQAEBSLDKTVKELAEQLEFIKNSDIQ 1316
Db 1269 IGEATEHLTQLEADLTVDQENFNANHALSGLERDRIALNLTQLRDLQHLKHSNFLG 1328
QY 1317 ALDSITKYFQMSLEAEKRVNASTTDPNSTVEQSAITRDRVEDLMLERESPKEQEEQAR 1376
Db 1329 AYDSIRHAHSQSAEAEERRANTSALAVPSPVNSASARHRTALMDACKEDFNKHEMANQR 1388
QY 1377 LIDELAGKLQSLDLASAAQMTCTGTPPGADCSSECGGPNCRDTDEGEKKCGGPGCGGLVTV 1436
Db 1389 ALGKLSARHTTSLTIDINELVCGAQLHHDRTSPCGGACRDEDDGPRCGGLSCNGAAT 1448
QY 1437 AHSWQKAMDFFDRDVLALAEVEQLSKMVSEAKVRADEAKQNAQDVLKTNATKEKYDKS 1496
Db 1449 ADLALGRARHTQAEQLRALAEGGSILSRVAETRRQASEAQQAQALDKANASRGQVEQA 1508
QY 1497 NEDLRNLKQIRNFLTSDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQ 1556
Db 1509 NOELQELIQSVKDFLNEGADPDSIEMVATRVLELSIPASAEQIQHLAGAIARVRSRAD 1568
QY 1557 VEVLQQAADIAARAEULLLEAKRASKSATDVKVTADMVKEALBEAEKAQVAEAKAIQA 1616
Db 1569 VDAILARTVGDVRRAEQLQDARRARSWAEDKQKAETVQAALBEAQAQGIAGAIQA 1628
QY 1617 DEDIQTNLLTSIETASAEETLTNASORISKLRNVEELKKAQNSGEAEYIEKV 1676
Db 1629 VADTRDTEQTLQVQERMAGAERALSAGERARQDLALLEALKLRAGNSLAASTAHETA 1688
QY 1677 YSVKQNAADDVKKTLGDELDEKYYKVESLIAQNTESADARRKAEALLQNEAKTLLAQANSK 1736
Db 1689 GSAQGRAQAEQELRLGQDQYQYTVKALAEKQAQGLVLAQARAEQLPDEARDLLOAQDK 1748
QY 1737 LQLEDLERKYEDNQYLEDKAQELVRLGEVRSLLKDISEKVAVYSTC 1785
Db 1749 LQRLQLEGTYEENERALESKAAQLDGLAEARMSVLQAINLQVQIYNTC 1797

RESULT 15

US-09-561-709B-1
; Sequence 1, Application US/09561709B
; Patent No. 6682911
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Champlaud, Marie-France
; APPLICANT: Olson, Pamela
; APPLICANT: Koch, Manuel
; APPLICANT: Brunken, William
; TITLE OF INVENTION: LAMININS AND USES THEREOF
; FILE REFERENCE: 10287-06001
; CURRENT APPLICATION NUMBER: US/09/561.709B
; CURRENT FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 09/168,949
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: US 60/061,609
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1761
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-561-709B-1

Query Match 39.1%; Score 3813.5; DB 4; Length 1761;
Best Local Similarity 41.1%; Pred. No. 9.6e-217;
Matches 743; Conservative 305; Mismatches 636; Indels 125; Gaps 30;

QY 30 CAEGSCYPATGDLIGRAQKLSVTSTCGLHKEPEYCIIVSHLQEDKKCFICDSRDPYHETL 89

Db 23 CNRGACHPTTGDLLVGRNTQMASSTCGLSRAQKYCILSYLEGEQKCSICDSRFPYDYPD 82
QY 90 NPDSHLIENVVTTFAPNRLKIWQSENGVENVTIQLDLEAEFHTLIMTFKTRPAAAML 149
Db 83 QPNSHTIENVTVSFEPDREKKWQSENGLDHVSIRLDEALFRSHLILTFKTRPAAAML 142
QY 150 IERSDFGKTWGVYRYFAYDCSSFFPGISTGPMKKVDDIICDSRYSDIEPSTEGEVIFRA 209
Db 143 VERSTDYGHNMWKFYFAKDCATSFNITSGQAQGVGDIVCDISKYSDIEPSTGGEVWLKV 202
QY 210 LDPAFKIEDPYSPRIQNLKLTNLRKFVKLHTLGNLLDSRM-EIREKYYAVYDMVVR 268
Db 203 LDPSFEIENPYSPIQDLVTLNLRINFTKLHTLGDALLGRRQNDSDLKYYIYALYEMIVR 262
QY 269 GNCFCYGHASECAPVDGVNEEV--EGMVHGHCMCRHNTKGLNCELMDYFHDLPWRPAE 325
Db 263 GSCFCNGHASECRPMQKMRGDFVSPPMVHGGVCVQCHNTDGNPCERCKDFQDAPWRPAA 322
QY 326 GRNSNACKKCNNEHSSSCHDFDMAVFLATGNVSGVCDNCQHNTMGRNCEQCKPFYFQHP 385
Db 323 DLQDNACRSCNSHSSRCHDFMTTYLASGGLSGVCEDCQHNTGQHCHDCRPLFYRDP 382
QY 386 ERDIRPDLCEPCTCDPAGSENGGICDGYTDFSVGLIAGQCRCKLHVEGERCDVCKEGFY 445
Db 383 LKTTSDPYACIPCECDPDGTISGGICVSHSDPALGSGVAGQCLCKENVEGAKCDQCKPNHY 442
QY 446 DLSAEDPYGCKSCACNPLGTIPGNPCDSETGYCYCKRLVTGQRCDCQLPQHWGLSNDLD 505
Db 443 GLSATDPLGQPCDCNPLGSLP-FLTCDVDTGQCLCLSYVTGAHCEEVTVGWLGNHLH 501
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Search completed: May 18, 2004, 15:02:09
Job time : 23.5107 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:	May 18, 2004, 14:56:24 ; Search time 45.4374 Seconds (without alignments) 10937.572 Million cell updates/sec
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 Perfect score: 9758
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	9758	100.0	1786	9	US-09-938-275-7	Sequence 7, Appli
2	9758	100.0	1786	14	US-10-037-182-10	Sequence 10, Appl
3	9429	96.6	1725	14	US-10-037-182-12	Sequence 12, Appl
4	9144	93.7	1786	9	US-09-873-676-113	Sequence 113, App
5	9144	93.7	1786	9	US-09-938-275-6	Sequence 6, Appli
6	9144	93.7	1786	14	US-10-037-182-6	Sequence 6, Appli
7	9092	93.2	1765	14	US-10-037-182-8	Sequence 8, Appli
8	5690.5	58.3	1196	16	US-10-443-349-4	Sequence 4, Appli
9	5087.5	52.1	1801	9	US-09-938-275-8	Sequence 8, Appli
10	5066.5	51.9	1799	9	US-09-845-583-6	Sequence 6, Appli
11	5031.5	51.6	1798	9	US-03-938-275-9	Sequence 9, Appli
12	4902	50.2	1798	9	US-09-845-583-8	Sequence 8, Appli
13	3742.5	38.4	1808	15	US-10-369-493-5986	Sequence 5986, Ap
14	3068.5	31.4	1101	12	US-10-287-971-18	Sequence 18, Appl
15	2154	22.1	527	12	US-09-925-298-703	Sequence 703, App

16	2154	22.1	527	14	US-10-102-806-703	Sequence 703, Appl
17	1751	17.9	3672	15	US-10-369-493-6146	Sequence 6146, Ap
18	1675	17.2	3712	12	US-10-037-417-48	Sequence 48, Appl
19	1675	17.2	3712	13	US-10-108-605-103	Sequence 103, App
20	1671	17.1	3712	12	US-10-037-417-51	Sequence 51, Appl
21	1661.5	17.0	1572	14	US-10-037-182-20	Sequence 20, Appl
22	1661.5	17.0	1605	14	US-10-037-182-18	Sequence 18, Appl
23	1651	16.9	1609	14	US-10-037-182-14	Sequence 14, Appl
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33	1577	16.2	3696	15	US-10-312-088-31	Sequence 31, Appl
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37	1572.5	16.1	3695	14	US-10-037-182-2	Sequence 2, Appl
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41	1555	15.9	3070	10	US-09-961-403-7	Sequence 7, Appl
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45	1550.5	15.9	1172	9	US-09-919-172-16	Sequence 16, Appl

ALIGNMENTS

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RESULT 1
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; Sequence 7, Application US/09938275
; Patent No. US20020111309A1
; GENERAL INFORMATION:
; APPLICANT: Gerardo Castillo
; APPLICANT: Alan Snow
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications
; TITLE OF INVENTION: of Laminin and Laminin-Derived Protein Fragments
; FILE REFERENCE: PROTEO.P03
; CURRENT APPLICATION NUMBER: US/09/938,275
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Mus Musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Swissprot P02469
; DATABASE ENTRY DATE: 1989-07-01

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; Publication No. US20030044899A1
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Doi, Masayuki
; APPLICANT: Thyboll, Jill
; TITLE OF INVENTION: Recombinant Laminin 10
; FILE REFERENCE: 99-274-F
; CURRENT APPLICATION NUMBER: US/10/037,182
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,449
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/279,282
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 36
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; TYPE: PRT
; ORGANISM: Mus musculus
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Db 661 SRYVVLPRPVCPEKGMNYYTVRLELPQYTAGSGDVESPYTFIDSLVLMPYCKSLDIFTVGG 720
QY 721 SGDGEVNTSAWETPQRYRCLENSRSVVKTPMTDVCRNIIIFSALIHQTGLACECDPQGS 780
Db 721 SGDGEVNTSAWETPQRYRCLENSRSVVKTPMTDVCRNIIIFSALIHQTGLACECDPQGS 780
QY 781 LSSVCDPNGGQCQCRPNVVGRTCNRCAPGTFGPGNGCKPCDCHLQGSASAFCAITGQC 840
Db 781 LSSVCDPNGGQCQCRPNVVGRTCNRCAPGTFGPGNGCKPCDCHLQGSASAFCAITGQC 840
QY 841 HCFQGIYARQCRLPGYWGFPSCQPCQCNHGDCTVTGECISQDQYTTGHNCRCL 900
Db 841 HCFQGIYARQCRLPGYWGFPSCQPCQCNHGDCTVTGECISQDQYTTGHNCRCL 900
QY 901 GYIGDPIIGSGDHCRPCPCPDGPDGSGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCAS 960
Db 901 GYIGDPIIGSGDHCRPCPCPDGPDGSGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCAS 960
QY 961 GFFGNPSDFGGSQPCQCHNIDTTDPEACDKDTGRCLKCLYHTEGDHCQLCQGYYGDA 1020
Db 961 GFFGNPSDFGGSQPCQCHNIDTTDPEACDKDTGRCLKCLYHTEGDHCQLCQGYYGDA 1020
QY 1021 LRQDCRKCVCNLYGTVKEHNGSDCHCDKATGQCSCCLPNVIGQNCDCRCAPNTWOLASGTG 1080
Db 1021 LRQDCRKCVCNLYGTVKEHNGSDCHCDKATGQCSCCLPNVIGQNCDCRCAPNTWOLASGTG 1080
QY 1081 CGPCNCNAAHSFGSCNEFTGQCQCMPGFGGRTCECQELFWGDPDVECRACDCDPRGIE 1140
Db 1081 CGPCNCNAAHSFGSCNEFTGQCQCMPGFGGRTCECQELFWGDPDVECRACDCDPRGIE 1140
QY 1141 TPQCDQSTGQCVCVEGVEGPRCDKCTRGYSGVFPDCTPCHQCQFALWDIAIGELTNRTHKF 1200
Db 1141 TPQCDQSTGQCVCVEGVEGPRCDKCTRGYSGVFPDCTPCHQCQFALWDIAIGELTNRTHKF 1200
QY 1201 LEKAKALKISGVIGPYRETVDSEKKNVEIKDILAQSPAAPLKNIGILFEEAEKLTADV 1260

Db 1201 LEKAKALKISGVIGPYRETVDSEKKNVEIKDILAQSPAAPLKNIGILFEEAEKLTADV 1260
QY 1261 TEKMAQVEVKLTDTASQSNSTAGELCALQAEASLDTKTVKELAEQLEFIKNSDIOGALDS 1320
Db 1261 TEKMAQVEVKLTDTASQSNSTAGELCALQAEASLDTKTVKELAEQLEFIKNSDIOGALDS 1320
QY 1321 ITKYFQMSLEAKRVNASTTDPNSIVESQALTRDRVEDLMLESPPFKEQEEQARLLDE 1380
Db 1321 ITKYFQMSLEAKRVNASTTDPNSIVESQALTRDRVEDLMLESPPFKEQEEQARLLDE 1380
QY 1381 LAGKLQSLDLSAAAQMTCTGTPPGADCESECGGPNCRCTDEGEKKCGGPGCGGLVTVAHSA 1440
Db 1381 LAGKLQSLDLSAAAQMTCTGTPPGADCESECGGPNCRCTDEGEKKCGGPGCGGLVTVAHSA 1440
QY 1441 WQKAMDFDRDVLALAEVEQLSKMWSEAKVRADEAKQNAQDVLLKTNATKEKVKDKSNEDL 1500
Db 1441 WQKAMDFDRDVLALAEVEQLSKMWSEAKVRADEAKQNAQDVLLKTNATKEKVKDKSNEDL 1500
QY 1501 RNLIKQIRNFLTSDADLDSIEAVANEVLKSGNASTPQQLQNLTDIEDIRERVETLSQVEVI 1560
Db 1501 RNLIKQIRNFLTSDADLDSIEAVANEVLKSGNASTPQQLQNLTDIEDIRERVETLSQVEVI 1560
QY 1561 LQQAADIAAEELLEEAKRASKSATDVKVTADMVKEALEEAEKQVAAEKAIKQADEDI 1620
Db 1561 LQQAADIAAEELLEEAKRASKSATDVKVTADMVKEALEEAEKQVAAEKAIKQADEDI 1620
QY 1621 QGTQNLTSIESETAAASEETLTNASQRISKLERNEVELKRAQNSGEAEYIEKVVSVK 1680
Db 1621 QGTQNLTSIESETAAASEETLTNASQRISKLERNEVELKRAQNSGEAEYIEKVVSVK 1680
QY 1681 QNADDVKITLDGELDEKYKKVESLIAQKTEESADARRKAEALLQNEAKTLLAQANSKLQLL 1740
Db 1681 QNADDVKITLDGELDEKYKKVESLIAQKTEESADARRKAEALLQNEAKTLLAQANSKLQLL 1740
QY 1741 EDLERKYEDNQKYLEDKAQELVRLEGEVRSLLKDISEKAVAVYSTCL 1786
Db 1741 EDLERKYEDNQKYLEDKAQELVRLEGEVRSLLKDISEKAVAVYSTCL 1786

RESULT 3
US-10-037-182-12
; Sequence 12, Application US/10037182
; Publication No. US20030044899A1
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Doi, Masayuki
; APPLICANT: Thyboll, Jill
; TITLE OF INVENTION: Recombinant Laminin 10
; FILE REFERENCE: 99-274-F
; CURRENT APPLICATION NUMBER: US/10/037,182
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,449
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/279,282
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1725
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-037-182-12

Query Match 96.6%; Score 9429; DB 14; Length 1725;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 62 EPYCIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVTTFAPNRLKIWMQSENGVENV 121
Db 1 EPYCIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVTTFAPNRLKIWMQSENGVENV 60
QY 122 TIQLDLAEAFHFTHLIMTFKTRPAAMLIERSSDFGKTGWVRYFAYDCSSFPFGISTGP 181

Db 61 TQLDLEAEFHTLIMTFKTRPAAMLIERSSDFKGTGWVYRYFAYDCSSFPGISTGP 120
QY 182 MKKVDIIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLLKITNLRIKFKVLH 241
Db 121 MKKVDIIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLLKITNLRIKFKVLH 180
QY 242 TLGDNLLDSRMEIREKYYVAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGVHGHCMCR 301
Db 181 TLGDNLLDSRMEIREKYYVAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGVHGHCMCR 240
QY 302 HNTKGLNCELMDFYHDLPRPAEGRNSNACKKNCNEHSSSCHFDMAVFLATGNVSGGV 361
Db 241 HNTKGLNCELMDFYHDLPRPAEGRNSNACKKNCNEHSSSCHFDMAVFLATGNVSGGV 300
QY 362 CDNCQHTMGRNCEQCKPFYFQHPERDIRDNLCEPCTCDPAGSENGGICDGYTDFSVGL 421
Db 301 CDNCQHTMGRNCEQCKPFYFQHPERDIRDNLCEPCTCDPAGSENGGICDGYTDFSVGL 360
QY 422 IAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGGNPCDSETGYCYC 481
Db 361 IAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGGNPCDSETGYCYC 420
QY 482 KRLVTGQRCDQCLPOHWGLSNDLDGCRPCDCDLGGALNNSCEDSGQCSCLPHMIGROCN 541
Db 421 KRLVTGQRCDQCLPOHWGLSNDLDGCRPCDCDLGGALNNSCEDSGQCSCLPHMIGROCN 480
QY 542 EVESGYFTTLDHYIYEAEANLPGVWVVERQYIQDRIPSWTGPGRVVRPEGAYLEFFI 601
Db 481 EVESGYFTTLDHYIYEAEANLPGVWVVERQYIQDRIPSWTGPGRVVRPEGAYLEFFI 540
QY 602 DNIPIYSMEYEILIRYEPQLPDHWEKAVITVORPGKIPASSRCGNTVPDDNQVVSLSPGS 661
Db 541 DNIPIYSMEYEILIRYEPQLPDHWEKAVITVORPGKIPASSRCGNTVPDDNQVVSLSPGS 600
QY 662 RYVVLPRPVCFEKGMNYYTVRLPELPQYTAGSDVESPYTFIDSLVLMPYCKSLDIFTVGS 721
Db 601 RYVVLPRPVCFEKGMNYYTVRLPELPQYTAGSDVESPYTFIDSLVLMPYCKSLDIFTVGS 660
QY 722 GDGEVYNSAWETFQRYRCLNSRSVVKTPMTDVCNIIIFSALIHQTLGACECDPQGS 781
Db 661 GDGEVYNSAWETFQRYRCLNSRSVVKTPMTDVCNIIIFSALIHQTLGACECDPQGS 720
QY 782 SSVCDPNGGQCQCRPNVVGRTCNRCAPGTGFGPNCGKPCDCHLQGSASFCDAITGQCH 841
Db 721 SSVCDPNGGQCQCRPNVVGRTCNRCAPGTGFGPNCGKPCDCHLQGSASFCDAITGQCH 780
QY 842 CFQGIYARQCDRLPGYWGFPSCQPCQCNHGDCTVTGECCLSCQDYTTGHCNRCERCLAG 901
Db 781 CFQGIYARQCDRLPGYWGFPSCQPCQCNHGDCTVTGECCLSCQDYTTGHCNRCERCLAG 840
QY 902 YYGDPRIIGSGDHCRPCPCPDGSDSGRQFARSCYQDPVTQLACVCDPBGYIGSRCDDCASG 961
Db 841 YYGDPRIIGSGDHCRPCPCPDGSDSGRQFARSCYQDPVTQLACVCDPBGYIGSRCDDCASG 900
QY 962 FFGNPSDFGSGCQPCQCHNITDTPDPEACDKDTGRCLKCLYHTEGDHCQLCOYGYGDAL 1021
Db 901 FFGNPSDFGSGCQPCQCHNITDTPDPEACDKDTGRCLKCLYHTEGDHCQLCOYGYGDAL 960
QY 1022 RQDCRKCVCNYLGTIVKEHCNGSDCHCDKATGQCSCCLPNVIGQNCDCRCAPNTWQLASGTGC 1081
Db 961 RQDCRKCVCNYLGTIVKEHCNGSDCHCDKATGQCSCCLPNVIGQNCDCRCAPNTWQLASGTGC 1020
QY 1082 GPCNCNAAHSFGPSCNEFTGQCQCMPPGFGGRTCECQELFWGDPDVECRACDCDPRGIET 1141
Db 1021 GPCNCNAAHSFGPSCNEFTGQCQCMPPGFGGRTCECQELFWGDPDVECRACDCDPRGIET 1080
QY 1142 PQCDQSTGQCVCVEGVGPRCDKCTRIGYSGVFPDCTPCHQCQFALWDAIIGELTNRTHKFL 1201
Db 1081 PQCDQSTGQCVCVEGVGPRCDKCTRIGYSGVFPDCTPCHQCQFALWDAIIGELTNRTHKFL 1140
QY 1202 EKAKALKISGVIPYRETVDVSEKKVNEIKDILAQSPAAEPLKNIGILFEEAEKLT KDVT 1261

Db 1141 EKAKALKISGVIPYRETVDVSEKKVNEIKDILAQSPAAEPLKNIGILFEEAEKLT KDVT 1200
QY 1262 EKMAQVEVKLTDTASQSNSTAGELGALQAEASLDKTVKELAEQLEFIKNSDIQGALDSI 1321
Db 1201 EKMAQVEVKLTDTASQSNSTAGELGALQAEASLDKTVKELAEQLEFIKNSDIQGALDSI 1260
QY 1322 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLERESPFKEQQEQEQLLDEL 1381
Db 1261 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLERESPFKEQQEQEQLLDEL 1320
QY 1382 AGKLOSLDLASAAQMTCTGTPPGADCSSECCGGPCNCRDEGEKKCGGPGCGGLVTVVAHSAM 1441
Db 1321 AGKLOSLDLASAAQMTCTGTPPGADCSSECCGGPCNCRDEGEKKCGGPGCGGLVTVVAHSAM 1380
QY 1442 QKAMDFDRDVLASAEVEQLSKMVSEAKVRADAKQNAQDVLLKTNATKEKVDKSNEDLR 1501
Db 1381 QKAMDFDRDVLASAEVEQLSKMVSEAKVRADAKQNAQDVLLKTNATKEKVDKSNEDLR 1440
QY 1502 NLTKQIRNFLTSDADLSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVIL 1561
Db 1441 NLTKQIRNFLTSDADLSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVIL 1500
QY 1562 QQSAADIARAELLLLEAKRASKSATDVKVTADMVKEALEEAEKAQVAAEKAIKQADEDIQ 1621
Db 1501 QQSAADIARAELLLLEAKRASKSATDVKVTADMVKEALEEAEKAQVAAEKAIKQADEDIQ 1560
QY 1622 GTONLLTSIESETAASEETLTNASQRI SKLERNVEELKRAAQNSGEAEYIEKVYYSVKQ 1681
Db 1561 GTONLLTSIESETAASEETLTNASQRI SKLERNVEELKRAAQNSGEAEYIEKVYYSVKQ 1620
QY 1682 NADDVVKKTLDGELDEKVKVESLIAQKTEESADARRKAELLQNEAKTLLAQANSKLQLE 1741
Db 1621 NADDVVKKTLDGELDEKVKVESLIAQKTEESADARRKAELLQNEAKTLLAQANSKLQLE 1680
QY 1742 DLERKYEDNQKYLEDKAQLVRLEGEVRSLLKDISEKVAVYSTCL 1786
Db 1681 DLERKYEDNQKYLEDKAQLVRLEGEVRSLLKDISEKVAVYSTCL 1725

RESULT 4

US-09-873-676-113
; Sequence 113, Application US/09873676
; Patent No. US20020077289A1
; GENERAL INFORMATION:
; APPLICANT: MacDonald, Nicholas J.
; APPLICANT: Sim, Kim L.
; TITLE OF INVENTION: Angiostatin and Endostatin Binding Proteins and Methods of Use
; FILE REFERENCE: 05213-0378 (43170-259333)
; CURRENT APPLICATION NUMBER: US/09/873,676
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 60/209,065
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/289,387
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 113
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-873-676-113

Query Match 93.7%; Score 9144; DB 9; Length 1786;
Best Local Similarity 92.7%; Pred. NO. 0;
Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;
QY 1 MGLQVPAFGVLA LWGTRVCAQEPESYCAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60
Db 1 MGLQLLAFSFLALCRARVRAQEPESYCAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60
QY 61 PEPYCIIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVVTTFAPNRLKIWQSENGVEN 120
Db 61 PEPYCIIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVVTTFAPNRLKIWQSENGVEN 120

QY 121 VTQLDLEAEFHFTHLIMTKTFRPAAMLIERSSDFGKTGWVRYRFAYDCESFPFGISTG 180
Db 121 VTQLDLEAEFHFTHLIMTKTFRPAAMLIERSSDFGKTGWVRYRFAYDCESFPFGISTG 180
QY 181 PMKQVDDIIICDSRYSDIEPSTGEVIFRALDPAPKIEDPYPRIQNLLKITNLRKIFVKL 240
Db 181 PMKQVDDIIICDSRYSDIEPSTGEVIFRALDPAPKIEDPYPRIQNLLKITNLRKIFVKL 240
QY 241 HTLGDNLLDSRMEIREKYYAVYDMVVRGNCFYGHASECAPVDGVNEEVEGMVGHCMC 300
Db 241 HTLGDNLLDSRMEIREKYYAVYDMVVRGNCFYGHASECAPVDGVNEEVEGMVGHCMC 300
QY 301 RHNTKGLNCELMDFFHDLPLWRPAEGRNSNACKKNCNEHSSSCHFDMAVFLATGNVSGG 360
Db 301 RHNTKGLNCELMDFFHDLPLWRPAEGRNSNACKKNCNEHSSSCHFDMAVFLATGNVSGG 360
QY 361 VCDNCQHNTMGRNCEQCKPFYFQHPERDIRDPNLCPECTCDPAGSENGGICDGYTDFSVG 420
Db 361 VCDNCQHNTMGRNCEQCKPFYFQHPERDIRDPNLCPECTCDPAGSENGGICDGYTDFSVG 420
QY 421 LIAGQCRCRLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGPNPCDSETGYCY 480
Db 421 LIAGQCRCRLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGPNPCDSETGYCY 480
QY 481 CKRLVTGQRCDQCLPQHGLSNDLDGCRPCDCLDGLGALNNSCSEDSGQCSCLPHMIGRQC 540
Db 481 CKRLVTGQRCDQCLPQHGLSNDLDGCRPCDCLDGLGALNNSCSEDSGQCSCLPHMIGRQC 540
QY 541 NEVESGYFTTLDHYIYEAEEANLPGVVVVERQXIQDRIPSWTGPGRVPEGAYLEFF 600
Db 541 NEVESGYFTTLDHYIYEAEEANLPGVVVVERQXIQDRIPSWTGPGRVPEGAYLEFF 600
QY 601 IDNTPYSMEYELIRYEPQLPDHWEKAVITVQRPKIPASSRCNGTVPDDNQVVSLSPG 660
Db 601 IDNTPYSMEYELIRYEPQLPDHWEKAVITVQRPKIPASSRCNGTVPDDNQVVSLSPG 660
QY 661 SRYVVLPRPVCFEKGMNYYTVELLPQYTASGSDVESPYTFIDSLVLMPCYCKSLDIFTVGG 720
Db 661 SRYVVLPRPVCFEKGMNYYTVELLPQYTASGSDVESPYTFIDSLVLMPCYCKSLDIFTVGG 720
QY 721 SGDGEVYNSAWETFORYRCLENSRSVVKTEPMTDVCNRIIFISALIHQTLGACBCDPQGS 780
Db 721 SGDGVVYNSAWETFORYRCLENSRSVVKTEPMTDVCNRIIFISALIHQTLGACBCDPQGS 780
QY 781 LSSVCDPNGGQCQCRPNVVGRTICNRCAPGTGFGPNCGKPCDCHLOGSASAFCDAITQC 840
Db 781 LSSVCDPNGGQCQCRPNVVGRTICNRCAPGTGFGPNCGKPCDCHLOGSASAFCDAITQC 840
QY 841 HCFQGIYARQCDRLCPGYWGFSPCQPCQNGHALDCDVTGTECLSCQDYYTTHNCERCLA 900
Db 841 HCFQGIYARQCDRLCPGYWGFSPCQPCQNGHALDCDVTGTECLSCQDYYTTHNCERCLA 900
QY 901 GYGDPIIGSGDHCRCPCPCPDGSDSGRQFARSCYQDPVTQLACVCDPGYIGSRCDDCAS 960
Db 901 GYGDPIIGSGDHCRCPCPCPDGSDSGRQFARSCYQDPVTQLACVCDPGYIGSRCDDCAS 960
QY 961 GFFGNPSDFGSSCQPCQCHNIIIDTDPACDKDTGRCLKCLYHTEGDHCQLCOGYGYGDA 1020
Db 961 GYFGNPSDFGSSCQPCQCHNIIIDTDPACDKDTGRCLKCLYHTEGDHCQLCOGYGYGDA 1020
QY 1021 LRQDCRKVCVNYLGTVQEHKNGSDCHCDKATGQCSCLEPNVIGQNCDCRCAPIWOLASGTG 1080
Db 1021 LRQDCRKVCVNYLGTVQEHKNGSDCHCDKATGQCSCLEPNVIGQNCDCRCAPIWOLASGTG 1080
QY 1081 CGPCNCAAHSGFSPSCNEFTGQCQCMFPGFGRTCTSECELFWDGPDVECRACDPRGIE 1140
Db 1081 CGPCNCAAHSGFSPSCNEFTGQCQCMFPGFGRTCTSECELFWDGPDVECRACDPRGIE 1140
QY 1141 TPQCDSGTGQVCVVEGPRCDKCTRGYSGVFPDCTPCHQCFCALWDIAIIGELTNRTHKF 1200
Db 1141 TPQCDSGTGQVCVVEGPRCDKCTRGYSGVFPDCTPCHQCFCALWDIAIIGELTNRTHKF 1200

QY 1201 LEKAKALKISGVIGPYRETVDVSEKKNVEIKDILAQSPAAEPLKNIGILFEEAEKLTADV 1260
Db 1201 LEKAKALKISGVIGPYRETVDVSEKKNVEIKDILAQSPAAEPLKNIGILFEEAEKLTADV 1260
QY 1261 TEKMAQVEVKLTDTASQSNSTAGELGALQAEAFSLDKTVKELAEQLEFIKNSDIQGALDS 1320
Db 1261 TEKMAQVEVKLTDTASQSNSTAGELGALQAEAFSLDKTVKELAEQLEFIKNSDIQGALDS 1320
QY 1321 ITKYFQMSLEAEKRVNASTTDPNSTVEQSAITRDRVEDLMLERESPFKEQEQEQAARLLDE 1380
Db 1321 ITKYFQMSLEAEKRVNASTTDPNSTVEQSAITRDRVEDLMLERESPFKEQEQEQAARLLDE 1380
QY 1381 LAGKLQSLDLSAAAQMTCTGPPGADCSSESCGGPNCRTDEGEKCKGPGCGGLVTVAHSA 1440
Db 1381 LAGKLQSLDLSAAAQMTCTGPPGADCSSESCGGPNCRTDEGEKCKGPGCGGLVTVAHSA 1440
QY 1441 WQKAMDFDRDVLALAEVQLSKMVSEAKVRADAKQNAQDVLKTNATKEKVDKSNEDL 1500
Db 1441 WQKAMDFDRDVLALAEVQLSKMVSEAKVRADAKQNAQDVLKTNATKEKVDKSNEDL 1500
QY 1501 RNLIKQIRNFLTQSDADLSIEAVANEVLKSGNASTPQOLQNLTEDIRERVETLSQVEVI 1560
Db 1501 RNLIKQIRNFLTQSDADLSIEAVANEVLKSGNASTPQOLQNLTEDIRERVETLSQVEVI 1560
QY 1561 LQSAADIAAEALLLEAKRASKSATDVKVTADMVKEALEEAEKAAQVAAEKAIKQADEDI 1620
Db 1561 LQSAADIAAEALLLEAKRASKSATDVKVTADMVKEALEEAEKAAQVAAEKAIKQADEDI 1620
QY 1621 QGTQNLTSIESETAASEETLTFNASQRISKLEARNVEELKRAAQNSEAEYIEKVYYSVK 1680
Db 1621 QGTQNLTSIESETAASEETLTFNASQRISKLEARNVEELKRAAQNSEAEYIEKVYYSVK 1680
QY 1681 QNADDVKKTLDELDEKYYKVESLIAQKTEESADARRKAEALLQNEAKTLLAQANSKLQLL 1740
Db 1681 QNADDVKKTLDELDEKYYKVESLIAQKTEESADARRKAEALLQNEAKTLLAQANSKLQLL 1740
QY 1741 EDLERKYEDNQYLEDKAEQELVRLGEVRSLLKDISKVAVYSTCL 1786
Db 1741 EDLERKYEDNQYLEDKAEQELVRLGEVRSLLKDISKVAVYSTCL 1786

RESULT 5

US-09-938-275-6
; Sequence 6, Application US/09938275
; Patent No. US20020111309A1
; GENERAL INFORMATION:
; APPLICANT: Gerardo Castillo
; APPLICANT: Alan Snow
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications
; TITLE OF INVENTION: of Laminin and Laminin-Derived Protein Fragments
; FILE REFERENCE: PROTEO.P03
; CURRENT APPLICATION NUMBER: US/09/938,275
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Swissprot P07942
; DATABASE ENTRY DATE: 1988-08-01
US-09-938-275-6

Query Match 93.7%; Score 9144; DB 9; Length 1786;
Best Local Similarity 92.7%; Pred. No. 0;
Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;
QY 1 MGLLQVFAFGVLALWGTRVCAQEPFESYCAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60
Db 1 MGLLQVFAFGVLALWGTRVCAQEPFESYCAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60
QY 61 PEPYCIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVVTTFAPNRLKIWWQSENGVEN 120

Db 61 PEPYCIVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVVTTFAPNRLKIHWQSENGVEN 120
QY 121 VTIQLDLEAEFFHFLIMTFKTFRPAAMLIERSSDFGKTGWYRYFAYDCESFPFGISTG 180
Db 121 VTIQLDLEAEFFHFLIMTFKTFRPAAMLIERSSDFGKTGWYRYFAYDCESFPFGISTG 180
QY 181 PMKQVDDIIICDSRYSDIEPSTEGEVI FRALDPAFKIEDPYSPRIQNLLKITNRIKFVKL 240
Db 181 PMKQVDDIIICDSRYSDIEPSTEGEVI FRALDPAFKIEDPYSPRIQNLLKITNRIKFVKL 240
QY 241 HTLGDNLLDSRMEIREKYIYAVYDMVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMC 300
Db 241 HTLGDNLLDSRMEIREKYIYAVYDMVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMC 300
QY 301 RHNTKGLNCEL CMDFYHDL PWRPAEGRNSNACKKCNNEHSSSCHFDMAVFLATGNVSGG 360
Db 301 RHNTKGLNCEL CMDFYHDL PWRPAEGRNSNACKKCNNEHSSI SCHFDMAVFLATGNVSGG 360
QY 361 VCDNCQHNTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVG 420
Db 361 VCDNCQHNTMGRNCEQCKPFYFQHPERDIRDPNFCERTCTDPAGSQNEGICDSYTDFTG 420
QY 421 LIAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGPNPCDSETGYCY 480
Db 421 LIAGQCRCKLHVEGERCDVCKEGFYDLSSEDFFGCKSCACNPLGTIPGPNPCDSETGHYCY 480
QY 481 CKRLVTGQRCDQCLPQHGLNSDL DGCRCPCDCDLGGALNNSCSEDSGQCSCLPHMIGRQC 540
Db 481 CKRLVTGQHCDQCLPEHWGLNSDL DGCRCPCDCDLGGALNNSCFAESGGQSCRPHMIGRQC 540
QY 541 NEVESGYFTTLDHYIYEAEEANLPGVAVVERQYIQDRIPSWTGPFGFVRVPEGAYLEFF 600
Db 541 NEVEPGYYFATLDHYLYEAEEANLPGGVSI VERQYIQDRIPSWTGAGFVRVPEGAYLEFF 600
QY 601 IDNIPYSMEYIILIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTVPPDDDNQVVSLSPG 660
Db 601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPTSRRCGNTIPDDDNQVVSLSPG 660
QY 661 SRYVVLPRPVCFEKGMNTYVRLELPQYTSDDSVESPYTIDSLVLMYPYCKSLDIFTVGG 720
Db 661 SRYVVLPRPVCFEKGTNTYVRLELPQYTSDDSVESPYTIDSLVLMYPYCKSLDIFTVGG 720
QY 721 SGDGEVNTSAWETFQYRCLENSRSVVKTEMTDVCRNII FSI SALLHQTGLACEDEPQGS 780
Db 721 SGDGVVNTSAWETFQYRCLENSRSVVKTEMTDVCRNII FSI SALLHQTGLACEDEPQGS 780
QY 781 LSSVCDPNGGCQCRPNVVGRTCNRCAPGTFGFGPNCKPCDCHLQGSASAFCDAITGQC 840
Db 781 LSSVCDPNGGCQCRPNVVGRTCNRCAPGTFGFGPSGCKPCCHLQGSVNAFCNPVTGQC 840
QY 841 HCFQGIYARQCDRCLPGYWGFPSCQPCQCNHGHALDCDVTGBCLSQDYYTGHNCERCLA 900
Db 841 HCFQGVYARQCDRCLPGHWGFPSCQPCQCNHGADDPCDPTGBCLNQDYYTGHNCERCLA 900
QY 901 GYGDPIIGSGDHCRPCPCPDGSDSGRQFARSCYQDPVTLQACVCDPDPGYIGSRCDDCAS 960
Db 901 GYGDPIIGSGDHCRPCPCPDGSDSGRQFARSCYQDPVTLQACVCDPDPGYIGSRCDDCAS 960
QY 961 GFFGNPSPDFGSSCQPCQCHNIDITDPEACDKDTGRCLKCLYHTEGDHCLQCYGYGDA 1020
Db 961 GYFGNPSEVGSCQPCQCHNIDITDPEACDKETGRCLKCLYHTEGEHCQCFRFGYGDA 1020
QY 1021 LRQDCRKVCVNLGTVKEHCNGSDCHCDKATGQCSCLPNVIGQNCDCRCAPNTWQLASGTG 1080
Db 1021 LRQDCRKVCVNLGTVQEHHCNGSDCQCDKATGQCLCLPNVIGQNCDCRCAPNTWQLASGTG 1080
QY 1081 CGPCNCNAHSFGPSCNEFTGQCQCMPPFGGRTCECQELFWGDPDVECRACDCDPRGIE 1140
Db 1081 CDFPCNCNAHSFGPSCNEFTGQCQCMPPFGGRTCECQELFWGDPDVECRACDCDPRGIE 1140
QY 1141 TPQCDQSTGQCVVEGVEGPRCDKCTRGYSGVFPDCTPCHQCFALWDIAIIGELTNRTHKF 1200

Db 1141 TPQCDQSTGQCVVEGVEGPRCDKCTRGYSGVFPDCTPCHQCFALWDVITIAELTNRTHRF 1200
QY 1201 LEKAKALKISGVIGPYRETVDVSVEKKVNEIKDILAQSPAAEPLKNIGILFEAEKLTQDV 1260
Db 1201 LEKAKALKISGVIGPYRETVDVSVERKVSEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDV 1260
QY 1261 TERMAQVEVKLTDTASQSNSTAGELGALQAAESLDKTVKELAEQLEFIKNSDIQCALDS 1320
Db 1261 TENMAQVEVKLSDTTQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDS 1320
QY 1321 ITRYFQMSLEAEKRVNASITDPNSTVEQSALTRDRVEDLMLERESPFEQEQEQARLLDE 1380
Db 1321 ITRYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVMVERESQFKEKQEQARLLDE 1380
QY 1381 LAGKIQSLDLSAAAQMTCCGPPGADCSSESCGPGNCRCTDEGEKKCGGPGCGGLVTVAHSA 1440
Db 1381 LAGKIQSLDLSAAAEMTCGTPPGASCSETECGPGNCRCTDEGERKCGGPGCGGLVTVAHNA 1440
QY 1441 WQKAMDPRDVL SALAEVEQLSKMVSEAKVRADAEAKONAQDVLLKTNATKEKVDKSNEDL 1500
Db 1441 WQKAMDLDQDVL SALAEVEQLSKMVSEAKLRADAEAKQSAEDILLKTNATKEKMDKSNEEL 1500
QY 1501 RNLIKQIRNFLTEDSADLDSIEAVANEVLKSGNASTPQOLQNLTEDIRERVETLSQVEVI 1560
Db 1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKMEMPTPQOLQNLTEDIRERVESLSQVEVI 1560
QY 1561 LQSAADIAEAELLLLEAAKASKSATDVKTADVMVKEALEEAEKAQVAEAKAIKQADEDI 1620
Db 1561 LQSAADIAEAEMLLLEAAKASKSATDVKTADVMVKEALEEAEKAQVAEAKAIKQADEDI 1620
QY 1621 QGTQNLTSIESETAASEEILFNASQRISELERNVBELKRAAQNSEAEYIEKVYVYTVK 1680
Db 1621 QGTQNLTSIESETAASEEILFNASQRISELERNVBELKRAAQNSEAEYIEKVYVYTVK 1680
QY 1681 QNADDVKKTLDGELDEKYKKVESLIAQKTEESADARRKAEALLQNEAKTLLAQANSKIQLL 1740
Db 1681 QSAEDVKKTLDGELDEKYKKVENLIAKTEESADARRKAEMLQNEAKTLLAQANSKIQLL 1740
QY 1741 EDLERKYEDNQKYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1786
Db 1741 KDLERKYEDNQRYLEDKAQELARLEGEVRSLLKDISEKVAVYSTCL 1786

RESULT 6

US-10-037-182-6
; Sequence 6, Application US/10037182
; Publication No. US20030044899A1
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Doi, Masayuki
; APPLICANT: Thyboll, Jill
; TITLE OF INVENTION: Recombinant Laminin 10
; FILE REFERENCE: 99-274-F
; CURRENT APPLICATION NUMBER: US/10/037,182
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,449
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/279,282
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-037-182-6

Query Match 93.7%; Score 9144; DB 14; Length 1786;
Best Local Similarity 92.7%; Pred. No. 0;
Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;

QY 1 MGLLQVFAFGVLALWGTGRVCAQEPESYGAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60

Db 1 MGLLQLLAFSLALCRARVRAQEPESYGAEGSCYPATGDLILIGRAQKLSVTSTCTGLHK 60
QY 61 PEPYCIIVSHLOEDKKCFICDSRDPYHETLNPDShLIENVVTTTFAPNRLKIWWQSENGVEN 120
Db 61 PEPYCIIVSHLOEDKKCFICNSQDPYHETLNPDShLIENVVTTTFAPNRLKIWWQSENGVEN 120
QY 121 VTIQLDLEAEFHFTHLIMTFKTRPAAMLIERSSDFGKTGWVRYPAYDCESFPGISTG 180
Db 121 VTIQLDLEAEFHFTHLIMTFKTRPAAMLIERSSDFGKTGWVRYPAYDCESFPGISTG 180
QY 181 PMKKVDDIICDSRYSDIEPSTEGEVI FRALDPAFKIEDPSPRIQNLKITNLRIKFVKL 240
Db 181 PMKKVDDIICDSRYSDIEPSTEGEVI FRALDPAFKIEDPSPRIQNLKITNLRIKFVKL 240
QY 241 HTLGDNLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGHC 300
Db 241 HTLGDNLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGHC 300
QY 301 RHNTKGLNCELMDFYHDLPRWPAEGRNSNACKKCNCHSSCHFDMAVFLATGNVSGG 360
Db 301 RHNTKGLNCELMDFYHDLPRWPAEGRNSNACKKCNCHSSCHFDMAVFLATGNVSGG 360
QY 361 VCDNCQHNTMGRNCEQCKPFYFQHPERDIRDNLCEPCTCDPAGSENGICDGYTDFSVG 420
Db 361 VCDNCQHNTMGRNCEQCKPFYFQHPERDIRDNLCEPCTCDPAGSENGICDGYTDFSVG 420
QY 421 LIAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGNGPCDSETGYCY 480
Db 421 LIAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGNGPCDSETGYCY 480
QY 481 CKRLVTGQRCDQCLPOHWGLSNDLDGCRPCDCLGGALNNSCEDSGQSCSLPHMIGRQC 540
Db 481 CKRLVTGQRCDQCLPOHWGLSNDLDGCRPCDCLGGALNNSCEDSGQSCSLPHMIGRQC 540
QY 541 NEVESGYFTTLDHYIYEAEANLPGVVVVERQYIQDRIPSWTGPGRVVRPEGAYLEFF 600
Db 541 NEVESGYFTTLDHYIYEAEANLPGVVVVERQYIQDRIPSWTGPGRVVRPEGAYLEFF 600
QY 601 IDNIPYSMEYIILIRYEPQLPDHWEKAVITVORPGKIPASSRCNGTVPDDDNQVVSLS 660
Db 601 IDNIPYSMEYIILIRYEPQLPDHWEKAVITVORPGKIPASSRCNGTVPDDDNQVVSLS 660
QY 661 SRYVVLPRPVCFEKGMNVTVRLELPQYTAGSDVESPYTFIDSLVLMPYCKSLDIFTVGG 720
Db 661 SRYVVLPRPVCFEKGMNVTVRLELPQYTAGSDVESPYTFIDSLVLMPYCKSLDIFTVGG 720
QY 721 SGDGEVNTSAWETFQYRCLENSRSVVKTPMTDVCNRIIFSISALIHQTGLACECDPQGS 780
Db 721 SGDGEVNTSAWETFQYRCLENSRSVVKTPMTDVCNRIIFSISALIHQTGLACECDPQGS 780
QY 781 LSSVCDPENGQCCQCRPNVVGRTCNRCAPGTFGFGNGCKPCDCHLQGSASAFDAITGQC 840
Db 781 LSSVCDPENGQCCQCRPNVVGRTCNRCAPGTFGFGNGCKPCDCHLQGSASAFDAITGQC 840
QY 841 HCFQGIYARQCDCRLPGYWGFPSPCQPCQCNCGHALDCTVTGECCLSCQDYTTGHNCECLA 900
Db 841 HCFQGIYARQCDCRLPGYWGFPSPCQPCQCNCGHALDCTVTGECCLSCQDYTTGHNCECLA 900
QY 901 GYGDPIIGSGDHCRPCPDGPDGSGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCAS 960
Db 901 GYGDPIIGSGDHCRPCPDGPDGSGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCAS 960
QY 961 GYFGNPSDFGSGCQPCQCHNIDTTPDPAECDKDTGRCLKCLYHTEGDHCLQCYGYGDA 1020
Db 961 GYFGNPSDFGSGCQPCQCHNIDTTPDPAECDKDTGRCLKCLYHTEGDHCLQCYGYGDA 1020
QY 1021 LRQDCKKVCNVLGTVQHEHNGSDCHCDKATGQCSCLPNVIGQNCDCRCAPNWQLASGTG 1080
Db 1021 LRQDCKKVCNVLGTVQHEHNGSDCHCDKATGQCSCLPNVIGQNCDCRCAPNWQLASGTG 1080
QY 1081 CGPCNCNAHSFGPSCNEFTGQCCQCMPPGFGGRTCTSECQELFWGDDVECRACDPRGIE 1140
Db 1081 CGPCNCNAHSFGPSCNEFTGQCCQCMPPGFGGRTCTSECQELFWGDDVECRACDPRGIE 1140

QY 1141 TPQCDQSTGQCVCVEGVGPRCDKCTRGYSVGFPPDCTPCHQCFAWDIAIIGELTNRTHKF 1200
Db 1141 TPQCDQSTGQCVCVEGVGPRCDKCTRGYSVGFPPDCTPCHQCFAWDIAIIGELTNRTHKF 1200
QY 1201 LEKAKALKISGVIQPYRETVDVSEKVKVNEIKDILAQSPAAEPLKNIGLFEAEKLTQDV 1260
Db 1201 LEKAKALKISGVIQPYRETVDVSEKVKVNEIKDILAQSPAAEPLKNIGLFEAEKLTQDV 1260
QY 1261 TEKMAQVEVKLTDTFASQSNSTAGELGALQABAEASLDKTVKELAEQLEFIKNSDIOGALDS 1320
Db 1261 TEKMAQVEVKLTDTFASQSNSTAGELGALQABAEASLDKTVKELAEQLEFIKNSDIOGALDS 1320
QY 1321 ITKYFQMSLEAEKRVNASTTDPNSTVEQSAALTRDRVEDLMLERESPFEKQEEQARLLDE 1380
Db 1321 ITKYFQMSLEAEKRVNASTTDPNSTVEQSAALTRDRVEDLMLERESPFEKQEEQARLLDE 1380
QY 1381 LAGKLQSLDLSAAAQMTCTGTPPGADCSSECGGPNCRDTDEGEKKCGGPGGGLVTVAHSA 1440
Db 1381 LAGKLQSLDLSAAAQMTCTGTPPGADCSSECGGPNCRDTDEGEKKCGGPGGGLVTVAHSA 1440
QY 1441 WQKAMDFDRDVL SALAEVQLSKMVSEAKVRADEAKQNAQDVLTKTNATKVKDKSNEDL 1500
Db 1441 WQKAMDFDRDVL SALAEVQLSKMVSEAKVRADEAKQNAQDVLTKTNATKVKDKSNEDL 1500
QY 1501 RNLIKQIRNFLTEDSADLDSIEAVANEVLKSGNASTPQQLQNLNLTEDIRERVETLSQVEVI 1560
Db 1501 RNLIKQIRNFLTEDSADLDSIEAVANEVLKSGNASTPQQLQNLNLTEDIRERVETLSQVEVI 1560
QY 1561 LQOQSAADIARAEELLEAEKRAKASKSATDVKTADVMVKEALEEAEKAAQVAAEKAIKQADEI 1620
Db 1561 LQOQSAADIARAEELLEAEKRAKASKSATDVKTADVMVKEALEEAEKAAQVAAEKAIKQADEI 1620
QY 1621 QGTQNLTLTSIESETAASEETLTFNASQRISELERNVVELKRKAAQNSGEAEYIEKVYTVK 1680
Db 1621 QGTQNLTLTSIESETAASEETLTFNASQRISELERNVVELKRKAAQNSGEAEYIEKVYTVK 1680
QY 1681 QNADDVKKTLTGELDEKYKKVESLIAQKTESADARRKAELLQNEAKTLAQANSKLQLL 1740
Db 1681 QNADDVKKTLTGELDEKYKKVESLIAQKTESADARRKAELLQNEAKTLAQANSKLQLL 1740
QY 1741 EDLERKYEDNQYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1786
Db 1741 EDLERKYEDNQYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1786

RESULT 7
US-10-037-182-8
; Sequence 8, Application US/10037182
; Publication No. US20030044899A1
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Doi, Masayuki
; APPLICANT: Thyboll, Jill
; TITLE OF INVENTION: Recombinant Laminin 10
; FILE REFERENCE: 99-274-F
; CURRENT APPLICATION NUMBER: US/10/037,182
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,449
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/279,282
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-037-182-8

Query Match 93.2%; Score 9092; DB 14; Length 1765;
Best Local Similarity 93.0%; Pred. No. 0;
Matches 1642; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

QY 22 QPEFSGCAEGSCYPATGDLIGRAQKLSVTSTCGLHKPEPYCIVSHLOEDKCKFCIDS 81
Db 1 QPEFSGCAEGSCYPATGDLIGRAQKLSVTSTCGLHKPEPYCIVSHLOEDKCKFCICS 60
QY 82 RDPYHETLNPDSLHNIENVVTFAPNRLKIWQSENGVENVTIQLDLAEFFHFTHLIMTFK 141
Db 61 QDPYHETLNPDSLHNIENVVTFAPNRLKIWQSENGVENVTIQLDLAEFFHFTHLIMTFK 120
QY 142 TERPAAMLIERSSDFGTGWVRYFAYDCESFFGTSTGPMKVVDDIICDSRYSDIERST 201
Db 121 TERPAAMLIERSSDFGTGWVRYFAYDCESFFGTSTGPMKVVDDIICDSRYSDIERST 180
QY 202 EGEVIFRALDPAFKIEDPSPRIQNLKITNLRIFKVLHTLGLDNLDSRMEIREKYAYA 261
Db 181 EGEVIFRALDPAFKIEDPSPRIQNLKITNLRIFKVLHTLGLDNLDSRMEIREKYAYA 240
QY 262 VYDMVVRGNCFCYGHASECAPVDGVNEEVEGVMHGMCRHNTKGLNCELCDWDFYHDLPW 321
Db 241 VYDMVVRGNCFCYGHASECAPVDGVNEEVEGVMHGMCRHNTKGLNCELCDWDFYHDLPW 300
QY 322 RPAEGRNSNACKKNCNEHSSCHFDMAVFLATGNVSGGVCDNCQHNTMGRNCEQCKPFY 381
Db 301 RPAEGRNSNACKKNCNEHSSCHFDMAVFLATGNVSGGVCDNCQHNTMGRNCEQCKPFY 360
QY 382 FOHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGLIAGQCRCKLHVEGERCDVCK 441
Db 361 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSTGLIAGQCRCKLHVEGERCDVCK 420
QY 442 EGFYDLSAEDPYGCKSCACNPLGTIPGPNPCDSETGYCYCKRLVTGQRCDQCLPQHGLS 501
Db 421 EGFYDLSAEDPYGCKSCACNPLGTIPGPNPCDSETGYCYCKRLVTGQRCDQCLPQHGLS 480
QY 502 NDLDGCRPCDCLGGALNNSCEDSGQCSCLPHMIGRQCNEVESGYFTTLDHYIYEAEE 561
Db 481 NDLDGCRPCDCLGGALNNSCPAESGQCSRPHMIGRQCNEVEPGYFATLDHYIYEAEE 540
QY 562 ANLPGVIVVERQYIQDRIPSWTGPFGFVRVPEGAYLEFFIDNIPYSMEYELIRYEPQLP 621
Db 541 ANLPGVIVVERQYIQDRIPSWTGPFGFVRVPEGAYLEFFIDNIPYSMEYELIRYEPQLP 600
QY 622 DHWEKAVITVQRPKIPASSRCGNTVPDDNQVSLSPGSRYVWLP RPVCPEKGMNVTVR 681
Db 601 DHWEKAVITVQRPKIPASSRCGNTIPDDNQVSLSPGSRYVWLP RPVCPEKGMNVTVR 660
QY 682 LELPQYTAGSDVESPYTFIDSLVLMYPYCKSLDIFTVGSGDGEVTNSAWETPQRYRCLE 741
Db 661 LELPQYTAGSDVESPYTFIDSLVLMYPYCKSLDIFTVGSGDGEVTNSAWETPQRYRCLE 720
QY 742 NSRSVVKTPMTDVCNRIIFSISALIHQTGLACECDPQGSLSVCDPNPGQCCQCRPNVWGR 801
Db 721 NSRSVVKTPMTDVCNRIIFSISALLHQTGLACECDPQGSLSVCDPNPGQCCQCRPNVWGR 780
QY 802 TCNRCAPGTGFGPNCKPCDCHLQGSASAFCDAITGQCHCFQGIYARQCDRCLPGYWGF 861
Db 781 TCNRCAPGTGFGPNCKPCDCHLQGSVNAFCNPVTGQCHCFQGIYARQCDRCLPGYWGF 840
QY 862 PSCQPCQCNHGLDCTVTGECCLSCQDYTTGHNRCERCLAGYGDPIIGSGDHCRPCPCPD 921
Db 841 PSCQPCQCNHGLDCTVTGECCLSCQDYTMGHNRCERCLAGYGDPIIGSGDHCRPCPCPD 900
QY 922 GPDSGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCASGFFGNPSPDFGSGCQPCQCHN 981
Db 901 GPDSGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCASGFFGNPSPDFGSGCQPCQCHN 960
QY 982 IDTTDPEACDKTGRCLKCLYHTEGHCQLCOYGYGDLRQDCRCKVCNLTGTVKEHCN 1041
Db 961 IDTTDPEACDKTGRCLKCLYHTEGHCQFCRFGYYGDLRQDCRCKVCNLTGTVKEHCN 1020
QY 1042 GSDCHCDKATGQCSCLPNVIGQNCRCAPNTWQLASGTGCGPCNCAHSGFSPSCNEFTG 1101
Db 1021 GSDCHCDKATGQCSCLPNVIGQNCRCAPNTWQLASGTGCGPCNCAHSGFSPSCNEFTG 1080

QY 1102 QCQMPGFGGRTCTSECOELFWGDDPDVECRACDCDPRGIETPQCDQSTQCVCVEGVEGPR 1161
Db 1081 QCQMPGFGGRTCTSECOELFWGDDPDVECRACDCDPRGIETPQCDQSTQCVCVEGVEGPR 1140
QY 1162 CDKCTRGYSYGVFPDCTPCHQCFALWDAIIGELTNRTHKFLEKAKALKISGVIGPYRETVD 1221
Db 1141 CDKCTRGYSYGVFPDCTPCHQCFALWDVIIAELTNRTHRFLEKAKALKISGVIGPYRETVD 1200
QY 1222 SVEKKNVNEIKDILAQSPAAEPLKNIGILFEEAEKLTVDVTEKMAQVEVKLTDTASQSNST 1281
Db 1201 SVEKKNVNEIKDILAQSPAAEPLKNIGILFEEAEKLTVDVTEKMAQVEVKLTDTASQSNST 1260
QY 1282 AGELGALQAEAESLDKTVKELAEQLEFIKNSDIOGALDSITKYFQMSLEAEKRVNASTTD 1341
Db 1261 AKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEKRVNASTTE 1320
QY 1342 PNSTVEQSALTRDRVEDLMLERESPFKEQOEQAEQALLDELAKGLOSLDLSAAQWTCGTP 1401
Db 1321 PNSTVEQSALMRDRVEDVVMERESQFKEQOEQARLLDELAKGLOSLDLSAAQWTCGTP 1380
QY 1402 PGADCSSESECGPNCRTEDEGKCKGPGCGGLVTVVAHSAWQKAMDFDRDVLALAEVEQL 1461
Db 1381 PGADCSSESECGPNCRTEDEGKCKGPGCGGLVTVVAHSAWQKAMDFDRDVLALAEVEQL 1440
QY 1462 SKMVSEAKVRADEAKQNAQDVLKTNATKEKVDKSNEDLRNLIKQIRNFLTQDSADLDSI 1521
Db 1441 SKMVSEAKVRADEAKQNAQDVLKTNATKEKVDKSNEDLRNLIKQIRNFLTQDSADLDSI 1500
QY 1522 EAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVILQQAADIAEAELLEEAKRA 1581
Db 1501 EAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVILQQAADIAEAELLEEAKRA 1560
QY 1582 SKSATDVKVTADVMKEALSEAEKQVAAEAKIAKQADEDIQGTQNLTSIESETAASEETL 1641
Db 1561 SKSATDVKVTADVMKEALSEAEKQVAAEAKIAKQADEDIQGTQNLTSIESETAASEETL 1620
QY 1642 TNASQRISEKLNVEELKRAQNSGEAEYIEKVYVVKQNAADDVKKTLDELDEKYYKV 1701
Db 1621 TNASQRISEKLNVEELKRAQNSGEAEYIEKVYVVKQNAADDVKKTLDELDEKYYKV 1680
QY 1702 ESLIAQKTEESADARRKAEMLQNEAKTLLAQANSKLQLEDLERYEDNQYLEDKAQEL 1761
Db 1681 ENLIAKTEESADARRKAEMLQNEAKTLLAQANSKLQLEDLERYEDNQYLEDKAQEL 1740
QY 1762 VRLEGEVRSLLKDISEKVAVYSTCL 1786
Db 1741 ARLEGEVRSLLKDISQKVAVYSTCL 1765

RESULT 8
US-10-443-349-4
; Sequence 4, Application US/10443349
; Publication No. US20040023856A1
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert E.
; APPLICANT: Wagon, David W.
; TITLE OF INVENTION: BLK CHAIN OF LAMININ AND METHODS OF USE
; FILE REFERENCE: 10287/021003
; CURRENT APPLICATION NUMBER: US/10/443,349
; CURRENT FILING DATE: 2003-05-22
; PRIOR APPLICATION NUMBER: US/09/161,872
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: US 08/735,893
; PRIOR FILING DATE: 1996-10-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1196
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(250)


```

; OTHER INFORMATION: Human B1 chain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (251)...(437)
; OTHER INFORMATION: Human B1 chain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (438)...(807)
; OTHER INFORMATION: Human B1 chain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (808)...(840)
; OTHER INFORMATION: Human B1 chain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (841)...(1196)
; OTHER INFORMATION: Human B1 chain
; US-10-443-349-4

Query Match      58.3%; Score 5690.5; DB 16; Length 1196;
Best Local Similarity 63.2%; Pred. No. 6.7e-314;
Matches 1116; Conservative 46; Mismatches 33; Indels 571; Gaps 2;

QY 22 QBEFYSYGAEGSCYPATGDLIGRAQKLSVTS-TCGLHKPEPYCIVSHLQEDKKCFICD 80
Db 1 QBEFYSYGAEGSCYPATGDLIGRAQKLSVTS-TCGLHKPEPYCIVSHLQEDKKCFICN 60

QY 81 SRDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENVTIQLDLAEFFHFTHLIMTF 140
Db 61 SODPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENVTIQLDLAEFFHFTHLIMTF 120

QY 141 KTFRPAAMLIERSSDFGKTGWGYRYFAYDCESPPGISTGPMKKVDDIICDSRYSDIEPS 200
Db 121 KTFRPAAMLIERSSDFGKTGWGYRYFAYDCESPPGISTGPMKKVDDIICDSRYSDIEPS 180

QY 201 TEGEVIFRALDPAFKIEDYSPRIQNLLKITNLRIFKVKLHTLGNLLDSRMEIREKYYY 260
Db 181 TEGEVIFRALDPAFKIEDYSPRIQNLLKITNLRIFKVKLHTLGNLLDSRMEIREKYYY 240

QY 261 AVYDMVVRGNCFCYGHASECAPVDGVNEEVEGVHGHCMCRHNTKGLNCELMDFFYHDL 320
Db 241 AVYDMVVRGNCFCYGHASECAPVDGVNEEVEGVHGHCMCRHNTKGLNCELMDFFYHDL 300

QY 321 WRPAEGRNSNACKKCNNEHSSCHFDMVFLATGNVSGGVCDNCQHNMTGRNCEQCKPF 380
Db 301 WRPAEGRNSNACKKCNNEHSSCHFDMVFLATGNVSGGVCDNCQHNMTGRNCEQCKPF 360

QY 381 YFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGLIAGQCRCCKLHVEGERCDVC 440
Db 361 YFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGLIAGQCRCCKLHVEGERCDVC 420

QY 441 KEGFYDLSEAEDPYGCKSCACNPLGTIPGGNPNCDSETGYCYCKRLVTGQRCDQCLPQH 500
Db 421 KEGFYDLSEAEDPYGCKSCACNPLGTIPGGNPNCDSETGYCYCKRLVTGQRCDQCLPQH 477

QY 501 SNDLDGCRPCDCDLGGLNNSCEDSGQCSCLPHMIGRQCNEVESGYFTTLDHYIYAE 560
Db 438 ----- 437

QY 561 BANLPGVVVVERQYIQDRIPSWTGPFGFVRVPEGAYLEFFIDNIPYSMEYELIRYEPQL 620
Db 438 ----- 437

QY 621 PDHWEKAVITVQRPKIPASSRCGNTVPDDNQVVSLSPGSRVYVLPVPRVCFEKGMYTV 680
Db 438 ----- 437

QY 681 RLELPQYTAGSDVESPYTFIDSLVLMFYCKSLDIFTVGGSGDGEVTSAWETFORYRCL 740
Db 438 ----- 437

QY 741 ENSRSVVKTPMTDVCRNIFISALIHQTGLACECDPQGSLSVCDPNPGGQCQCRPNVVG 800
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Db 438 ----- 437
QY 801 RTCNRCAPGTFGFGPNCGCKPCDCHLQGSASAFCDAITQCHCFQGIYARQCDRCLPGYWG 860
Db 438 ----- 437
QY 861 FPSCQPCQCNGHALDCDVTGTGECLSCQDYTTTGHNCERCLAGYYGDPPIIGSGDHCRPCPCP 920
Db 438 ----- 437
QY 921 DGPDGSRQFARSCYQDPVTLQACVCDPGYIGSRCDDCASGFFGNPSPDFGGSCQPCQCHH 980
Db 438 ----- 437
QY 981 NIDTTPDPEACDKDTGRCCLKCLYHTEGDHCQLCQYGYGDALRQDCRKCVCNVLGTVKEHC 1040
Db 438 -----CVCNVLGTVQEH 450
QY 1041 NGSDCHCDKATGQCSCLEPNVIGQNCDCRCAPNTWQLASGTGCGPCNCNAHSGFSCNEFT 1100
Db 451 NGSDCQCDKATGQCCLPNVIGQNCDCRCAPNTWQLASGTGCGPCNCNAHSGFSCNEFT 510
QY 1101 GQCQMPGFGGRTCECQELFWGDPDVECRACDPRGIETPQCDQSTGQCVCVEGVEGP 1160
Db 511 GQCQMPGFGGRTCECQELFWGDPDVECRACDPRGIETPQCDQSTGQCVCVEGVEGP 570
QY 1161 RCDKCTRGYSGVFPDCTPCHQCFALWDVIAIELTNRTHRFLKAKALKISGVIGPYRET 1220
Db 571 RCDKCTRGYSGVFPDCTPCHQCFALWDVIAIELTNRTHRFLKAKALKISGVIGPYRET 630
QY 1221 DSVKVKVNEIKDILAQSPAAEPLKNIGILFEEAEKLTVDTEKMAQVEVKLTDTSQSNS 1280
Db 631 DSVKVKVSEIKDILAQSPAAEPLKNIGILFEEAEKLTVDTEKMAQVEVKLTDTSQSNS 690
QY 1281 TACELGALQAEAESLDTVKELAEQLEFINKNSDIQALDLSITKYFQMSLEAEKRVNASTT 1340
Db 691 TACELDLSLQTEAESLDTVKELAEQLEFINKNSDIQALDLSITKYFQMSLEAEKRVNASTT 750
QY 1341 DPNSTVEQSALTRDRVEDIMLERESPFEKEQEEQARLLDELAKLQSLDLSAAQMTCTG 1400
Db 751 EBNSTVEQSALMRDRVEDVMVERESQFKEKEQEEQARLLDELAKLQSLDLSAAQMTCTG 810
QY 1401 PGADCSSECGGPNCRIDEGEKKCGGPGCGGLVTVVAHSAWQKAMDFDRDVLALAEVEQ 1460
Db 811 PGASCSETECGGPNCRIDEGERKCGGPGCGGLVTVVAHNAWQKAMDLDDQDVLALAEVEQ 870
QY 1461 LSKMVSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDLRNLKQIRNFLETDSADLDS 1520
Db 871 LSKMVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNEDLRNLKQIRNFLETDSADLDS 930
QY 1521 IEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVILQQSAADIARAEELLLEAKR 1580
Db 931 IEAVANEVLKMEMPSTPQQLQNLTEDIRERVESLSQVEVILQHSAAADIARAEMLLEAKR 990
QY 1581 ASKSATDVKVTDVMTADMVKEALEEAEKAQVAAEKAQADEDIQGTQNLTSIESETAASEET 1640
Db 991 ASKSATDVKVTDVMTADMVKEALEEAEKAQVAAEKAQADEDIQGTQNLTSIESETAASEET 1050
QY 1641 LTNASQRISKLERNVVEELKRAAQNNGEAEYIEKVYVSVKQNAADDVKKTLTGELDEKYYK 1700
Db 1051 LFNASQRISSELERNVVEELKRAAQNNGEAEYIEKVYVSVKQNAADDVKKTLTGELDEKYYK 1110
QY 1701 VESLIAQKTEESADARRKAEELLQNEAKTLLAQANSKLQLEDLERKYEDNQKYLEDKAQE 1760
Db 1111 VENLIAKTEESADARRKAEMLQNEAKTLLAQANSKLQLEDLERKYEDNQKYLEDKAQE 1170
QY 1761 LVRLEGEVRSLLKDISEKVAVYSTCL 1786
Db 1171 LARLEGEVRSLLKDISQKVAVYSTCL 1196
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RESULT 9
US-09-938-275-8

; Sequence 8, Application US/09938275
; Patent No. US20020111309A1
; GENERAL INFORMATION:
; APPLICANT: Gerardo Castillo
; APPLICANT: Alan Snow
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications
; TITLE OF INVENTION: of Laminin and Laminin-Derived Protein Fragments
; FILE REFERENCE: PROTEO.P03
; CURRENT APPLICATION NUMBER: US/09/938,275
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1801
; TYPE: PRT
; ORGANISM: Rattus No. US20020111309A1vegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Swissprot P15800
; DATABASE ENTRY DATE: 1990-04-01
US-09-938-275-8

Query Match 52.1%; Score 5087.5; DB 9; Length 1801;
Best Local Similarity 51.2%; Pred. No. 1.7e-279;
Matches 920; Conservative 303; Mismatches 544; Indels 29; Gaps 11;

QY 1 MGLQVAFPGVLAWGTRVCAQEPESY-GCAEGSCYFATGDLIIIGRAQKLSVTSTCGLH 59
Db 23 LGLL-----LSVLA----ATLAQVPSLDVPGCSRGSCYFATGDLIIIGRADRLTASSTCGLH 74

QY 60 KPEPYCIVSHLQEDKKCFICSDRDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVE 119
Db 75 SPQPYCIVSHLQEDKKCFICSDRDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVP 134

QY 120 NVTIQLDLAEAFHFTHLIMTFKTRPAAMLIERSDFGTWGVYRYFAYDCSEFPFGIST 179
Db 135 MVTIQLDLAEAFHFTHLIMTFKTRPAAMLIERSDFGTWGVYRYFAYDCSEFPFGIPL 194

QY 180 GPMKKVDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSRIQNLLKITNLRKIFVK 239
Db 195 APPRRWDDVCESTRYSIEPSTEGEVIVRVLDPAIPIDPYSRIQNLLKITNLRVNLTR 254

QY 240 LHTLGDNLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCM 299
Db 255 LHTLGDNLDPREIREKYYALVELVIRGNCFCYGHASQCAPAPGAPAHAEGMVHGACI 314

QY 300 CRHNTKGLNCELCMDYHDLPRPAEGRNSNACKKNCNEHSSSCHFDMAVFLATGNVSG 359
Db 315 CKHNTKGLNCEQCQDFYQDLPHWPAEDGHTHACRKECNGHSHSCHFDMAVFLASGNVSG 374

QY 360 GVCNDCQNTWGRNCEQCKPFYFQHPERDIRDPLNLCPECTCDPAGSENGGICDGYTDFSV 419
Db 375 GVCNDCQNTWGRNCEQCKPFYFQHPERDIRDPLNLCPECTCDPAGSENGGICDGYTDFSV 434

QY 420 GLIAGQCRCKLHVEGERCDVCKEGFYDLAEADPYGCKSCACNPLGTIPGGNCPDSETYC 479
Db 435 GLVSGQCRCKEHVVGTRCQCRDGFGLSASNPRGCQRCQNSRGTVPGGTPCDSSTGTC 494

QY 480 YCKRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCDLGGALNNSCSEDSGQCSCLPHMIGRQ 539
Db 495 FCKRLVTGDCDRCLPGHWGLSHDLGCRPCDCDLGGALNNSCSEDSGQCSCLPHMIGRR 554

QY 540 CNEVESGYFTTLDHYIYEAEANLPGVWVVERQYIQDIRIPSWTGPGRVVRPEGAYLEF 599
Db 555 CEQVQPGYFRPFLDHLTWEAEGAH-CQVLEVVRLVNTRETPSWTGVGFVRLREGQVEF 613

QY 600 FIDNIPYSMEYELIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTVPDDDNQVVSLS 659
Db 614 LVTSLPRAMDYDILLRWEPOVPEQWAELELVVQRPGPVSAHSPCGHVLPRDDRIQGM 673

QY 660 GSRVTVLPRPVCFEKGMNVTVRLELPQYTAGSDVESPYT----FIDSLVLMPCYCKSLDI 715
Db 674 NTRVLVFPFRPVCLEPGLSKLKLTLG-TGGRAPHPETPYSGSILIDSLVLQPHVLMLEM 732

QY 716 FTVGSGDGEVTNSAWETPQRYRCLENSRSVVKTPMTDVCRNIIIFSISALIHQTGLACEC 775
Db 733 F-----SGDAAALERRTTTFERYRCHEEGLMPSKTPLSEACVPLISASSLVYNGALPCQC 788

QY 776 DPQSLSSVCDPNGGQCQCRPNVVRGTCNRCAPGTGFGPNGCKPCDCDCHLQGSASAFCD 835
Db 789 DPQSLSSVCDPNGGQCQCRPNVVRGTCNRCAPGTGFGPNGCKPCDCDCHLQGSASAFCD 848

QY 836 ITGQCHCFQGIYARQCRCLEPGYWGFPSPCQPCQCNHGLDCTVTGECCLSCQDYTTGHC 895
Db 849 TSGQCLCRTGAFGLRCHCQRCQGWGFPNCRPCVNCGRADCDHTGACLGCRDYTTGHEHC 908

QY 896 ERCLAGYVGDPIIGSGDHCRPCPCPDGDSGRQFARSCYQDPVTLQACVCDPFGYISRC 955
Db 909 ERCLAGYVGDPIIGSGDHCRPCPCPDGDSGRQFARSCYQDPVTLQACVCDPFGYISRC 968

QY 956 DDCASGFFGNPSDFGSCCQPCQCHHNIIDTDPACDQDTRGCLKLYHTEGHDHCLCQYG 1015
Db 969 EACAPGHFGDPSKPGGRCQLCECSGNIIDTDPGACDPHTGQCLRLHHTGPHGCHCKPG 1028

QY 1016 YYGDALRQDCRCKVCNLYLGTVKEHCNGSD-CHCDKATGQCSCLPNVIGQNCDCRCA 1074
Db 1029 FHGQAAQSCCHRCTCNLLGTDPQRCPTDLCHCDPSTGQCPCLPHVQGLSCDRCA 1088

QY 1075 LASGTGCGPCNCAAHSGFSCNEFTGQCQCMPPGFGGRTCECQELFWGDPDVECRACDC 1134
Db 1089 FTSGRGQPCACHPSRARGPTCNEFTGQCHAGFGGRTCECQELFWGDPDVECRACDC 1148

QY 1135 DPRGIETPQCDQSTGQCVVEGVEGPRCDKCTRGYSVGFDPDCTPCHQCFCALWDALIGELT 1194
Db 1149 DPRGIDKPQCHRSTGHGCRPGVSVGRCDQCARGFSGVFPACHPCFACFGDWRVVDLA 1208

QY 1195 NRTHKFEKAKALKISGVIQRETVDVSVEKKNVNEIKDILA--QSPAAEPLKNIGILFEE 1252
Db 1209 ARTRRLQWAEQELQQTGVLGAFESSFLNLQKLGVMQAIVAARNTSAASTAK----LVEA 1264

QY 1253 AEKLTQDV--TEKMAQVEVKLTDTASQSNSTAGELGALQAEASLDKTVKELAEQLEFI 1309
Db 1265 TEGLRHEIGKTERLTQLEAELTDVQDENFNANHALSGLERDGLALNLTLRQLDQHL 1324

QY 1310 KNSDIQALDSITKYFQMSLEAEKRVNASTTDPNSTVQSALTRDRVEDLMLERESPKE 1369
Db 1325 KHSNFLGAYDSIRHAHSQSTEARRANASTFAIPSPVNSADTRRRRAEVLMGQARENFR 1384

QY 1370 QQEEQARLLDELAKGLQSLDLSAAQWTCGTPPGADCESECGGPNCRCTDEGEKKGPG 1429
Db 1385 QHLANQALGRLSTHTLTSLTGVELVCGAPDAPCATSPCGGAGCRDEDEGPRCGLG 1444

QY 1430 CGGLVTVAHSAWQKAMDFDRDVLALAEVEQLSKMVSEAKVRADEAKQNAQDVLLKTNAT 1489
Db 1445 CSGAAATADLALGRARHTQAEIQRALVEGGILSRVSETRRQAEAAQQAALDKANAS 1504

QY 1490 KEKVDKSNEDLRNLKQIRNFLTSDSADLDSIEAVANEVLKSGNASTPQQLQNLTEIRE 1549
Db 1505 RGQVEQANQELRELIONVXDFLSQEGADPDSIEMVATRVLDISIPASPEIQRLASEIAE 1564

QY 1550 RVETLSQVEVILQOSAADIARAEFLLEAEAKRASKSATDVKVTADMVKEALEAEAKQVAA 1609
Db 1565 RVRSLADVDTILAHMTMGDVRRAEQLLODAQARARSRAEGRQKAETVQAALAEAAQQA 1624

QY 1610 EKAIKQADEDIQGTQNLTSISEETAASEETLTNASQRISKLERNVVEELKRKAQNSGEA 1669
Db 1625 QGAIRGAVVDTKNTEQTLLQVQERMAGTEQSLNSASERARQLHALLKLRAGNSLAA 1684

QY 1670 EYIEKVYVVKQNAADDVKKTLDELDDEKYYKVESLIAQKTEESADARRKAELLQNEAKTL 1729
Db 1685 STAEETAGSAQSRAREAEKQLREQVGDQYQTVRALAERKAEGVLAQAARAEQLRDEARGL 1744

QY 1730 LAQANSKLQLELDERKYNQKYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTC 1785
Db 1745 LQAAQDKLQRLQLELEGTYEENERELEVKAAQLDGLAERMRSVLQAINLQVQIYNTC 1800

RESULT 11
US-09-938-275-9
; Sequence 9, Application US/09938275
; Patent No. US20020111309A1
; GENERAL INFORMATION:
; APPLICANT: Gerardo Castillo
; APPLICANT: Alan Snow
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications
; OF Laminin and Laminin-Derived Protein Fragments
; FILE REFERENCE: PROTEO.P03
; CURRENT APPLICATION NUMBER: US/09/938,275
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1798
; TYPE: PRT
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: P55268
; DATABASE ENTRY DATE: 1996-10-01
US-09-938-275-9
Query Match 51.6%; Score 5031.5; DB 9; Length 1798;
Best Local Similarity 50.4%; Pred. No. 2.6e-276;
Matches 903; Conservative 313; Mismatches 556; Indels 19; Gaps 9;
QY 1 MGLQVFAFGVLALWGTRVCAQEPFSGYCAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60
Db 20 LGLL-----LSVLA--ATLAQAPADVP-GCSRGSCYPATGDLVGRADLTASSTCGLNG 72
QY 61 PEPYCIIVSHLQEDKKCFICSDRDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVEN 120
Db 73 PQPYCIIVSHLQDEKKCFICSDRDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGIPA 132
QY 121 VTIQDLEAEFFHFTLIMTKTFRPAAMLIERSSDFGKTGWVYRYFAYDCBSSPPGISTG 180
Db 133 VTIQDLEAEFFHFTLIMTKTFRPAAMLVERSADFGRTWHVYRYSYDCGADFPVPLA 192
QY 181 PMKKVDDIICDSRYSYDIEPSTGEVIFRALDPAFKIEDPYSPRIQNLLKIINLRKIFVKL 240
Db 193 PPRHWDVVCEYSYSEIEPSTGEVYRVLDPAPIPIPDYSSRIQNLLKIINLRVNLTRL 252
QY 241 HTLGNLLDSRMEIREKYYVAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVGHGCMC 300
Db 253 HTLGNLLDPRREIREKYYVAVYELVVRGNCFCYGHASECAPAPGAPAHAEVGHGACIC 312
QY 301 RHNTKGLNCELMDFFYHDLWPFAEAGRNNSACKKCNNEHSSSCHDFMAVFLATGNVSGG 360
Db 313 KENTRGLNCEQCQDFYRDLWPFAEDGHSHACRCKCECHGTHSCHDFMAVYLAGNVSGG 372
QY 361 VCDNCOHNTMGRNCEQCKPFYFQHPERDIRDNLCEPCTCDPAGSENGGICDGYTDFSVG 420
Db 373 VCDGCOHNTAGRHCELCRPFYFVDPTKDLRDPAVCRSCDCDPMGSDGGRCDSDHDDPALG 432
QY 421 LIAGQCRCKLHVEGERCDVCKEGFYDLSEADPYGCKSCACNPLGTIPGGNPCDSETGYCY 480
Db 433 LVSGQCRCKEHVVGTRCQCQCRDGFGLSISDRLGRCRCQCNARGTVPGSTPCDPSGSCY 492
QY 481 CKRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCDLGGALNNSCSEDSGQCSCLPHMIGRQC 540
Db 493 CKRLVTGRGCDRCLPGHWGLSHDLGCRPCDCDVGGALDPQCDEGTGQCHCRQHWVGRRC 552
QY 541 NEVESGYFTTLDHYIYEAEEANLPGVGVVVERQYIQDRIPSWTGPFGFVRVPEGAYLEFF 600
Db 553 EQVQPGYFRPFLDHLIWEAEDTR-GQVLDVVERLVTPGETPSTGSGFVRLQEGQTLLEFL 611
QY 601 IDNIPYSMEYELIRYEPQLPDHWEKAVITVQRPKGIIPASSRCGNTVPDDDNQVVSLSPG 660
Db 612 VASVPKAMDYDLLRLLEPQVPEQWAELELIVQRPFGVPAHSLCGHLVPKDDRIQGTLOPH 671

QY 661 SRYVVLPRPVCPEKGMNVTVRLELPQYTAGSDVESPYT-----FIDSLVLMPYCKSLDIF 716
Db 672 ARYLIFPNPVCLEPGISYKHLHLKLV- TGSSAQPETPYSGPGLLDLSVLLPRVLVLEMF 730
QY 717 TVGSGDGEVTNSAWETFORYRCLENSRSVVTKPMTDVCNIIIFSISALIHQTGLACECD 776
Db 731 ----SGDAAALERQATPERYQCHEEGLVPSKTSPPSEACAPLLISLSTLYNGALPCQC 786
QY 777 PQGSLSSVCDPNGGQCCQCRPNVGRTCNRCAPGTFGFGPNGCKPCDCHLQGSASAFCDAI 836
Db 787 PQGSLSSVCDPNGGQCCQCRPNVGRTCNRCAPGTFGFGPNGCKPCDCHLQGSASAFCDAI 846
QY 837 TGOCHCFQGIYARQCDRLCPGYWGFPPSCQPCQCNHGHALDCDVTGECSCQDYTTGHNCE 896
Db 847 SGQCLCRTGAFGLRCDCRCQRCQGWGFPPSCPCVCNCHADECNTHTGACLCGRDHTGGEHCE 906
QY 897 RCLAGYGGDPIIGSGDHCRPCPCPDGPDGSRGRQFARSCYQDPVTLQACVCDPGYIGSRCD 956
Db 907 RCIAGFHRDPRLPYGGQCRPCPCPEGPGSQRHFATSCHQDEYSQQIVCHCRAGYTGRLRCE 966
QY 957 DCASGFFGNPSDFGSCQPCQCHHNIDTTPDPEACDKDTGRCLKCLYHTEGHCQLCQYGY 1016
Db 967 ACAPGHFGDPSRPGRCQLCECSGNIDPMDPDACDPHTGQCLRLCHHTTEGPHCAHCKPGF 1026
QY 1017 YGDALRQDCRKVCNLYLTVKEHCNGSD-CHCDKATGQCSCLPNVIGQNCDCRCAENTWQL 1075
Db 1027 HGQAARQSCHRCTCNLLGTNPQCCPSPDQCHCDPSSGQCPCLPNVQGPSDCRCAFNFWNL 1086
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Db 1087 TSGHGCQPCACHPSRARGPTCNEFTGQCHCRAGFGGRTCECQELHWGDDPGLQCHACDGD 1146
QY 1136 PRGIETPQCDQSTGQCVVEGVEGPRCDKCTRGYSGVFPDCTPCHQCFALWDALIGELTN 1195
Db 1147 SRGIDTPQCHRTGHCSCRCFVSGVRCDCQCARGFSGIFPACHPCFACFGDWDVVDLAA 1206
QY 1196 RTHKELEKAKALKISGIVGYPRETVDVSEKKVNEIKDIL-AQSPAAEPLKNIGILFEEAE 1254
Db 1207 RTQRLQRAQELQQTGVLGAFESSFWHMQEKLGIVQIVGARNTSAASTAQLVEATEELR 1266
QY 1255 KLTKDVTEKMAQVEVKLTDTASQSNSTAGELGALQAEASLDKTVKELAEQLEPIKNSDI 1314
Db 1267 REIGEATEHLTQLEADLTVDQDENFNANHALSGLERDLALNLTLRQLDQHLDLKHSNF 1326
QY 1315 QGALDSITKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRVEDLMLERESPFEKQEEQ 1374
Db 1327 LGVDSIRHAHSQSAEAEERRANTSALAVSPVSNASARHRTALMDAQKEDFNSKHMAM 1386
QY 1375 ARLLDELAKLQSLDLASAAQMTCTGTPPGADCSSECGPNCRTDEGEKKCGGPGCGGLV 1434
Db 1387 ORALCKLSAHTHTLSLTDINELVCGAPDAPCATSPCGAGCRDEDGQPCGGLSCNGAA 1446
QY 1435 TVAHSAWQKAMDFRDVLALAEVEQLSKMVSEAKVRADEAKQNAQDVLLKTNATREKVD 1494
Db 1447 ATADLALGRARHTQAELOALAEAGSILSRVAETRRRQASEAQQAALDKANASRGQVE 1506
QY 1495 KSNEDLRNLIKQIRNFLTEDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETL 1554
Db 1507 QANQELQELIQSVKDFLNQEGADPDSIEMVATRVLELSIPASAEQIOHLAGAIAERVSL 1566
QY 1555 SQVEVILQQAADIARAELLEEAKRASKSATDVKTADVMVKEALEEAEKAAQVAAEKAIK 1614
Db 1567 ADVDAILARTVGDVRRAEQLQDARRARSWAEDKOKAETVQAALAEQAQAGIAQGAIR 1626
QY 1615 QADEDIQCTQNLLTSIETSAASEETLTNASQRIKSLERNVEELKRAAQNQSGAEVIEK 1674
Db 1627 GAVADTRDTEQTLVQVQERMAGAERALSAGERARQLDALLEALKLKRAGNSLAATAEE 1686
QY 1675 VVYSVKQNAADDVKTLTLDGELDEKYKKVESLIAQKTESADARRKAEALLQNEAKTLQAQAN 1734
Db 1687 TAGSAQGRAQEAELRLRPLGQYQTVKALAEKAAQGVLAQAARAEQLRDEARDLLQAAQ 1746
QY 1735 SKLQLELDERKYEDNQKYLEDKAQELVRLGEVRSLLKDISEKVAVYSTC 1785

Wed May 19 10:47:32 2004

1747 DKLORLOELEGTYEENERALESKAAQLDGLEARNKFSVLQAINLQVOYNTC 1797

RESULT 12

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RES001 12
US-09-845-583-8
; Sequence 8, Application US/09845583
; Patent No. US20020142954A1
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Brunken, William Joseph
; APPLICANT: Champlaud, Marie-France
; APPLICANT: Hunter, Dale
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
; FILE REFERENCE: 10287-056001
; CURRENT APPLICATION NUMBER: US/09/845,583
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/200,863
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 4.0

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; SEQ ID NO: 1
: LENGTH: 1798

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; LENGTH: 1
; TYPE: PRT

LIFE: FRI
ORGANISM: Homo sapiens

ORGANISM: IN
US-09-845-583-8

Query Match	50.2%;	Score 4902;	DB 9;	Length 1798;
Best Local Similarity	49.6%;	Pred. No. 5.6e-269;		
Matches 887;	Conservative 308;	Mismatches 574;	Indels 20;	Gaps 8;

QY	3	LLQVFAFGVLALWGRVCAQEPFESYCAEGSCYPATGDLILLIGRAQKLSVTSTCGLHKPE	62
Db	23	LLSVLA-----ATLAQAPAPDVP-GCSRGSCYPATADLLVGRADRLTASSTCGLNGRQ	74
QY	63	PYCIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVVTTFAPNRLKIWWQSENGVENVT	122
Db	75	PYCIVSHLQDEKKCFCLDSRRPFSARDNPHTHRIQNVTTSFAPQRRAAWQSQNGIPAVT	134
QY	123	IQLDLEAEFHFTHLIMTFKTRPAAAMLIERSDFGKTGWVYRYFAYDCESFPFGISTGPM	182
Db	135	IQLDLEAEFHFTHLIMTFKTRPAAAMLVERSADFGRTWHVYRYFSYHCGADFPGVPLAPP	194
QY	183	KKVDDIICDSRYSIDIEPSTEGEVIFRALDPAFKIEDPYSPRIQNLLKIITNLRKIFVKLHT	242
Db	195	RHWDVVCESRYSIEPSTEGEVIYRVLDPAIPIPDPSYSSRIQNLLKIITNLRVNLTRLHT	254
QY	243	LGDNLDDSRMEIREKYYYAVYDMVVVRGNCFCYGHASECAPVDGVNEEVEGMVHGHCMRH	302
Db	255	LGDNLDDPRREIREKYYYALVELVVRGNCFCYGHASECAPAPGAPAHAEVMVHGACICKH	314
QY	303	NTKGLNCELCMDFYHDLWPRPAEGRNSNACKKCNCEHSSSCHDFMAVFLATGNVSGGVC	362
Db	315	NTRGLNCEQCQDFYRDLWPRPAEDGHSHACKRCDKRHGHTHSCHFDMAYVLGSGNVSGGVC	374
QY	363	DNCQHTWGRNCEQCKPFYFQHPERDIRDENLCEPCTCDPAGSENGGICDGYTDFSVGLI	422
Db	375	DGCQHTAWRHCELCRPFYFDRPTKDLRDPAVCRSCDCDPMGSDQDGGRCDSHDDPALGLV	434
QY	423	AGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGPNPCDSETGYCYCK	482
Db	435	SGQCRCKEHVVGTRCQOQCRDGFGLSISDPGSCRRQCQCNARGTVPGSTPCDPNPGSCYCK	494
QY	483	RLVTGQRCDQCLPQHWGLSNDLDGCRPCDCLGGALNNSCSEDSGQCSCLPHMIGRQCNE	542
Db	495	RLVTGRGDRCLPGHWGLSLDLLGCRPCDCDVGGLDPCQDEGTGQCHCRQHVMVGRRC EQ	554
QY	543	VESGYFTTLDHYIYEAEANLGPVVVVERQYIQDRIPSWTGPGFVRVPEGAYLEFFID	602
Db	555	VQPGYFRPFLDHLIWEAENR-GQVLDVVERLVTPGETPSWTGSGFVRLQEGQITLEFLVA	613
QY	603	NIPYSMEYELLIRYEPQLPDHWEKAVITVQRPCKIPASSRCGNTVPDDDNQVVSLSPGSR	662

Qy	1737	LQLEDLERKYEDNQKYLEDKAQLVRLGEVRSLIKDISKVAVSTC	1785
Dd	1749	LORLQELEGTYEENRERALESKAAQLDGLERNRSVLOAINLOVOYINTC	1797

RESULT 13
US-10-369-493-5986
; Sequence 5986, Application US/10369493
; Publication No. US20030233675A1

APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng

NO.	TITLE OF INVENTION:	EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
1	TITLE OF INVENTION:	PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/1

;
CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 13254

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; NUMBER OF SEQ ID NOS: 47374
; SEQ TO NO E99C

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SEQUENTIAL LENGTH: 18085986

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; LENGTH: 1808
; TYPE: PRT

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ORGANISM: *Caenorhabditis elegans*

US-10-369-493-5986

Query Match 38.4%; Score 3742.5; DB 15; Length 1808;
Best Local Similarity 39.5%; Pred. No. 3e-203;
Matches 746; Conservative 315; Mismatches 635; Indels 193;

Qy	1	MGLQLVFAFGVLALWGTRVCQP--EFSYGAEGSCYPATGDLIGRAQKLVTSTCGL	58
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		: : : : : : : : : :	
Dd	8	LGLJ-----LSLLLVFIEAQHPLOQNEDRCQDRSCVPITGNLLIGRKSQLKATSTCGS	60

Qy 59 HKPEPYCIVSHLQEDKKCFICDSRDPYHETLNPDP--SHLIENVTTFAPNRLKIWQSEN 116

Dbb 61 QGRQFCIVSHLEEQTCKFCYCDSRTEWKQREPYRLSHRIENVVTEVMDDKGNRWYQSEN 120

Qy 117 GVENVTIQDLEAEFHFTHLINTFKTRPPAAMLIERSDFGKTGWYRYFAYDCESSFPG 176

Db 121 GAQNVSI SFDLEAEFFHFLIMTFKSFRAAMIERSADFGKTQVRYRFAYDCDSSFFG 180

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QY      177  ISTGPMKKVDDIIICDSRYSJIEPSTEGEVIFRALDPAFKIEDPSPRIQNLLKITNLRK 236

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Db      181  IPEGPKKHTDVICTSQYSDVAPSTGGEIVYKVISHVIVTENPYADEISTLKITNLRN 240

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QY      237 FVKLHTLGDNLLDSRMEIREKYYYAVYDMVRGNCFCYGHASECAPVD---GVNEEVE-- 291
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241 FTKLHTLGDDLLDYRPEIDKYYAYEIVRGSCYGHASRCIPIDPHVSPNTVMRA 300

[illegible]

301 DIVGRCECMHTEGLNCEKCAFYNLWPRPAIGDEKNECQCNCNRHALLRCHFDRVY 360

QY 352 LATGN-----VSGVCDCNQHNTWGRNCEQCKPFYFOHPERDIRDPN 393
::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:

Db 361 ESSGNTSSFSKSFSSGFSYFSGFVSGVCDDCMNTQGNCEQCKPFFYRDPRTIDDPH 420

394 LCEPCTCDPAGSENGGICDGYTDFSVGLIAGQCRCKLHVEGERCDVCYKEGYDLSAEDPY 455

421 VCLPCECDKAGSQNKGI^{CEGEEDA}ERGLVAGKCY^{CTNVDGN}RCDCRCKNGY^{WNL}TETNVD 480

454 GCKSACACNPLGTIPGSGNRCDSSETGYCYCKRLVTGTGRCDQCLPQHWGLSLNDLIGCRPCDCD 513

DB 481 GCVACTCNLLGTY - NNEGDKYTGMCCTCKRLVTGNCDCQLPEHYGLSEHVDGCKACDCD 539

[illegible]

340 1995IDN1CE111GQACKEGFSGRKCE1ADSSFCAD11H1VIEAEYANDIKGEVKIRE 599

QY	574	QYIQDRIPSWTGPGRVVRVPEGAYLEFFIDN--IPYSMEYEILIRYE-PQLPDHWEKAVIT	630
DB	600	WPSQPHETFTGEGFAQAVEGTIITV---NPIVEVSQXNVNIIHRDGDARDPVGVENIQIT	656
QY	631	VORPGKIPASSRCGNTVPDDDNQVVSLSPPGSRVYVLP RPVCPEKGMNVTYVRLEL	684
DB	657	VVRP-EAEGDSCSDAPSDDFLIARIYPGSRYIEVQPAICLEAGVQYELRIQFNEXRGN	715
QY	685	--POYTASGSDVESPYTFIDSLVLMPYCKSLDIFTVGGSGDGEVTNSAWETFORYRC--L	740
DB	716	SHPOERAAN-----ILIDSILLAPPTSELHIFQGSARAEQHLTE---YNYRQCRHL	764
QY	741	ENSRSVVKTPTMTDVCNRIIFSISALIHQTGLACECDPQGSLSVCDPNGGQCQCRPNVVG	800
DB	765	ALSLSLFKDORNEVCERYVCPIAAALLNKTSECNCDATGSVSGICNVGGQCECKPNVVG	824
QY	801	RTCNRCAPGTGFGPNCKPCDCHLQGSASAFCDAITGQCHCFQ-GIYARQCDRCLPGYW	859
DB	825	RRCDOCAIGTYGFGPSGCKKCDODAVGSLGNDCDKQSGQCVCBREKGIYGRQCNQCQPGFW	884
QY	860	GFPSCQPCQCNHALDCDVTVTGECLSQDYYTTHGNCEERCLAGYGDPIIGSGDHCRPCPC	919
DB	885	GFPECRICQCNHDANICDQSSGACIECRDLTTGHYCDRCQDQGYGDPRLGVGIPCKPCPC	944
QY	920	PDGPDSGRQFARSCY---QDPVTIQLACVCDPGYIGSRCDDCASGFFGNPSDFGGSCQPC	976
DB	945	PGGPTSGYQHADTCYLRNSGNTQDIVCNCKSGYQGERCECAQNHMGSPREVGGTCERC	1004
QY	977	QCHENIDTDPEACDKDTGRCLKCLYHTEGDHCOLQYGYGDALRQDRCKVCVNYLGTV	1036
DB	1005	DCNGNIDMAMEGSCDAATGECCLKLHHTEGAQCEHCVDGYGDAKLKTCQRCVCNELGT-	1063
QY	1037	KEHCNGSDCHCDKATQCSCLPNVIGQNCDCRCAPNTWQLASGTGCGPCNCNA-----	1091
DB	1064	----NSTKGACDRVSGQCPCHDNIIGMQCDQCAENHFNLASGAGCEACGCDNSGVVLNHE	1119
QY	1092	FGP--SCNEFTGQCQCMPPGFGGRTCSQCQLFWGDDPVE--CRACDCDPRGIETPQCDQS	1147
DB	1120	GVPHLQCNIFDQCQCCKPGRGRKCDQCEDLYWGDPTTPDGCCHRCECNPTGSKSLQCHRN	1179
QY	1148	TGQCVCEGVEGPRCDKCTRYSGVFPDCTPCHQCQFALWDALIGELTNRTHKFLKAKAL	1207
DB	1180	NGTCEQAGSGGALCNECARGYTGQWPYCNPCGCECFHQWDNIMOKLQKVHALIDTANNI	1239
QY	1208	KISGVIGPYRETVDVSVEKKVNEIKDILAQSPAABPLKNIGILFEEAEKLTKDVT-----	1261
DB	1240	EDTGVASAYDADFQMBETLKETK-----KALSDANISKEDIEMSKLALLKKQV	1290
QY	1262	----EKVAQVEVKLTDTASQSNSTAGELGALQABESLDKTVKELAEQLEFIKNSDIQGA	1317
DB	1291	IAGREKLGAETRISNITQAVDFAQKLEHLQKEVDKVTYKATIELEDKASKIKEADVIGA	1350
QY	1318	LDSITKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRVEDLMLERESPFKEQBEQARL	1377
DB	1351	FNITRESASKSLDAQRRTDAA-IGKLA AENQAL---RASELLEKNKNDFEKYVYENEEA	1406
QY	1378	LDE---LAGKLQSLDLSAAQMTCGTPPGADCSSECGGNCRDTDEGEKKCGGPG-----	1430
DB	1407	LNEAETLLGGLESV-LPKLNEQVCG-----ASSAPC-----DALCGGPGSCGFC	1449
QY	1431	GGLVTVHAHSAWQAMDFDRDVL SALAEVQLSKMVSEAKVRADEAKQNAQ-----DVL	1483
DB	1450	GG-----QSCME-----GAVSKANQAKSFATEADTRLDEKQKEAEVLSIVRDVL	1494
QY	1484	LKTNATKEKVDKSNE-----DLRNIKQIRNFLTDSADLDSIEAVANEVL	1529
DB	1495	TETTKAKAKAEKAYEVAKNTAQRANSSRAELDKIABEIGEFLLTAQSSPEQIRNLAEVL	1554
QY	1530	KSGNASTPQQLQNLTEDIRERVETLSQVEVILQOQAADIARAELLLLEAKRASKSATDVK	1589
DB	1555	GKEISLTPDQITDLTGKIKESLAKINNIDEILNETRGNKSI AANLESRAVKANKBAELLQ	1614

263	GSCFCNGHASECRPMQMRGDVFPFGVMVHGQCVCQHNTDGNPCERCKDFQDAPWRPAA	322
326	GRNSNAKKKNCNEHSSSCHFDMAVFLATGNVSGGVCNCOHNTWGRNCEOCKPFYFQHP	385
323	DLQDNACRSCSNSSHRRCHFDMTYLASGGLSGGVCCDCQHTEGOHCDCRPLFYRDP	382
386	ERDIRDNLCPECTCDPAGSENGGICDGYTDFSUGLIAQCRCKLHVEGERCDVCKEGFY	445
383	LKTISDPYACIPCECDPDGTISGGICVSHSDPALGSVAGCQLCKENVEGAACKDOCKPNHY	442
446	DLSAEDPYGCKSCACNPGLTTPGGNPPCDSETGYCYCKRLVTGORCDQCLPOHWGLSNDLD	505
443	GLSATDPLGCQPCCCNPLGSLP-FLTCDVDTGQCLCLS YVTGAHCEECTVGWGLGNHLH	501
506	GCRPCDDLGALNNCSSEDSSGQCSCLPHMIGRCQNEVESGYVFTTLDDHIYEAEEAN--	563
502	GCSPCDCDIGGAYSNVCSFKXGQCCECPHVTVGRSCSEPAPGVFFAPLNFYLYEAEZATTL	561
564	--LG-----PGVVVERQYIQDRIPSWTGPGFVRVPEGAYLEFFIDNIPIYSMEYE	611
562	QGLAPLGSETFGQSPA VHHVLGEVPVGNPVTVTWPGFARVLP GAGLRFAVN NIFFPVDF	621
612	ILIRYEPQLPDHWEKAVITVORPGKIPASSRCGNTPVDDDQNVVLSLSPGSRYVVLPRPVC	671
622	I AIHYETQSAADWTQIV-VNPPG--GSEHCIPKTLQSKPOSFALPAATRIMLLPTPIC	677
672	FEKGMYTVRLLELPQTASGSDVESPYTFIDS LVLMPYCKSLDI FTVGGSGDGEV TNSAW	731
678	LEPDVQYSIDVYFSQPLQGESHHS-HVLVDSLGLIPIQINSLENF-----CSKQDL	727
732	ETFORYRCLENSRSVVKTPMTDVCRNII FSI SALIHQTGLACEBDDPQGSLSVCDPNGGQ	791
728	DEYQLHNVCVEIASAMGPQVLP GACERLIISM SAKLHDGAVACKCHPQGSVSGSSCSRLGGQ	787
792	CQCRPNVVGRTCNRCAPGTFGFGPNCKPCDCHLQGSASAFCDAITGQCHCFQGIYARQC	851
788	CQCKPLVVGRCDDR CSTGSYDLGHGCHPCHPQGS KDTVCDQVTGQCPCHGEVSRRRC	847
852	DRCLPGYWGFPSPCOPCQCNGHALDCDVTVTGECLSCQDYTTGHN CERC LAGYYG DPIIGSG	911
848	DRCLAGYFGFPSPCHPCPNRFAELCDPETGSCFNCGGFTTGRNCERCIDGYGNP--SSG	905
912	DHCRPCPDGPDGDSGRQFARS CYQDPVTLOLACVDPGYIGSRCDDCASGFFGNPSDFGG	971
906	QPCRPLCLPDDPSSNQYFAHSCYQNLSWDVICNLQGYTGTQCGECSTGFYGNPRI SGA	965
972	SCQPCQCHNIDTDDPEACDKDTGRCLKCLYHTEGDH CQLCOYG YGDALRD CRKCVCN	1031
966	PCQPCACNNIDVTDPESCSRVTGBECLRCLHNTQGAN CQLCKEPHYGSALNQT CRRCSCH	1025
1032	YLGTVKEHC--NGSDCHCDKATGQCSCLPNVIGNQNC DRCA PNTWQLASGTGCGPCNCNAA	1089
1026	ASGVSPMECPGPGGACLCDPVTGACPCLPNVTGLACDRCADGYWNLV PGRG-----	1076
1090	HSFGPSCNEFTGQCQCM PGFGGRTCSECQELFWGDPDVECRACDCDPRGIET PQCDQS	1147
1077	-----CQSCDCDPRTSQSSHCDQA 1095	
 RESULT 15 US-09-925-298-703 ; Sequence 703, Application US/09925298 ; Publication No. US20020039764A1 ; GENERAL INFORMATION: ; APPLICANT: Rosen et al. ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies ; FILE REFERENCE: PA103 ; CURRENT APPLICATION NUMBER: US/09/925,298 ; CURRENT FILING DATE: 2001-08-10 ; PRIOR APPLICATION NUMBER: PCT/US00/05881 ; PRIOR FILING DATE: 2000-03-08 ; PRIOR APPLICATION NUMBER: 60/124,270 ; PRIOR FILING DATE: 1999-03-12		

NUMBER OF SEQ ID NOS: 846
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 703
LENGTH: 527
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (243)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (257)
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LOCATION: (259)
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NAME/KEY: SITE
LOCATION: (519)
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US-09-925-298-703

Query Match 22.1%; Score 2154; DB 12; Length 527;
Best Local Similarity 79.7%; Pred. No. 6.7e-114;
Matches 437; Conservative 33; Mismatches 42; Indels 36; Gaps 3;
1151 CVCVEGVEGPRCDKCTRGYSGVFPDCTPCHQCFCALWDIAIGELTNRTHKFLKAKALKIS 1210
1 CVCVEGVEGPRCDKCTRGYSGVFPDCTPCHQCFCALWDVIIAELTNRTHRFLERKAKALKIS 60
1211 GVIGPYRETVDSEKKVNEIKDILAQSPAAEPLKKNIGILFEEAEKLTQDVTEKMAQVEVK 1270
61 GVIGPYRETVDSEKKVNEIKDILAQSPAAEPLKKNIGILFEEAEKLTQDVTEKMAQVEVK 120
1271 LTDTASQSNSTAGELGALQAEASLDKTVKELAEQLEFIKNSDIQALDLSITKYFQMSLE 1330
121 LSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDLSITKYFQMSLE 180
1331 AEKRVNASTTDPNSTVEQSAITRDRVEDLMLERESPFKEQCEEQARLLDELAKLQSLDL 1390
181 AEKRVNASTTDPNSTVEQSAITRDRVEDVMMERESQFKEQCEEQARLLDELAKLQSLDL 240
1391 SAAQMTCTGTPPGADCESECEGPNCRDTDEGEKCGGCGGLVTVVAHSAWQKAMDFFDRD 1450
241 SAXAEMTCTGTPPGASCXEXECCGPNCRDTDEGERKCGGCGGLVTVVAHNAWQKAMDLDQD 300
1451 VLSALAEVEQLSKMWSEAKVRADEAKQNAQDVLLKTNAFKVKDKSNEDLRNLKQIRNF 1510
301 VLSALAEVEQLSKMWSEAKVRADEAKQSAEDILLKTNAFKVKDKSNEELRNLIKQIRNF 360
1511 LTEDSADLDSIEAVANEVLKSGNASTPQQLNLTEDIRRVETLSQVEVILQSSAADIAI 1570
361 LTQDSADLDSIEAVANEVLKMEPSTPQQLNLTEDIRRVESLSQVEVILQSSAADIAI 420
1571 AELLLEAKRASKSATDVKVTAADMVKEALEEAEAKQVAEAKAIKQADEDIQGTQNLTSI 1630
421 AEMLLLEAKRASKSATDVKVTAADMVKEALEEAEAKQVAEAKAIKQADEDI----- 470
1631 ESETAASBETLTNASQRISKLRNVE---ELKRKAAQNSGEAEYIEKVVSVKQNADDV 1686

Db 471 -----XRNPEPXNFXLEFXKQQLSG-GNLVQVPRASSEFREDV 508
Qy 1687 KKTLDGEL 1694
Db 509 GRXLSGKL 516
Search completed: May 18, 2004, 15:42:38
Job time : 54.4374 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:49:23 ; Search time 10.1546 Seconds
(without alignments)
6313.134 Million cell updates/sec

Title: US-10-037-182-10
Perfect score: 9758
Sequence: 1 MGLLQVAFGVLALWGTRVC.....EVRSLKDISKVAVYSTCL 1786

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 240604 seqs, 35894274 residues

Total number of hits satisfying chosen parameters: 240604

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents AA New:
1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
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6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9140	93.7	1786	6 US-10-796-280-770	Sequence 770, App
2	5690.5	58.3	1196	6 US-10-841-139-4	Sequence 4, Appli
3	5039.5	51.6	1798	6 US-10-796-307-899	Sequence 899, App
4	5039.5	51.6	1798	6 US-10-796-307-900	Sequence 900, App
5	3610	37.0	1670	1 PCT-US02-39555A-917	Sequence 917, App
6	1675	17.2	3712	6 US-10-108-605A-103	Sequence 103, App
7	1645	16.9	1573	6 US-10-796-280-1353	Sequence 1353, App
8	1645	16.9	1573	6 US-10-796-280-1354	Sequence 1354, App
9	1576.5	16.2	3690	6 US-10-796-280-1384	Sequence 1384, App
10	1576.5	16.2	3690	7 US-60-568-219-509	Sequence 509, App
11	1569	16.1	885	1 PCT-US02-39555A-2483	Sequence 2483, App
12	1567.5	16.1	3690	1 PCT-US02-22858A-347	Sequence 347, App
13	1567.5	16.1	3717	6 US-10-821-234-1076	Sequence 1076, App
14	1555	15.9	2107	6 US-10-796-280-1108	Sequence 1108, App
15	1555	15.9	2107	6 US-10-796-307-671	Sequence 671, App
16	1555	15.9	2107	7 US-60-568-219-409	Sequence 409, App
17	1555	15.9	2480	6 US-10-796-280-1106	Sequence 1106, App
18	1555	15.9	2480	6 US-10-796-307-669	Sequence 669, App
19	1555	15.9	2480	7 US-60-568-219-407	Sequence 407, App
20	1555	15.9	3116	6 US-10-796-280-1107	Sequence 1107, App
21	1555	15.9	3116	6 US-10-796-307-670	Sequence 670, App
22	1555	15.9	3116	7 US-60-568-219-408	Sequence 408, App
23	1511.5	15.5	3714	6 US-10-796-280-1383	Sequence 1383, App
24	1511.5	15.5	3714	7 US-60-568-219-508	Sequence 508, App
25	1475	15.1	1165	6 US-10-841-139-2	Sequence 2, Appli
26	1468.5	15.0	1147	6 US-10-841-139-3	Sequence 3, Appli

27	1468	15.0	3332	1 PCT-US02-39555A-1160	Sequence 1160, Ap
28	1330	13.6	249	6 US-10-841-139-6	Sequence 6, Appli
29	1096	11.2	1486	1 PCT-US02-39555A-2658	Sequence 2658, Ap
30	1009	10.3	250	6 US-10-841-139-7	Sequence 7, Appli
31	987.5	10.1	628	6 US-10-100-683-8634	Sequence 8634, Ap
32	987.5	10.1	628	6 US-10-831-979-2	Sequence 2, Appli
33	986.5	10.1	628	6 US-10-831-979-5	Sequence 5, Appli
34	674.5	6.9	1653	6 US-10-453-372-866	Sequence 866, App
35	673.5	6.9	1620	6 US-10-453-372-868	Sequence 868, App
36	668	6.8	1547	6 US-10-453-372-886	Sequence 886, App
37	668	6.8	1577	6 US-10-453-372-882	Sequence 882, App
38	668	6.8	1577	6 US-10-453-372-884	Sequence 884, App
39	662.5	6.8	1594	6 US-10-453-372-860	Sequence 860, App
40	649	6.7	1418	6 US-10-453-372-864	Sequence 864, App
41	647.5	6.6	4265	7 US-60-563-440-1664	Sequence 1664, Ap
42	647.5	6.6	4346	7 US-60-548-091-384	Sequence 384, App
43	647.5	6.6	4346	7 US-60-568-219-343	Sequence 343, App
44	647.5	6.6	4347	7 US-60-548-091-383	Sequence 383, App
45	647.5	6.6	4347	7 US-60-568-219-342	Sequence 342, App

ALIGNMENTS

RESULT 1
US-10-796-280-770
; Sequence 770, Application US/10796280
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001510
; CURRENT APPLICATION NUMBER: US/10/796,280
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 68533
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 770
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-796-280-770

Query Match 93.7%; Score 9140; DB 6; Length 1786;
Best Local Similarity 92.6%; Pred. No. 0;
Matches 1654; Conservative 73; Mismatches 59; Indels 0; Gaps 0;

QY	1	MGLLQVAFGVLALWGTRVCAQEPESYGCAGSCYPATGDLIGRAQKLSVTSTCGLHK	60
Db	1	MGLLQVAFGVLALWGTRVCAQEPESYGCAGSCYPATGDLIGRAQKLSVTSTCGLHK	60
QY	61	PEPYCIVSHLQEDKKCFICDSRDPYHETLNPNDSHLIENVTTTAPNRLKIWQSENGVEN	120
Db	61	PEPYCIVSHLQEDKKCFICDSRDPYHETLNPNDSHLIENVTTTAPNRLKIWQSENGVEN	120
QY	121	VTIQLDLAEFFHFTLIMTFKTRPAAMLIERSDDFGKTGWVRYFYAYDCESFPFGISTG	180
Db	121	VTIQLDLAEFFHFTLIMTFKTRPAAMLIERSDDFGKTGWVRYFYAYDCESFPFGISTG	180
QY	181	PMKKVDDIICDSRYSYSDIEPSTEGEVIFRALDPAFKIEDPYSPRIQNLLKITNLRKFVKL	240
Db	181	PMKKVDDIICDSRYSYSDIEPSTEGEVIFRALDPAFKIEDPYSPRIQNLLKITNLRKFVKL	240
QY	241	HTLGNLLDSRMEIREKYYAVYVDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMC	300
Db	241	HTLGNLLDSRMEIREKYYAVYVDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMC	300
QY	301	RHNTKGLNCELMDIFYHDLWPRAEGRNSACKKCNENHSSSCHFDMAVFLATGNVSGG	360
Db	301	RHNTKGLNCELMDIFYHDLWPRAEGRNSACKKCNENHSSSCHFDMAVFLATGNVSGG	360
QY	361	VCNDCQHTMTGRNCEQCKPFFYQHPERDIRDPNLCPECTCDPAGSENGGICDGYTDFSVG	420
Db	361	VCNDCQHTMTGRNCEQCKPFFYQHPERDIRDPNLCPECTCDPAGSENGGICDGYTDFSVG	420

QY 421 LIAGQCRCKLHVEGERCDVCKEGFYDLAEDPYGCKSCACNPLGTIPGGNCPDSETGYCY 480
Db 421 LIAGQCRCKLHVEGERCDVCKEGFYDLAEDPYGCKSCACNPLGTIPGGNCPDSETGYCY 480
QY 481 CKRLVTGQRCDOCLPQHGLSNDLDGCRPCDCLGGALNNSCEDSGQCSCLPHMIGRQC 540
Db 481 CKRLVTGQRCDOCLPQHGLSNDLDGCRPCDCLGGALNNSCEDSGQCSCLPHMIGRQC 540
QY 541 NEVESGYFTTLDHYIYEAEANLPGVWVVERQYIQRIPSWTGPGRVVRPEGAYLEFF 600
Db 541 NEVESGYFTTLDHYIYEAEANLPGVWVVERQYIQRIPSWTGPGRVVRPEGAYLEFF 600
QY 601 IDNIPYSMEYEILIRYEPQLPDHWEKAVITVQRPKIPASSRCNGTVPDDNQVVSLSPG 660
Db 601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPKIPASSRCNGTVPDDNQVVSLSPG 660
QY 661 SRYVVLPRPVCFEKGMNVTYVLELPOYTASGSDVESPYTFIDSLVLMPCYCKSLDIFTVGG 720
Db 661 SRYVVLPRPVCFEKGMNVTYVLELPOYTASGSDVESPYTFIDSLVLMPCYCKSLDIFTVGG 720
QY 721 SGDGEVNTSAWETFQYRCLNRSRVVKTPTMTDVCNRIIFSISALIHOTGLACECDPQGS 780
Db 721 SGDGVNTSAWETFQYRCLNRSRVVKTPTMTDVCNRIIFSISALIHOTGLACECDPQGS 780
QY 781 LSSVCDPENGQCCQCRPNVGRICNRCAPGTGFGPGNGKPCDCHLQGSASAFCDAITQC 840
Db 781 LSSVCDPENGQCCQCRPNVGRICNRCAPGTGFGPGNGKPCDCHLQGSASAFCDAITQC 840
QY 841 HCFQGIYARQCDRCRLPGYWGFPSPCQPCQNGHALDCDVTGECCLSCQDYTTGHCNCRCLA 900
Db 841 HCFQGVYARQCDRCRLPGYWGFPSPCQPCQNGHALDCDVTGECCLSCQDYTTGHCNCRCLA 900
QY 901 GYGDPITIGSGDHCRCPCPDGDSGRQFARSCYQDPVTQLACVCDPGYIGSRCDCCAS 960
Db 901 GYGDPITIGSGDHCRCPCPDGDSGRQFARSCYQDPVTQLACVCDPGYIGSRCDCCAS 960
QY 961 GFFGNPSPFGGSCQPCQCHNIDTTDPEACDKDTGRCLKLYHTEGDHQCQLCYGYGDA 1020
Db 961 GYFGNPSEVGGSCQPCQCHNIDTTDPEACDKETGRCLKLYHTEGEHCQCFRGYGYGDA 1020
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Db 1021 LQQDCRKVCNYLGTVEHCNGSDCQCDKATGQCCLPNVIGQNCDCRCAPNTWQLASGTG 1080
QY 1081 CGPCNCNAAHSPGSCNEFTGQCQCMGFGGRTCECQELFWGDPDVECRACDCDPRGIE 1140
Db 1081 CDPCNCNAAHSPGSCNEFTGQCQCMGFGGRTCECQELFWGDPDVECRACDCDPRGIE 1140
QY 1141 TPQCDQSTGQCVCEGVEGPRCDKCTRGYSVGFPPDCTPCHQCFALWDIAIIGELTNRTHKF 1200
Db 1141 TPQCDQSTGQCVCEGVEGPRCDKCTRGYSVGFPPDCTPCHQCFALWDVIIAELTNRTHRF 1200
QY 1201 LEKAKALKISGVIQPYRETVDVSEKKNVNEIKDILAQSPAEPKKNIGILFEEAEKLTADV 1260
Db 1201 LEKAKALKISGVIQPYRETVDVSEKKNVNEIKDILAQSPAEPKKNIGILFEEAEKLTADV 1260
QY 1261 TEKMAQVEVKLTDTASQSNSTAGELGALQAEAESLDKTVKELAEQLEFIKNSDIOGALDS 1320
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QY 1321 ITKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRDRVEDLMLERESPFEKQEQEQARLDE 1380
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QY 1381 LAGKLOSLDLSAAQMTCTGTPPGADCSSECGGPNCRCTDEGERKCGGPGCGGLVTVAHSA 1440
Db 1381 LAGKLOSLDLSAAEMTCTGTPPGASCSETECGGPNCRCTDEGERKCGGPGCGGLVTVAHNA 1440
QY 1441 WQKAMDFDRDVL SALAEVEQLSKMVSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDL 1500
Db 1441 WQKAMDLDQDVL SALAEVEQLSKMVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNEDL 1500

QY 1501 RNLIKQIRNFLTSDSADLDSIEAVANEVLKSGNASTPQQLQNLTDIRIRVETLSQVEVI 1560
Db 1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKMEMBSTPQQLQNLTDIRIRVESLSQVEVI 1560
QY 1561 LQQAADIARAELLLEAKRASKSATDVKVTADVMYKEALEEAEKAQVAEKAIKOADEDI 1620
Db 1561 LQHAADIARAELLLEAKRASKSATDVKVTADVMYKEALEEAEKAQVAEKAIKOADEDI 1620
QY 1621 QGTQNLTSISETAASEETLTNASQRIKSLERNVEELKRKAAQNSGEAEYIEKVYYSVK 1680
Db 1621 QGTQNLTSISETAASEETLTNASQRISELERNVEELKRKAAQNSGEAEYIEKVYYSVK 1680
QY 1681 QNADDVKKTLDELDEKYYKVESLIAQKTEESADARRKAELLQNEAKTLLAQANSKLQLL 1740
Db 1681 QSAEDVKKTLDELDEKYYKVENLIAKTEESADARRKAEMLQNEAKTLLAQANSKLQLL 1740
QY 1741 EDLERKYEDNQYLEDKAQELVRLGEVRSLLKXDISKVAVYSTCL 1786
Db 1741 KDLERKYEDNQRYLEDKAQELARLEGEVRSLLKDISOKVAVYSTCL 1786

RESULT 2

US-10-841-139-4
; Sequence 4, Application US/10841139
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert E.
; APPLICANT: Wagnan, David W.
; TITLE OF INVENTION: BLK CHAIN OF LAMININ AND METHODS OF USE
; FILE REFERENCE: 10287/021003
; CURRENT APPLICATION NUMBER: US/10/841,139
; CURRENT FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US/10/443,349
; PRIOR FILING DATE: 2003-05-22
; PRIOR APPLICATION NUMBER: US/09/161,872
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: US 08/735,893
; PRIOR FILING DATE: 1996-10-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1196
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(250)
; OTHER INFORMATION: Human B1 chain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (251)...(437)
; OTHER INFORMATION: Human B1 chain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (438)...(807)
; OTHER INFORMATION: Human B1 chain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (808)...(840)
; OTHER INFORMATION: Human B1 chain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (841)...(1196)
; OTHER INFORMATION: Human B1 chain
US-10-841-139-4

Query Match 58.3%; Score 5690.5; DB 6; Length 1196;
Best Local Similarity 63.2%; Pred. No. 2.5e-235;
Matches 1116; Conservative 46; Mismatches 33; Indels 571; Gaps 2;
QY 22 QEPFSGYCAEGSCYPATGDLILIGRAQKLSVTS-TCGLHKPEPYCIVSHLQEDKKCFICD 80
Db 1 QEPFSGYCAEGSCYPATGDLILIGRAQKLSVTS-TCGLHKPEPYCIVSHLQEDKKCFICN 60

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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:58 ; Search time 16.4366 Seconds
(without alignments)
10452.141 Million cell updates/sec

Title: US-10-037-182-10
Perfect score: 9758
Sequence: 1 MGLLQVFAFGVLALWGTRVC.....EVRSLKDISKVAVYSTCL 1786

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	9758	100.0	1786	1 MMMSB1	laminin beta-1 cha
2	9144	93.7	1786	1 MMHUB1	laminin beta-1 cha
3	5087.5	52.1	1801	1 MMRTS	laminin beta-2 cha
4	5033.5	51.6	1798	2 S53869	laminin beta-2 cha
5	4870.5	49.9	1797	2 A55677	laminin beta-2 cha
6	3858.5	39.5	1790	1 MMFFB1	laminin beta-1 cha
7	3742.5	38.4	1808	2 T15099	hypothetical prote
8	1751	17.9	3672	2 T23433	hypothetical prote
9	1751	17.9	3704	2 T37316	probable laminin a
10	1704	17.5	1639	1 MMFFB2	laminin gamma-1 ch
11	1675	17.2	3712	2 S18253	laminin alpha-1 ch
12	1647	16.9	1609	1 MMHUB2	laminin gamma-1 ch
13	1645.5	16.9	1557	2 T28811	hypothetical prote
14	1634.5	16.8	1607	1 MMMSB2	laminin gamma-1 ch
15	1584	16.2	3635	2 T10053	laminin alpha 5 ch
16	1575	16.1	303	2 B45067	laminin B1 chain -
17	1573.5	16.1	3075	2 S14458	laminin alpha-1 ch
18	1541.5	15.8	1170	2 A53612	laminin B1k chain
19	1524	15.6	3106	1 S53868	laminin alpha-2 ch
20	1520.5	15.6	1168	2 I56985	laminin B1 - mouse
21	1510	15.5	3084	1 MMMSA	laminin alpha-1 ch
22	1305.5	13.4	2823	2 T23064	hypothetical prote
23	1305.5	13.4	2823	2 F87908	protein T22A3.8 [i
24	1305.5	13.4	3102	2 T43291	laminin alpha chai
25	978.5	10.0	616	2 I38231	S-laminin - human
26	858.5	8.8	1193	2 A44018	laminin B2t chain
27	850.5	8.7	1192	2 S69000	laminin gamma 2 ch
28	686	7.0	606	2 A54665	netrin-1 precursor
29	682.5	7.0	1620	2 T27283	hypothetical prote

30	680	7.0	1574	2 T13954	MEGF6 protein - ra
31	661.5	6.8	1111	2 T26972	hypothetical prote
32	656	6.7	3707	2 S18252	heparan sulfate pr
33	647.5	6.6	4391	2 A38096	perlecan precursor
34	617	6.3	612	2 JH0799	laminin-related pr
35	608.5	6.2	581	2 B54665	netrin-2 precursor
36	561	5.7	400	2 T46383	hypothetical prote
37	560.5	5.7	1816	1 S68960	laminin alpha-4 ch
38	555.5	5.7	1751	1 MMHUMH	laminin alpha-2 ch
39	531	5.4	2524	2 A35844	Xotch protein - Af
40	527	5.4	2321	2 S78549	notch3 protein - h
41	520.5	5.3	198	2 A45067	laminin B1 chain v
42	511.5	5.2	2703	1 A24420	notch protein - fr
43	510	5.2	2295	2 C88369	protein unc-52 [im
44	510	5.2	3375	2 T19821	hypothetical prote
45	508.5	5.2	2531	2 T31070	notch homolog - se

ALIGNMENTS

RESULT 1

MMMSB1
laminin beta-1 chain precursor - mouse
N;Alternate names: laminin chain B1
C;Species: Mus musculus (house mouse)
C;Date: 28-Feb-1986 #sequence revision 30-Jun-1991 #text change 10-Dec-1999
C;Accession: A26413; S02679; S05326; S14877; A02871; S02036; S13543
R;Sasaki, M.; Kato, S.; Kohno, K.; Martin, G.R.; Yamada, Y.
Proc Natl Acad Sci U S A. 84, 935-939, 1987
A;Title: Sequence of the cDNA encoding the laminin B1 chain reveals a multidomain protein.
A;Reference number: A26413; MUID:87147212; PMID:3493487
A;Accession: A26413
A;Molecule type: mRNA
A;Residues: 1-1786 <SAS>
A;Cross-references: EMBL:M15525; NID:G198700
A;Note: translation in GenBank has additional 48 residues at the amino end
R;Fujiwara, S.; Shinkai, H.; Deutzmann, R.; Paulsson, M.; Timpl, R.
Biochem J. 252, 453-461, 1988
A;Title: Structure and distribution of N-linked oligosaccharide chains on various domain
A;Reference number: S02678; MUID:88326259; PMID:2458101
A;Accession: S02679
A;Molecule type: protein
A;Residues: 28-42;932-946 <FUJ>
R;Hartl, L.; Oberbaumer, I.; Deutzmann, R.
Eur J Biochem. 173, 629-635, 1988
A;Title: The N terminus of laminin A chain is homologous to the B chains.
A;Reference number: S00624; MUID:88225080; PMID:3267223
A;Accession: S05326
A;Molecule type: protein
A;Residues: 457-466;854-868;932-946 <HAR>
R;Mann, K.; Deutzmann, R.; Timpl, R.
Eur J Biochem. 178, 71-80, 1988
A;Title: Characterization of proteolytic fragments of the laminin-nidogen complex and th
A;Reference number: S08895; MUID:89078415; PMID:2462498
A;Accession: S14877
A;Molecule type: protein
A;Residues: 590-620 <MAN>
R;Barlow, D.P.; Green, N.M.; Kurkinen, M.; Hogan, B.L.M.
EMBO J. 3, 2355-2362, 1984
A;Title: Sequencing of laminin B chain cDNAs reveals C-terminal regions of coiled-coil a
A;Reference number: A02870; MUID:85051302; PMID:6209134
A;Accession: A02871
A;Molecule type: mRNA
A;Residues: 1292-1530, 'MEMP', 1535-1691, 'C', 1693-1748, 'N', 1750-1786 <BAR>
A;Cross-references: EMBL:X05212; NID:G52861; PIDN:CAA28839.1; PID:G809042
R;Deutzmann, R.; Huber, J.; Schmetz, K.A.; Oberbaumer, I.; Hartl, L.
Eur J Biochem. 177, 35-45, 1988
A;Title: Structural study of long arm fragments of laminin. Evidence for repetitive C-te
A;Reference number: S01790; MUID:89030693; PMID:3181157
A;Accession: S02036
A;Molecule type: protein
A;Residues: 1561-1587 <DEU>

R;Paulsson, M.; Deutzmann, R.; Timpl, R.; Dalzoppo, D.; Odermatt, E.; Engel, J.
EMBO J. 4, 309-316, 1985
A;Title: Evidence for Coiled-coil alpha-helical regions in the long arm of laminin.
A;Reference number: S13543; MUID:85257455; PMID:3848400
A;Accession: S13543
A;Molecule type: protein
A;Residues: 1700-1748, 'N', 1750-1759 <PAU>
C;Genetics:
A;Gene: Lamb-1
A;Map position: 12
A;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C;Function:
A;Description: interact with cells and with other basement membrane proteins to promote
C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-1786/Product: laminin beta-1 chain #status predicted <MAT>
F;22-270/Domain: VI <DOM6>
F;271-540/Domain: V <DOM5>
F;271-332/Domain: laminin-type EGF-like homology <LE01>
F;335-395/Domain: laminin-type EGF-like homology <LE02>
F;398-455/Domain: laminin-type EGF-like homology <LE03>
F;458-507/Domain: laminin-type EGF-like homology <LE04>
F;510-540/Domain: laminin-type EGF-like homology #status atypical <LE05>
F;541-772/Domain: IV <DOM4>
F;773-1182/Domain: III <DOM3>
F;773-818/Domain: laminin-type EGF-like homology <LE06>
F;821-864/Domain: laminin-type EGF-like homology <LE07>
F;867-914/Domain: laminin-type EGF-like homology <LE08>
F;917-973/Domain: laminin-type EGF-like homology <LE09>
F;976-1025/Domain: laminin-type EGF-like homology <LE10>
F;1028-1081/Domain: laminin-type EGF-like homology <LE11>
F;1084-1129/Domain: laminin-type EGF-like homology <LE12>
F;1132-1176/Domain: laminin-type EGF-like homology <LE13>
F;1183-1397/Domain: II <DOM2>
F;1183-1397/Region: heptad repeats
F;1398-1430/Domain: alpha <ALP>
F;1431-1786/Region: heptad repeats
F;1431-1786/Domain: I <DOM1>
F;22/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;30-35/Disulfide bonds: #status predicted
F;120,356,519,677,1041,1195,1279,1336,1343,1487,1533,1542,1643/Binding site: carbohydra
F;1179,1182,1785/Disulfide bonds: interchain #status predicted

Query Match 100.0%; Score 9758; DB 1; Length 1786;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MGLQVAFGV LALWGTRVCAQEPEFSYGCAGSCYPATGDL LIGRAQLSVTSTCGLHK 60

QY 61 PEPYCIIVSHLQEDKKCFICDSRDPPYHETLNPD SHLIENVTTFAPNRLKIWQSENGVEN 120
Db 61 PEPYCIIVSHLQEDKKCFICDSRDPPYHETLNPD SHLIENVTTFAPNRLKIWQSENGVEN 120

QY 121 VTIQDLLEAEFHFTLINTFKTFRPAAMLIERSSDFGKTGWVRYFAYDCESFPFGISTG 180
Db 121 VTIQDLLEAEFHFTLINTFKTFRPAAMLIERSSDFGKTGWVRYFAYDCESFPFGISTG 180

QY 181 PMKKVDDIIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPIQNLLKITNLRIFVKL 240
Db 181 PMKKVDDIIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPIQNLLKITNLRIFVKL 240

QY 241 HTLGDNLLDSRMEIREKYIYAYVDMVVRGNCFYGHASECAPVDGVNEEVEGMVHGCMC 300
Db 241 HTLGDNLLDSRMEIREKYIYAYVDMVVRGNCFYGHASECAPVDGVNEEVEGMVHGCMC 300

QY 301 RHNTKGLNCELMDFYHDLPLWRPAEGRNSACKNCNEHSSSCHDFMAVFLATGNVSGG 360
Db 301 RHNTKGLNCELMDFYHDLPLWRPAEGRNSACKNCNEHSSSCHDFMAVFLATGNVSGG 360

QY 361 VCDNCQHTMGRNCEQCKPFYFQHPERDIRDNLCEPCTCDPAGSENGGICDGYTDFSVG 420

Db 361 VCDNCQHTMGRNCEQCKPFYFQHPERDIRDNLCEPCTCDPAGSENGGICDGYTDFSVG 420

QY 421 LIAGQCRCKLHVGERCDVCKEGFYDLSEAEDPYGCKSCACNPLGTIPGNGPCDSETGYCY 480

Db 421 LIAGQCRCKLHVGERCDVCKEGFYDLSEAEDPYGCKSCACNPLGTIPGNGPCDSETGYCY 480

QY 481 CKRLVTGQRCDQCLPQHGLSNDLDGCRPCDCDLGGALNNSCEDSGQCSCLPHMIGRQC 540

Db 481 CKRLVTGQRCDQCLPQHGLSNDLDGCRPCDCDLGGALNNSCEDSGQCSCLPHMIGRQC 540

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Db 541 NEVESGYFTTLDHYIYEAEANLPGVGVVVERQYIQRIIPSWTGPFGFVRVPEGAYLEFF 600

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QY 661 SRYVLP RPVCFEKGMNYYT RLELPQYTASGSDVESPYTFIDSLVLMPYCKSLDIFTVGG 720

Db 661 SRYVLP RPVCFEKGMNYYT RLELPQYTASGSDVESPYTFIDSLVLMPYCKSLDIFTVGG 720

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Db 781 LSSVCDPNCGGQCCRPNVVGRITCNRCAPGTGFGPNCKPCDCHLQGSASAFCDAITGQC 840

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QY 1501 RNLIKOIRNFLTEDSADLDSIEAVANEVLKSGNASTPQOLQNLTEDIRERVETLSQVEVI 1560

Db 1501 RNLIKOIRNFLTEDSADLDSIEAVANEVLKSGNASTPQOLQNLTEDIRERVETLSQVEVI 1560

QY 1561 LQOAAADIARAELILEEAKRASKSATDVKTADVMVKEALEEAEKAAQVAAEKAIKQADEDI 1620

Db 1561 LQOAAADIARAELILEEAKRASKSATDVKTADVMVKEALEEAEKAAQVAAEKAIKQADEDI 1620

QY 1621 QGTQNLTSIESETAASEETLTNASORISKLERNVEELKRKAAQNSGAEAYIEKVVYSVK 1680

Db 1621 QGTQNLTSIESETAASEETLTNASORISKLERNVEELKRKAAQNSGAEAYIEKVVYSVK 1680

QY 1681 QNADDVKKTLDGELDEKYKVESLIAQKTESADARRKAEALLQNEAKTLLAQANSKLQLL 1740

Db 1681 QNADDVKKTLDGELDEKYKVESLIAQKTESADARRKAEALLQNEAKTLLAQANSKLQLL 1740

QY 1741 EDLERKYEDNQYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1786

Db 1741 EDLERKYEDNQYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1786

RESULT 2

MMHUB1

laminin beta-1 chain precursor - human

N;Alternate names: laminin chain B1

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text_change 19-Jan-2001

C;Accession: S13547; A28483; A26994; S23566

R;Vuolteenaho, R.; Chow, L.T.; Tryggvason, K.

J. Biol. Chem. 265, 15611-15616, 1990

A;Title: Structure of the human laminin B1 chain gene.

A;Reference number: S13547; MUID:90368768; PMID:1975589

A;Accession: S13547

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-1786 <VUO>

A;Cross-references: GB:M61951; GB:J02778; NID:G186911; PIDN:AAA59486.1; PID:G186913

A;Note: the nucleotide sequence was submitted to GenBank, February 1991

R;Pikkarainen, T.; Eddy, R.; Fukushima, Y.; Byers, M.; Shows, T.; Pihlajaniemi, T.; Sara

J. Biol. Chem. 262, 10454-10462, 1987

A;Title: Human laminin B1 chain. A multidomain protein with gene (LAMB1) locus in the q2

A;Reference number: A28483; MUID:87280097; PMID:3611077

A;Accession: A28483

A;Molecule type: mRNA

A;Residues: 1-1786 <PIK>

A;Cross-references: GB:M61951; GB:J02778; NID:G186911; PIDN:AAA59486.1; PID:G186913

R;Jaye, M.; Modi, W.S.; Ricca, G.A.; Mudd, R.; Chiu, I.M.; O'Brien, S.J.; Drohan, W.N.

Am. J. Hum. Genet. 41, 605-615, 1987

A;Title: Isolation of a cDNA clone for the human laminin-B1 chain and its gene localizat

A;Reference number: A26994; MUID:88021029; PMID:3661559

A;Accession: A26994

A;Molecule type: mRNA

A;Residues: 1276-1469, 'V', 1471-1695, 'G', 1697-1709 <JAY>

A;Cross-references: EMBL:M20206; NID:G186914; PIDN:AAA59487.1; PID:G186915

R;Vuolteenaho, R.; Kallunki, T.; Chow, L.; Ikonen, J.; Pikkarainen, T.; Tryggvason, K.

in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp. 175-193, Academic P

A;Title: Genes for the human laminin B1 and B2 chains.

A;Reference number: S23566

A;Accession: S23566

A;Molecule type: DNA

A;Residues: 762-1786 <VU2>

A;Note: mRNA was also sequenced

C;Genetics:

A;Gene: GDB:LAMB1

A;Cross-references: GDB:119357; OMIM:150240

A;Map position: 7q31.1-7q31.3

A;Introns: 13/1; 71/3; 117/1; 141/3; 204/3; 226/1; 293/3; 334/1; 397/1; 457/1; 494/3; 52

64/3; 1513/1; 1582/2; 1629/3; 1688/3; 1742/1

C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin

C;Function:

A;Description: interact with cells and with other basement membrane proteins to promote

C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology

C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-1786/Product: laminin beta-1 chain #status predicted <MAT>

F;22-270/Domain: VI <DOM6>

F;271-548/Domain: V <DOM5>

F;271-332/Domain: laminin-type EGF-like homology <LE01>

F;335-395/Domain: laminin-type EGF-like homology <LE02>

F;398-455/Domain: laminin-type EGF-like homology <LE03>

F;458-507/Domain: laminin-type EGF-like homology <LE04>

F;463-468/Region: cell adhesion #status predicted

F;510-540/Domain: laminin-type EGF-like homology #status atypical <LE05>

F;549-774/Domain: IV <DOM4>

F;662-668/Region: cell adhesion #status predicted

F;773-818/Domain: laminin-type EGF-like homology <LE06>

F;775-1178/Domain: III <DOM3>

F;821-864/Domain: laminin-type EGF-like homology <LE07>

F;867-914/Domain: laminin-type EGF-like homology <LE08>

F;917-973/Domain: laminin-type EGF-like homology <LE09>

F;923-927/Region: cell adhesion #status predicted

F;950-954/Region: cell adhesion #status predicted

F;976-1025/Domain: laminin-type EGF-like homology <LE10>

F;1028-1081/Domain: laminin-type EGF-like homology <LE11>

F;1084-1129/Domain: laminin-type EGF-like homology <LE12>

F;1132-1176/Domain: laminin-type EGF-like homology <LE13>

F;1179-1397/Domain: II <DOM2>

F;1179-1397/Region: heptad repeats

F;1398-1430/Domain: alpha <ALP>

F;1431-1786/Domain: I <DOM1>

F;1431-1786/Region: heptad repeats

F;30-35/Disulfide bonds: #status predicted

F;120,356,519,677,965,1041,1195,1279,1336,1343,1487,1542,1643/Binding site: carbohydrate

F;1179,1182,1785/Disulfide bonds: interchain #status predicted

Query Match 93.7%; Score 9144; DB 1; Length 1786;

Best Local Similarity 92.7%; Pred. No. 0;

Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;

QY 1 MGLQVAFAGVLALWGTRVCAQEPFESYGAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60

Db 1 MGLQLLAFSLALCRARVRAQEPFESYGAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60

QY 61 PEPYCIIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVVTTTFAPNRLKIWQSENGVEN 120

Db 61 PEPYCIIVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVVTTTFAPNRLKIWQSENGVEN 120

QY 121 VTQLDLEAEFHTLINTFKTRPAAMLIERSDFGKTGWYRYFAYDCSSFPFGISTG 180

Db 121 VTQLDLEAEFHTLINTFKTRPAAMLIERSDFGKTGWYRYFAYDCSEAFPGISTG 180

QY 181 PMKKVDDIICDSRYSDIEPTEGEVIFRALDPAFKIEDPSPRIQNLKLTNLRKFKVKL 240

Db 181 PMKKVDDIICDSRYSDIEPTEGEVIFRALDPAFKIEDPSPRIQNLKLTNLRKFKVKL 240

QY 241 HTLGNLLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMC 300

Db 241 HTLGNLLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGCMC 300

QY 301 RHNTKGLNCELMDFYHDLVWRPAEGRNSNACKKCNCHSSCHDFMAVFLATGNVSGG 360

Db 301 RHNTKGLNCELMDFYHDLVWRPAEGRNSNACKKCNCHSSCHDFMAVFLATGNVSGG 360

QY 361 VCDNCQHNTMGRNCEQCKPFYFQHPERDIRDPNLCPCTCDPAGSENGGICDGYTDFSVG 420

Db 361 VCDNCQHNTMGRNCEQCKPFYFQHPERDIRDPNLCPCTCDPAGSENGGICDGYTDFSTG 420

QY 421 LIAGQCRCKLHVEGERCDVCKEGFYDLSEADPYGCKSCACNPLGTIPGNPCDSETKGYC 480

Db 421 LIAGQCRCKLHVEGERCDVCKEGFYDLSEADPYGCKSCACNPLGTIPGNPCDSETKGYC 480

QY 481 CKRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCLGGALNNSCEDSGQCSCLPHMIGRQC 540

Db 481 CKRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCLGGALNNSCEDSGQCSCLPHMIGRQC 540

QY 541 NEVESGYFTTLDHYIYBAEANLPGVWVVERQYIQDRIPSWTGPGRVPEGAYLEFF 600
Db 541 NEVEPGYYFATLDHYLYBAEANLPGVSIVERQYIQDRIPSWTGAGFVRPEGAYLEFF 600
QY 601 IDNIPYSMEYEILIRYEPQLPDHWEKAVITVORPGKIPASSRCNGTVPDDNQWWSLSPG 660
Db 601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVORPGRIPTSSRCNGTIPDDNQWWSLSPG 660
QY 661 SRYVVLPRPVCFEKGMNVTYRLELPQYTAGSDVESPFTFIDSLVLMYPYKSLDIFTVGG 720
Db 661 SRYVVLPRPVCFEKGTNYRLELPQYTTSSDVSPEPYTLIDSLVLMYPYKSLDIFTVGG 720
QY 721 SGGEVTNSAWETFORYRCLENSRSVVKTPMTDVCNIIIFSISALIHQTGLACECDPQGS 780
Db 721 SGGVVTNSAWETFORYRCLENSRSVVKTPMTDVCNIIIFSISALLHOTGLACECDPQGS 780
QY 781 LSSVCDPNGGCQCRPNVVGRTCNRCAPGTFGFGNGCKPCDCHLQGSASAFCDAITGQC 840
Db 781 LSSVCDPNGGCQCRPNVVGRTCNRCAPGTFGFGSGCKPCECHLQGSVNAFCNPVTGQC 840
QY 841 HCFQGIYARQCRLPGYWGPPSPCQCQNGHALDCDVTGECISLQCDYTTGHCNRCCLA 900
Db 841 HCFQGVYARQCRLPGHWGFPSCQPCQNGHADDCDVPVTGECINQCDYTTGHCNRCCLA 900
QY 901 GYVGDPIIGSDHCRPCPCPDGSDSGRQFARSCYQDPVTQLACVCDPFGYIGSRCDCCAS 960
Db 901 GYVGDPIIGSDHCRPCPCPDGSDSGRQFARSCYQDPVTQLACVCDPFGYIGSRCDCCAS 960
QY 961 GFFGNPSDFGSCQPCQCHNIDTDPDPEACDKDTGRCLKCLYHTEGDHCLQCYGYGDA 1020
Db 961 GYFGNPSEVGGSCQPCQCHNIDTDPDPEACDKETGRCLKCLYHTEGEHCQCFRGYGYGDA 1020
QY 1021 LRQDRKVCVNYLGTVKEHNGSDCHCDKATGQCSCLPNVIGQNCDCRCAPNTWQLASGTG 1080
Db 1021 LRQDRKVCVNYLGTVQVQEHNGSDCQCDKATGQCLCLPNVIGQNCDCRCAPNTWQLASGTG 1080
QY 1081 CGPCNNAHSFGPSCNEFTGQCQCMFPGGRTCTSEQELFWGDPDVECRACDCDPRGIE 1140
Db 1081 CDPNCNAAHSFGPSCNEFTGQCQCMFPGGRTCTSEQELFWGDPDVECRACDCDPRGIE 1140
QY 1141 TPQCDSGTGQVCVVEGVEGPRCDKCTRGYSVFPDCTPCHQCFCALWDIAIIGELTNRTHKF 1200
Db 1141 TPQCDSGTGQVCVVEGVEGPRCDKCTRGYSVFPDCTPCHQCFCALWDVIIAELTNRTHRF 1200
QY 1201 LEKAKALKISGVIGPYRETVDSEKVVNEIKDILAQSPAAPLKNIGILFEAEKLTQDV 1260
Db 1201 LEKAKALKISGVIGPYRETVDSEKVVSEIKDILAQSPAAPLKNIGNLFEAEKLIKDV 1260
QY 1261 TERMAQVEVKLTDTASQSNSTAGELGALQAEASLDKTKVKELAEQLEFIKNSDIQCALDS 1320
Db 1261 TENMAQVEVKLSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDS 1320
QY 1321 ITKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLERESPFEQOEQARLLDE 1380
Db 1321 ITKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVMMERESQFKEQOEQARLLDE 1380
QY 1381 LAGKLSLDLSAAAQMTCTGTPPGADCSSECEGPNCRITDGEKKCGGPGCGGLVTVAHSA 1440
Db 1381 LAGKLSLDLSAAAEMTCGTPPGASCSETECGGPNCRITDGERKCGGPGCGGLVTVAHNA 1440
QY 1441 WQKAMDFDRDVLALAEVEQLSKMVSEAKVRADEAKQNAQDVLKTNATKEKVDKSNEDL 1500
Db 1441 WQKAMLDQDVLALAEVEQLSKMVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNEL 1500
QY 1501 RNLIKQIRNFLETSDADLDSIEAVANEVLKSGNASTPQQLQNLITEDIRERVETLSQVEVI 1560
Db 1501 RNLIKQIRNFLETQDSADLDSIEAVANEVLKWMFPSTPQQLQNLITEDIRERVESLSQVEVI 1560
QY 1561 LQOSAADIARAEALLLEAKRASKSATDVKVTADMVKEALEAEKAOVAEKAQKQADEDI 1620
Db 1561 LQHSAAADIARAEMLLEAKRASKSATDVKVTADMVKEALEAEKAOVAEKAQKQADEDI 1620

QY 1621 QGTQNLLTSIESETAASEETLTNASQRIKLERNVVELKRKAAQNSGEAEYIEKVVSVK 1680
Db 1621 QGTQNLLTSIESETAASEETLTNASQRISELERNVVELKRKAAQNSGEAEYIEKVVTVK 1680
QY 1681 QNADDVKKTLDGELDEKYKVESLIAQKTEESADARRKAEALLQNEAKTLAQANSKLQLL 1740
Db 1681 QSAEDVKKTLDGELDEKYKVENLIAKTEESADARRKAEMLQNEAKTLAQANSKLQLL 1740
QY 1741 EDLERKYEDNQYLEDKACELVRLEGEVRSLLKDISQKVAVYSTCL 1786
Db 1741 KLERKYEDNQYLEDKACELARLEGEVRSLLKDISQKVAVYSTCL 1786
RESULT 3
MMETS
laminin beta-2 chain precursor - rat
N:Alternate names: laminin chain B3; S-laminin
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 10-Dec-1999
C:Accession: S03539
R:Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.
Nature 338, 229-234, 1989
A:Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the neuro
A:Reference number: S03539; MUID:89159410; PMID:2922051
A:Accession: S03539
A:Molecule type: mRNA
A:Residues: 1-1801 <HUN>
A:Cross-references: EMBL:X16563; NID:G57250; PIDN:CAA34561.1; PID:G57251
C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C:Function:
A:Description: Interact with cells and with other basement membrane proteins to promote
C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular
F:1-35/Domain: signal sequence #status predicted <SIG>
F:36-1801/Product: laminin beta-2 chain #status predicted <MAT>
F:36-285/Domain: VI <DOM6>
F:286-555/Domain: V <DOM5>
F:286-347/Domain: laminin-type EGF-like homology <LE01>
F:350-410/Domain: laminin-type EGF-like homology <LE02>
F:413-470/Domain: laminin-type EGF-like homology <LE03>
F:473-522/Domain: laminin-type EGF-like homology <LE04>
F:525-555/Domain: laminin-type EGF-like homology #status atypical <LE05>
F:556-784/Domain: IV <DOM4>
F:786-831/Domain: laminin-type EGF-like homology <LE06>
F:788-1196/Domain: III <DOM3>
F:834-877/Domain: laminin-type EGF-like homology <LE07>
F:880-927/Domain: laminin-type EGF-like homology <LE08>
F:930-986/Domain: laminin-type EGF-like homology <LE09>
F:989-1038/Domain: laminin-type EGF-like homology <LE10>
F:1041-1095/Domain: laminin-type EGF-like homology <LE11>
F:1098-1143/Domain: laminin-type EGF-like homology <LE12>
F:1146-1190/Domain: laminin-type EGF-like homology <LE13>
F:1197-1412/Domain: II <DOM2>
F:1197-1412/Region: heptad repeats
F:1413-1445/Domain: alpha <ALP>
F:1446-1801/Region: heptad repeats
F:1446-1801/Domain: I <DOM1>
F:45-50/Disulfide bonds: #status predicted
F:251,371,1088,1252,1311,1351,1502/Binding site: carbohydrate (Asn) (covalent) #status p
F:1193,1196,1800/Disulfide bonds: interchain #status predicted

Query Match 52.1%; Score 5087.5; DB 1; Length 1801;
Best Local Similarity 51.2%; Pred. No. 2.8e-188;
Matches 920; Conservative 303; Mismatches 544; Indels 29; Gaps 11;
QY 1 MGLLQVFAFGVLALWGTRVCAQEPEFSY-GCAEGSCYPATGDLIGRAQKLSVTSTCGLH 59
Db 23 LGLL----LSVLA---ATLAQVPSLDVPGCSRGSCYPATGDLVGRADRLTASSTCGLH 74
QY 60 KPEPYCIVSHLQEDKKCFICDSRDPYHETLNPDShLIENVVTFAPNRLKIWQSENGVE 119
Db 75 SPQPYCIVSHLQDEKKCFCLDSRRRPSARDNPNSHRIQNVVTSFAPQRTAWQSENGVP 134

QY	120	NVTIQLDLEAEFHTHLIMTFKTRPAAMLIERSDPGKTGWVYRYFAYDCSSFPGIST	179
DB	135	MVTIQLDLEAEFHTHLIMTFKTRPAAMLVERSADFGTRWVRYFSDYDCGADFPGL	194
QY	180	GPMKKVDDIICDSRYSDIEPSTEGEVIFRALDPAPKIEDPPYSPRIQNLLKITNLRIFVK	239
DB	195	APRRWDDVVCESRYSEIEPSTEGEVIYRVLDPAIPDPYSSRIQNLLKITNLRVNLTR	254
QY	240	LHTLGDNLLDSRMEIREKYVYAVYDMVVRGNCFYGHASECAPVDGVNEEVEGMVHGCM	299
DB	255	LHTLGDNLLDPRREIREKYVYALYELVIRGNCFYGHASQCAPAGAPAAHAEGMVHGACI	314
QY	300	CRHNTKGLNCELMDPFYHDLPRPAPAGRNSNACKKCNHSSSCHFDMVFLATGNVSG	359
DB	315	CKHNRGLNCEQCQDFYQDLPWHPAEDGHTHACKCKECNGHSHSCHFDMVYLASGNVSG	374
QY	360	GVCDNCOHNTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSV	419
DB	375	GVCDGCOHNTAGHCELCRPFYRDPTKDMRDPAAACFPDCDPMGSDGGRCDSDHDPVL	434
QY	420	GLIAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGPNPCDSETYC	479
DB	435	GLVSGQCRCKEHVGTRCQQCRDGFGLSASNPRGQRCQCNSRGTVPGGTPCDDSSSGTC	494
QY	480	YKRLVTGORCDQCLPQHWGLSNDLDGCRPCDCLGGALNNSCEDSGQCSCLPHMIGRQ	539
DB	495	FKRLVTGDGCDRCLPGHWGLSHDLLGCRPCDCLVGGALDPQCDEATGQCPCRPMMIGRR	554
QY	540	CNEVESGYFTTLDHYIYEABEANLPGVVVVERQIQDRIPSWTGPGFVRVPEGAYLEF	599
DB	555	CEQVQPGYFRPFJDLHTWEABGAH-GQVLEVVERLVTNRETPTSWTGVGFVRLREGQVEF	613
QY	600	FIDNIPYSMEYELIRYEPQLPDHWEKAVITVORPGKIPASSRCGNTPVDDDNQVVSLS	659
DB	614	LVTSLPRAMDYDLLLLRWEPPQVPEQWAELELVQRPGPVSAHSPCGHVLPRRDDRIQGM	673
QY	660	GSRYVLP RPVCFEKGMNYTVRLELPQYTAGSDVESPYT- - - FIDSLVLMPCXSLDI	715
DB	674	NTRVLVFRPVCLEPGLSYKCLKLTG-TGGRAHPETPYSGSGILIDSLVLQPHVLMDEM	732
QY	716	FTVGGSGDGEVNTSAWETFRYRCLENSRSVVKTPTMTDVCRNIIFSISALIHQTGLACEC	775
DB	733	F- - - SGGDAAALERRTTFERYRCHEEGLMPSKTPLEBACVPLLIASASSLVYNGALP	788
QY	776	DPQGSLSVCDPNGGQOCQRPVNVGRTCNRCAPGTFGFGPNGCKPCDCHLQGSASAFCD	835
DB	789	DPQGSLSSECNPHGGQCRCKPGVWVRRCDACATGYGFGPAGCQACQSPDGALSALCEG	848
QY	836	ITQCHCFQGIYARQCDRCLPGYWGFPSCQPCQCNHGHALDCDVTVTGECLSCQDYTTG	895
DB	849	TSGQCLCRTGAFGLRCDHCQRQGWGFPNCRPCVCNCGRADECAHTGACGLGCRDYG	908
QY	896	ERCLAGYGDPIIGSGDHCRCPCPDGPDSSGRQFARSQYQDPVTLQACVCDPGYISRC	955
DB	909	ERCIAGFHGDPRLPYGGQCRPCPCPEGGPSQRHFATSHRDGYSQQIVCHCRAGYTG	968
QY	956	DDCASGFFGNPSDFGSSQCPQCHHNIDTTPDPEACDKDTGRCLKLYHTEGDHQCQLQY	1015
DB	969	EACAPGHGDPSPKPGRCQLCECSGNIDPTDPGACDPHTGQCLRCLHHTEGPHCGHCK	1028
QY	1016	YGDALRQDCRCKVCNVLGTVKEHNGSD-CHCDKATGQCSCLPNVIGONCDRCAPNTW	1074
DB	1029	FHQAAARQSCHRCTNLLGTDPQRCPSTDLCHCDPSTGQCPCLPHVQGLSCDRCAPNFW	1088
QY	1075	LASGTGCGPCNCAHSPGSCNEFTGQCQCMPFGGRTCSCEQELFWGDDPDVECRACDC	1134
DB	1089	FTSGRCQPCACHPSRARGPTCNEFTGQCHCHAGFGGRTCSCEQELHWGDPGLQCRACDC	1148
QY	1135	DPRGIETPQCDQSTGQCVVEGVGPRCDKCTRGYSGVFPDCTPCHQCFALWDAIIGELT	1194
DB	1149	DPRGIDKPQCHRSTGHGSCRPVGVGRCDQCARGFSGVFPACHPCHACFGDWRVVQDLA	1208
QY	1195	NRTHKFLEKAKALKTSGVIGPYRETVDVSVEKKVNEIKDILA--QSPAAEPLKNIGILFEE	1252

Db	1209	ARTRLEQWAQELQOTGVLAGFESSFLNLQKLGVMQVAIVARPNTSAASTAK---	1264
QY	1253	AEKLTADV--TEKMAQVEVKLTDTASQSNSTAGELGALQAEAESLDKTVKELAEQLEFI	1309
Db	1265	TEGLRHEIGKTTERTLTQLEAELTDVQDENFNANHALSGLERDGLAINTLRLQDLQHLDIL	1324
QY	1310	KNSDIOGALDSITKYFQMSLEAEKRVNASATDNPSTVEQSALTRDRVEDLMLERESPFXE	1369
Db	1325	KHSNFTGAYDSIRHAHSQSTEAEERRANASTFAIPSPVNSADTRRRRAEVLMGQAORENFR	1384
QY	1370	QEEQARLLDELAKGLQSLDLSAAAQMTCGTPPGADCSESECGGPNCRITDEGEKKCGPG	1429
Db	1385	QHLANQOALGRLSTHTTSLTGVNELVCGAPDAPCATSPCGGACGRDEGQPRCGGLG	1444
QY	1430	CGGLTVVAHSAWQKAMDFDRDVLSSALAEVEQLSKMVSEAKVRADEAKQNAQDVLKTNAT	1489
Db	1445	CSGAAATADLALGRARHTQAELORALVEGGILSRVSETRRRQAEBAQORAALDKANAS	1504
QY	1490	KEKVDKSNEDLRNLIKQIRNFLTEDSADLDSIEAVANEVLKSGNASTPQOLQNLTEDIRE	1549
Db	1505	RGQVEQANQELRELIONVKDFLSQEGADPDSIEMVATRVLDISIPASPEQIQRLASEIAE	1564
QY	1550	RVETLSQVEVILQCSAADIAARAELLEEAKRASKSATDVKVTDVMVKEALEEAEKAQVAA	1609
Db	1565	RVRSLADVDTILAHTMGDVRRAEQLQDAQRARSRAEGERQKAEVTQAALEEAQRAQGAA	1624
QY	1610	EKAIKQADEDIQGTQNLTSIESETAASEETLTNASQRIKSLERNVEELKRKAAQNSGEA	1669
Db	1625	QGAIRGAVVDTKNTEQTLQQVQERNAGTEQSLNSASERARQLHALLEALKLKRAAGNSLAA	1684
QY	1670	EYIEKVYSVKQNADDVKKTLDGELDEKYYKVESLIAQKTESADARRKAEALLQNEAKTL	1729
Db	1685	STAETAGSAQSRAREAEKQLREQVGDQYQTVTRALAERKAEGLVLAQAQARAQELRDEARGL	1744
QY	1730	LAQANSKLQLEDLERKYEDNQYLEDKAQELVRLEGEVRSLLKDISSEKVAVYSTC	1785
Db	1745	LOAAQDKLORLOELEGTYEENERELEVKAAOLDGLLEARMSRVLOAINLQVQVYNTC	1800

RESULT 4

laminin beta-2 chain precursor (version 2) - human
 S53869
 N/Alternate names: s-laminin
 C/Species: Homo sapiens (man)
 C/Date: 27-Oct-1995 #sequence_revision 23-Feb-1996 #text_change 24-Sep-1998
 C/Accession: S53869
 R/Iivanainen, A.; Vuolteenaho, R.; Sainio, K.; Eddy, R.; Shows, T.B.; Sario
 M/Title: The human laminin beta-2 chain (S-laminin): structure, expression
 A/Reference number: S53869
 A/Accession: S53869
 A/Molecule type: mRNA
 A/Residues: 1-1798 <IIV>
 C/Genetics:
 A/Gene: GDB:LAMB2
 A/Cross-references: GDB:132363; OMIM:150325
 A/Map position: 3p21.3-3p21.2
 C/Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
 C/Keywords: basement membrane; extracellular matrix; glycoprotein; heterotrimeric
 F/1-32/Domain: signal sequence #status predicted <SIG>
 F/33-1798/Product: laminin beta-2 chain #status predicted <MAT>
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 F/470-519/Domain: laminin-type EGF-like homology <LE04>
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 F/877-924/Domain: laminin-type EGF-like homology <LE08>
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 F/986-1035/Domain: laminin-type EGF-like homology <LE10>
 F/1038-1092/Domain: laminin-type EGF-like homology <LE11>

F;1095-1140/Domain: laminin-type EGF-like homology <LE12>
F;1143-1187/Domain: laminin-type EGF-like homology <LE13>

Query Match 51.6%; Score 5033.5; DB 2; Length 1798;
Best Local Similarity 50.4%; Pred. No. 3.3e-186;
Matches 903; Conservative 313; Mismatches 556; Indels 19; Gaps 9;

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QY 1 MGLQVFAFGLWALWTRVCAQAEPEFSYGCAESCYPATCDLLIGRAQKLSVTSTCGLHK 60
D 20 LGLL---LSVLA--ATLAQAPADVP-GCSRGSCTPATGDLVVGADRLTASSTCGLNG 72
QY 61 PEPYCIIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVEN 120
D 73 POPYCIIVSHLQDEKKCFICDSRRPFSARDNPHSHRIQNVVTSFAPQORAAWQSENGIPA 132
QY 121 VTIQLDLEAEFHTHLIMTFKTRPAPAMLIERSDFGKTGWVYRYPAYDCSSFPGISGT 180
D 133 VTIQLDLEAEFHTHLIMTFKTRPAPAMLIERSDFGKTGWVYRYPAYDCSSFPGISGT 192
QY 181 PMKKVDDIIICDSRYSDIEPSTEGEVIIFRALDPAPKIEDPYSPRIQNLKITNLRIKFVKL 240
D 193 PPRHWDVVCESEYSEIEPSTEGEVIYRVDPAIPDPYSSRIQNLKITNLRLNTRL 252
QY 241 HTLGNLLDSRMEIREKYYAVYDMVVRGNCFYGHASECAPVDGVNEVEGMVHGCMC 300
D 253 HTLGNLLDPRREIREKYYALVELVVRGNCFYGHASECAPAPGAHAEGMVHGCACIC 312
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D 313 KHNTKGLNCELMDYFHDLPWRPAEGRNSNACKKCNHSSSCHFDMAVFLATGNVSGG 372
QY 361 VCDNCOHNTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVG 420
D 373 VCDGCOHNTAGRHCELCPFFYRDPDKLDRDPAVCRSCDCDPMGSDGGRCDSHDDPALG 432
QY 421 LIAGQCRCKLHVEGERCDVCKEFGYDLSAEDPYGCKSCACNPLGTIPGNGNPDSETGYCY 480
D 433 LVSGQCRCKEHVGTGRCQQCRGFFGLSISDRLGCRRCQCNARGTVPGSTPCDPSNGSCY 492
QY 481 CKRLVTGQRCDQCLPOHWGLSNDLDGCRPCDCLGGLNNSCEDSGQSCCLPHMIGRQC 540
D 493 CKRLVTGRCDCRLPGHWGLSHLLGCRPCDCLVGGALDPQCDEGTGQCHCRQHVGRRC 552
QY 541 NEVESGYFTTLDHYIYEAEANLPGVWVVERQYIQDRIPSWTGPFGFVRVPEGAYLEFF 600
D 553 EQVQPGYFRPFLDHLIWEAEDTR-GQVLDVVERLVTPGTPTSWTSGSFVRLQEGQTLFL 611
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QY 717 TVGGSGDGEVTNSAWETPQRYRCLENSRSVVKTPMTDVCNIIIFSISALIHQTGLACECD 776
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D 847 SGQCLCRTGAFGLRCDRCQRGQWGFPSRCPCVNCNGHADECNTHTGACGLCRDHTGHEHCE 906
QY 897 RCLAGYGDPIIGSDHCRPCPCPDGDSGRQFARSCYQDPVTLQLACVCDPGYIGSRCD 956
D 907 RCIAGFHGDPRLPYGGQCRPCPCPEGSGQRHFATSCHQDEYSQQIVCHCRAGYTLGRCE 966
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QY 1196 RTHKFLEKAKALKISGVIQPYRETVDVSVEKKVNEIKDIL-AQSPAAEPLKNIGILFEEAE 1254
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D 1267 REICEATEHLTQLEADLTVDQDENFNANHALSGLERDLALNLTLRQLDQHLDKHSNF 1326
QY 1315 QGALDSITKYFQMSLEAEKRVNASTTDPNSTVEQSGALTRDRVEDLMLERESPKEQEEQ 1374
D 1327 LGAYDSIRHAHSQSAEAEERRANTSALAVSPVSNASARHRTALMDAQEKEDNSKHWAN 1386
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D 1687 TAGSAQGRAQAEAEQLLRGFLGQYQTVKALAEKAAQGVLAQAQAEQLRDEARDLQAAQ 1746
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RESULT 5

A55677
laminin beta-2 chain precursor (version 1) - human
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 17-Mar-1999
C;Accession: A55677
R;Wewer, U.M.; Gerecke, D.R.; Durkin, M.E.; Kurtz, K.S.; Mattei, M.G.; Champliand, M.F.;
Genomics 24, 243-252, 1994
A;Title: Human beta2 chain of laminin (formerly S chain): cDNA cloning, chromosomal loca-
A;Reference number: A55677; MUID:95213013; PMID:7698745
A;Accession: A55677
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1797 <WEW>
A;Cross-references: GB:X79683
C;Genetics:
A;Gene: GDB:LAMB2
A;Cross-references: GDB:132363; OMIM:150325

OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:58 ; Search time 16.4366 Seconds
(without alignments)
10452.141 Million cell updates/sec

Title: US-10-037-182-6
Perfect score: 9754
Sequence: 1 MGLIQLLAFLALCRARV.....EVRSLIKDISQKVAVYSTCL 1786

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: Pirl:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	9754	100.0	1786	1 MMHUB1	laminin beta-1 cha
2	9144	93.7	1786	1 MMMSB1	laminin beta-1 cha
3	5088.5	52.2	1801	1 MMRTS	laminin beta-2 cha
4	5054.5	51.8	1798	2 S53869	laminin beta-2 cha
5	4888	50.1	1797	2 A55677	laminin beta-2 cha
6	3846	39.4	1790	1 MMFFB1	laminin beta-1 cha
7	3772.5	38.7	1808	2 T15099	hypothetical prote
8	1758.5	18.0	1639	1 MMFFB2	laminin gamma-1 ch
9	1729.5	17.7	3672	2 T23433	hypothetical prote
10	1729.5	17.7	3704	2 T37316	probable laminin a
11	1696.5	17.4	1557	2 T28811	hypothetical prote
12	1676.5	17.2	1609	1 MMHUB2	laminin gamma-1 ch
13	1658	17.0	1607	1 MMMSB2	laminin gamma-1 ch
14	1645.5	16.9	3712	2 S18253	laminin alpha-1 ch
15	1605	16.5	3635	2 T10053	laminin alpha 5 ch
16	1583	16.2	303	2 B45067	laminin B1 chain -
17	1543.5	15.8	1170	2 A53612	laminin B1k chain
18	1539	15.8	3106	1 S53868	laminin alpha-2 ch
19	1529.5	15.7	3075	2 S14458	laminin alpha-1 ch
20	1510	15.5	3084	1 MMMSA	laminin alpha-1 ch
21	1485.5	15.2	1168	2 I56985	kalinin B1 - mouse
22	1307.5	13.4	2823	2 T23064	hypothetical prote
23	1307.5	13.4	2823	2 F87908	protein T22A3.8 li
24	1307.5	13.4	3102	2 T43291	laminin alpha chai
25	1001.5	10.3	616	2 I38231	S-laminin - human
26	871	8.9	1193	2 A44018	laminin B2t chain
27	862.5	8.8	1192	2 S69000	laminin gamma 2 ch
28	692	7.1	606	2 A54665	netrin-1 precursor
29	679	7.0	1620	2 T27283	hypothetical prote

30	669.5	6.9	1574	2 T13954	MEGF6 protein - ra
31	666	6.8	3707	2 S18252	heparan sulfate pr
32	663.5	6.8	1111	2 T26972	hypothetical prote
33	657	6.7	4391	2 A38096	perlecan precursor
34	608	6.2	581	2 B54665	netrin-2 precursor
35	580.5	6.0	1816	1 S68960	laminin alpha-4 ch
36	579	5.9	612	2 JH0799	laminin-related pr
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39	527	5.4	2555	2 A40043	notch protein homo
40	526	5.4	2295	2 C88369	protein unc-52 [im
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44	509	5.2	2524	2 A35844	notch protein - Af
45	506.5	5.2	2703	1 A24420	notch protein - fr

ALIGNMENTS

RESULT 1

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laminin beta-1 chain precursor - human
N;Alternate names: laminin chain B1
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text_change 19-Jan-2001
C;Accession: S13547; A28483; A26994; S23566
R;Vuolteenaho, R.; Chow, L.T.; Tryggvason, K.
J. Biol. Chem. 265, 15611-15616, 1990
A;Title: Structure of the human laminin B1 chain gene.
A;Reference number: S13547; MUID:90368768; PMID:1975589
A;Accession: S13547
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1786 <VUO>
A;Cross-references: GB:M61951; GB:J02778; NID:gl86911; PIDN:AAA59486.1; PID:gl86913
A;Note: the nucleotide sequence was submitted to GenBank, February 1991
R;Pikkarainen, T.; Eddy, R.; Fukushima, Y.; Byers, M.; Shows, T.; Pihlajaniemi, T.; Sarz
J. Biol. Chem. 262, 10454-10462, 1987
A;Title: Human laminin B1 chain. A multidomain protein with gene (LAMB1) locus in the q2
A;Reference number: A28483; MUID:87280097; PMID:3611077
A;Accession: A28483
A;Molecule type: mRNA
A;Residues: 1-1786 <PIK>
A;Cross-references: GB:M61951; GB:J02778; NID:gl86911; PIDN:AAA59486.1; PID:gl86913
R;Jaye, M.; Modi, W.S.; Ricca, G.A.; Mudd, R.; Chiu, I.M.; O'Brien, S.J.; Drohan, W.N.
Am. J. Hum. Genet. 41, 605-615, 1987
A;Title: Isolation of a cDNA clone for the human laminin-B1 chain and its gene localizat
A;Reference number: A26994; MUID:88021029; PMID:3661559
A;Accession: A26994
A;Molecule type: mRNA
A;Residues: 1276-1469, 'V', 1471-1695, 'G', 1697-1709 <JAY>
A;Cross-references: EMBL:M20206; NID:gl86914; PIDN:AAAS9487.1; PID:gl86915
R;Vuolteenaho, R.; Kallunki, T.; Chow, L.; Ikonen, J.; Pikkarainen, T.; Tryggvason, K.
in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp. 175-193, Academic P
A;Title: Genes for the human laminin B1 and B2 chains.
A;Reference number: S23566
A;Accession: S23566
A;Molecule type: DNA
A;Residues: 762-1786 <VU2>
C;Genetics:
A;Gene: GDB:LAMB1
A;Cross-references: GDB:119357; OMIM:150240
A;Map position: 7q31.1-7q31.3
A;Introns: 13/1; 71/3; 117/1; 141/3; 204/3; 226/1; 293/3; 334/1; 397/1; 457/1; 494/3; 52
64/3; 1513/1; 1582/2; 1629/3; 1688/3; 1742/1
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C;Function:
A;Description: interact with cells and with other basement membrane proteins to promote
C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular

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F;398-455/Domain: laminin-type EGF-like homology <LE03>			
F;458-507/Domain: laminin-type EGF-like homology <LE04>			
F;463-468/Region: cell adhesion #status predicted			
F;510-540/Domain: laminin-type EGF-like homology #status atypical <LE05>			
F;549-774/Domain: IV <DOM4>			
F;662-668/Region: cell adhesion #status predicted			
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F;775-1178/Domain: III <DOM3>			
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F;867-914/Domain: laminin-type EGF-like homology <LE08>			
F;917-973/Domain: laminin-type EGF-like homology <LE09>			
F;923-927/Region: cell adhesion #status predicted			
F;950-954/Region: cell adhesion #status predicted			
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F;1028-1081/Domain: laminin-type EGF-like homology <LE11>			
F;1084-1129/Domain: laminin-type EGF-like homology <LE12>			
F;1132-1176/Domain: laminin-type EGF-like homology <LE13>			
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F;1398-1430/Domain: alpha <ALP>			
F;1431-1786/Domain: I <DOM1>			
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QY	181	PMKKVDDIICDSRYSIDIEPSTEGEVIFRALDPAFKIEDPYPSPRIQNLKITNLRKFVKL	240
Db	181	PMKKVDDIICDSRYSIDIEPSTEGEVIFRALDPAFKIEDPYPSPRIQNLKITNLRKFVKL	240
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QY	361	VCDDCOHNTMGRNCEQCKPFYYQHPERDIRDNPFCERCTCDPAGSQNEGICDSYTDFTG	420
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Db	601	IDNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPRTSSRCGNTIPDDNQVWSLSPG	660
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Db	661	SRVWVLPVPCFEKGTNYTVRLELPQYTSDDSDVESPYTLIDSLVLMPYCKSLDIFTVGG	720
QY	721	SGDGWVTNSAWETFORYRCLENSRSVVKTMTDVCVCRNIIFSISALLHQTGLACECDPQGS	780
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QY	841	HCFQGVYARQCDCRLPGHWGFPSPCQPCQCNHADDCCDPVTGECINLCODYTMGHNCERCLA	900
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QY	901	GYGDPPIIGSGDHCRPCPCPDGPDGDSGRQFARSCYQDPVTIQLACVCDPGYIGSRCDDCAS	960
Db	901	GYGDPPIIGSGDHCRPCPCPDGPDGDSGRQFARSCYQDPVTIQLACVCDPGYIGSRCDDCAS	960
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Db	961	GYFGNPSEVGGSCQPCQCHNNIDTTDPEACDKETGRCLKCLYHTEGHCQFCRFGYYGDA	1020
QY	1021	LRQDCRKVCVNYLGTIVQEHCHNGSDCCQDKATGQCCLCLPNVIGQNCDCRCAPNTWQLASGTG	1080
Db	1021	LRQDCRKVCVNYLGTIVQEHCHNGSDCCQDKATGQCCLCLPNVIGQNCDCRCAPNTWQLASGTG	1080
QY	1081	CDPCNCNAHSGFSGSCNEFTGQCQCMPGFGGRTCSQCQELFWGDDPVECRACDCDPRGIE	1140
Db	1081	CDPCNCNAHSGFSGSCNEFTGQCQCMPGFGGRTCSQCQELFWGDDPVECRACDCDPRGIE	1140
QY	1141	TPQCDQSTGQCVCVEGVEGPRCDKCTRGVSGVFPDCTPCHQCQFALWDVIIAELTNRTHRF	1200
Db	1141	TPQCDQSTGQCVCVEGVEGPRCDKCTRGVSGVFPDCTPCHQCQFALWDVIIAELTNRTHRF	1200
QY	1201	LEKAKALKISGVIGPYRETVDSEVERKVSEIKDILAQSPAAEPLKNIGNLFEAEKLIKDV	1260
Db	1201	LEKAKALKISGVIGPYRETVDSEVERKVSEIKDILAQSPAAEPLKNIGNLFEAEKLIKDV	1260
QY	1261	TEMMAQVEVKLSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDS	1320
Db	1261	TEMMAQVEVKLSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDS	1320
QY	1321	ITKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVMMERESQFKEKQEEQARLLDE	1380
Db	1321	ITKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVMMERESQFKEKQEEQARLLDE	1380
QY	1381	LAGKLQSLDLSAAAEAMTCGTPPGASCSETGCGGPNCRCTDEGERKCGGPGCGGLVTVAHNA	1440
Db	1381	LAGKLQSLDLSAAAEAMTCGTPPGASCSETGCGGPNCRCTDEGERKCGGPGCGGLVTVAHNA	1440
QY	1441	WQKAMDLDQDVLALAEVEQLSKMVSEAKLRADEAKQSAEDILLKTNAKTKMKDKSNEEL	1500
Db	1441	WQKAMDLDQDVLALAEVEQLSKMVSEAKLRADEAKQSAEDILLKTNAKTKMKDKSNEEL	1500
QY	1501	RNLIKQIRNFLTQDSADLDSIEAVANEVLKMEPSTPQQLQNLNLTEDIRERVESLSQVEVI	1560
Db	1501	RNLIKQIRNFLTQDSADLDSIEAVANEVLKMEPSTPQQLQNLNLTEDIRERVESLSQVEVI	1560
QY	1561	LQHSAAADIARAEMLLEAKRASKSATDVKVTDVMVKEALEEAEAKAQVAEAKAIKQADEDI	1620
Db	1561	LQHSAAADIARAEMLLEAKRASKSATDVKVTDVMVKEALEEAEAKAQVAEAKAIKQADEDI	1620
QY	1621	QGTQNLITTSIESETAAASEETLFNASQRISIELERNVEELKRKAAQNSGEAEYIEKVYTVK	1680
Db	1621	QGTQNLITTSIESETAAASEETLFNASQRISIELERNVEELKRKAAQNSGEAEYIEKVYTVK	1680

Db 1621 QGTQNLLTSIESETAASEETLFNASQRISELERNVBELKRKAAQNSGEAEYIEKVYTVK 1680

Qy 1681 QSAEDVKKTLDCGELDEKYKKVENLIAKKTESADARRKAEMLQNEAKTLLAQANSKIQLL 1740

Db 1681 QSAEDVKKTLDCGELDEKYKKVENLIAKKTESADARRKAEMLQNEAKTLLAQANSKIQLL 1740

Qy 1741 KDLERKYEDNQRYLEDKAQELARLEGEVRSLLKDISQKVAVYSTCL 1786

Db 1741 KDLERKYEDNQRYLEDKAQELARLEGEVRSLLKDISQKVAVYSTCL 1786

RESULT 2

MMMSB1

laminin beta-1 chain precursor - mouse

N;Alternate names: laminin chain B1

C;Species: Mus musculus (house mouse)

C;Date: 28-Feb-1986 #sequence revision 30-Jun-1991 #text change 10-Dec-1999

C;Accession: A26413; S02679; S05326; S14877; A02871; S02036; S13543

R;Sasaki, M.; Kato, S.; Kohn, K.; Martin, G.R.; Yamada, Y.

Proc Natl. Acad. Sci. U.S.A. 84, 935-939, 1987

A;Title: Sequence of the cDNA encoding the laminin B1 chain reveals a multidomain protein

A;Reference number: A26413; MUID:87147212; PMID:3493487

A;Accession: A26413

A;Molecule type: mRNA

A;Residues: 1-1786 <SAS>

A;Cross-references: EMBL:M15525; NID:G198700

A;Note: translation in GenBank has additional 48 residues at the amino end

R;Fujiwara, S.; Shinkai, H.; Deutzmann, R.; Paulsson, M.; Timpl, R.

Biochem. J. 252, 453-461, 1988

A;Title: Structure and distribution of N-linked oligosaccharide chains on various domain

A;Reference number: S02678; MUID:88326259; PMID:2458101

A;Accession: S02679

A;Molecule type: protein

A;Residues: 28-42;932-946 <FUJ>

R;Hartl, L.; Oberbaeumer, I.; Deutzmann, R.

Eur. J. Biochem. 173, 629-635, 1988

A;Title: The N terminus of laminin A chain is homologous to the B chains.

A;Reference number: S00624; MUID:88225080; PMID:3267223

A;Accession: S05326

A;Molecule type: protein

A;Residues: 457-466;854-868;932-946 <HAR>

R;Mann, K.; Deutzmann, R.; Timpl, R.

Eur. J. Biochem. 178, 71-80, 1988

A;Title: Characterization of proteolytic fragments of the laminin-nidogen complex and th

A;Reference number: S08895; MUID:89078415; PMID:2462498

A;Accession: S14877

A;Molecule type: protein

A;Residues: 590-620 <MAN>

R;Barlow, D.P.; Green, N.M.; Kurkinen, M.; Hogan, B.L.M.

EMBO J. 3, 2355-2362, 1984

A;Title: Sequencing of laminin B chain cDNAs reveals C-terminal regions of coiled-coil a

A;Reference number: A02870; MUID:85051302; PMID:6209134

A;Accession: A02871

A;Molecule type: mRNA

A;Residues: 1292-1530, 'MEMP', 1535-1691, 'C', 1693-1748, 'N', 1750-1786 <BAR>

A;Cross-references: EMBL:X05212; NID:G52861; PIDN:CAA28839.1; PID:G809042

R;Deutzmann, R.; Huber, J.; Schmetz, K.A.; Oberbaeumer, I.; Hartl, L.

Eur. J. Biochem. 177, 35-45, 1988

A;Title: Structural study of long arm fragments of laminin. Evidence for repetitive C-te

A;Reference number: S01790; MUID:89030693; PMID:3181157

A;Accession: S02036

A;Molecule type: protein

A;Residues: 1561-1587 <DEU>

R;Paulsson, M.; Deutzmann, R.; Timpl, R.; Dalzoppo, D.; Odermatt, E.; Engel, J.

EMBO J. 4, 309-316, 1985

A;Title: Evidence for coiled-coil alpha-helical regions in the long arm of laminin.

A;Reference number: S13543; MUID:85257455; PMID:3848400

A;Accession: S13543

A;Molecule type: protein

A;Residues: 1700-1748, 'N', 1750-1759 <PAU>

C;Genetics:

A;Gene: Lamb-1

A;Map position: 12

C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin

C;Function:

A;Description: interact with cells and with other basement membrane proteins to promote

C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology

C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-1786/Product: laminin beta-1 chain #status predicted <MAT>

F;22-270/Domain: VI <DOM6>

F;271-540/Domain: V <DOM5>

F;271-332/Domain: laminin-type EGF-like homology <LE01>

F;335-395/Domain: laminin-type EGF-like homology <LE02>

F;398-455/Domain: laminin-type EGF-like homology <LE03>

F;458-507/Domain: laminin-type EGF-like homology <LE04>

F;510-540/Domain: laminin-type EGF-like homology #status atypical <LE05>

F;541-772/Domain: IV <DOM4>

F;773-1182/Domain: III <DOM3>

F;773-818/Domain: laminin-type EGF-like homology <LE06>

F;821-864/Domain: laminin-type EGF-like homology <LE07>

F;867-914/Domain: laminin-type EGF-like homology <LE08>

F;917-973/Domain: laminin-type EGF-like homology <LE09>

F;976-1025/Domain: laminin-type EGF-like homology <LE10>

F;1028-1081/Domain: laminin-type EGF-like homology <LE11>

F;1084-1129/Domain: laminin-type EGF-like homology <LE12>

F;1132-1176/Domain: laminin-type EGF-like homology <LE13>

F;1183-1397/Domain: II <DOM2>

F;1183-1397/Region: heptad repeats

F;1398-1430/Domain: alpha <ALP>

F;1431-1786/Region: heptad repeats

F;1431-1786/Domain: I <DOM1>

F;22/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted

F;30-35/Disulfide bonds: #status predicted

F;120,356,519,677,1041,1195,1279,1336,1343,1487,1533,1542,1643/Binding site: carbohydrat

F;1179,1182,1785/disulfide bonds: interchain #status predicted

Query Match 93.7%; Score 9144; DB 1; Length 1786;

Best Local Similarity 92.7%; Pred. No. 0;

Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;

Qy 1 MGLQLLAFSLALCRARVRAQEPESYCAEGSCYPATGDLIGRAQLSVTSCGLHK 60

Db 1 MGLQVFAFGVLALWGTRVCAQEPESYCAEGSCYPATGDLIGRAQLSVTSCGLHK 60

Qy 61 PEPYCIVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVVTTFAPNRLKIWQSENGVEN 120

Db 61 PEPYCIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVVTTFAPNRLKIWQSENGVEN 120

Qy 121 VTIQDLEAEFFHFTLIMTFKTRPAAMLIERSDPGKTGWYRYFAYDCEASFPFGISTG 180

Db 121 VTIQDLEAEFFHFTLIMTFKTRPAAMLIERSDPGKTGWYRYFAYDCEASFPFGISTG 180

Qy 181 PMKKVDDIICDSRYSDIESTEGEVI FRALDPAFKIEDPYPSPRIQNLLKIINRIKFVKL 240

Db 181 PMKKVDDIICDSRYSDIESTEGEVI FRALDPAFKIEDPYPSPRIQNLLKIINRIKFVKL 240

Qy 241 HTLGDNLDSRMEIREKYVYAVYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGCHMC 300

Db 241 HTLGDNLDSRMEIREKYVYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCHMC 300

Qy 301 RHNTKGLNCEL CMDFYHDL PWRPAEGRNSNACKKCNCHSISCHFDMAVYLATGNVSGG 360

Db 301 RHNTKGLNCEL CMDFYHDL PWRPAEGRNSNACKKCNCHSISCHFDMAVYLATGNVSGG 360

Qy 361 VCDDCQHTMGRNCEQCKPFPYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSTG 420

Db 361 VCDNCQHTMGRNCEQCKPFPYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVG 420

Qy 421 LIAGQCRCKLNVEGEHCDVCKEGFYDLSSDPFGCKSCACNPLGTIPGGNPCDSETHCY 480

Db 421 LIAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGGNPCDSETHCY 480

Qy 481 CKRLVTGQHCDQCLPEHFWGLSNDLDGCRPCDCLGGALNNSCFAESGCSCRPHMIGRQC 540

Db 481 CKRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCLGGALNNSCSEDSGCSCSLPHMIGRQC 540

QY 541 NEVEGYPATLDHYLYEAEANLGPVSIIVERQYIQDRIPSWTGAQFVRVPEGAYLEFF 600
Db 541 NEVEGYPATLDHYLYEAEANLGPVSIIVERQYIQDRIPSWTGAQFVRVPEGAYLEFF 600
QY 601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPRTSSRCNGTIPDDDNQVVSISPG 660
Db 601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPRTSSRCNGTIPDDDNQVVSISPG 660
QY 661 SRYVVLPRPVCFEKGNTYVRLELPOYTSSDSDVESPYTLLDLSLVLMPCYCKSLDIFTVGG 720
Db 661 SRYVVLPRPVCFEKGNTYVRLELPOYTSSDSDVESPYTLLDLSLVLMPCYCKSLDIFTVGG 720
QY 721 SGDGVTNSAWETFORYRCLNSRSVVKTPTMTDVCNIIIFSISALLHQTGLACECDPOGS 780
Db 721 SGDGVTNSAWETFORYRCLNSRSVVKTPTMTDVCNIIIFSISALLHQTGLACECDPOGS 780
QY 781 LSSVCDPNNGGQCCRPNNVGRITCNRCAPGTGFGPSGCKPCECHLQGSVNAFCNPVTGQC 840
Db 781 LSSVCDPNNGGQCCRPNNVGRITCNRCAPGTGFGPSGCKPCECHLQGSVNAFCNPVTGQC 840
QY 841 HCFQGVYARQCRLPGHWGFPSCQPCQNGHADDPCDPTVTEGCLNCODYTMGHNCERCLA 900
Db 841 HCFQGVYARQCRLPGHWGFPSCQPCQNGHADDPCDPTVTEGCLNCODYTMGHNCERCLA 900
QY 901 GYGDPIIGSGDHCRPCPCPDGSDSGRQFARSCYQDPVTTLQACVCDPGYIGSRCDDCAS 960
Db 901 GYGDPIIGSGDHCRPCPCPDGSDSGRQFARSCYQDPVTTLQACVCDPGYIGSRCDDCAS 960
QY 961 GYFNGPSEVGSQCPCQCHNNIDTTDPEACDKETGRCLKCLYHTEGEHCQFCRFGYIGDA 1020
Db 961 GYFNGPSEVGSQCPCQCHNNIDTTDPEACDKETGRCLKCLYHTEGEHCQFCRFGYIGDA 1020
QY 1021 LRQDCRKVCNVLGTVQEHCHNGSDCQCKATGQCLCLPNVIGQNCDCRCAPNTWQLASGTG 1080
Db 1021 LRQDCRKVCNVLGTVQEHCHNGSDCQCKATGQCLCLPNVIGQNCDCRCAPNTWQLASGTG 1080
QY 1081 CDPNCNAAHSFGPSCNEFTGQCQMPGFGRTCECQELFWGDPDVECRACDCDPRGIE 1140
Db 1081 CDPNCNAAHSFGPSCNEFTGQCQMPGFGRTCECQELFWGDPDVECRACDCDPRGIE 1140
QY 1141 TPQCDQSTGQCVVEGVGPRCDKCTRGVSGVFPDCTPCHQCFALWDVIIAELTNRTHRF 1200
Db 1141 TPQCDQSTGQCVVEGVGPRCDKCTRGVSGVFPDCTPCHQCFALWDVIIAELTNRTHRF 1200
QY 1201 LEKAKALKISGVIGPYRETVDVSVERKVSSEIKDILAQSPAAPLKNIGNLFEEAEKLIKDV 1260
Db 1201 LEKAKALKISGVIGPYRETVDVSVERKVSSEIKDILAQSPAAPLKNIGNLFEEAEKLIKDV 1260
QY 1261 TEMMAQVEVKLSDTTSQSNSTAKELDSLQTEABESLDNTVKELAEQLEFIKNSDIRGALDS 1320
Db 1261 TEMMAQVEVKLSDTTSQSNSTAKELDSLQTEABESLDNTVKELAEQLEFIKNSDIRGALDS 1320
QY 1321 ITKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVMMERESOPKEKQBEQARLLDE 1380
Db 1321 ITKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVMMERESOPKEKQBEQARLLDE 1380
QY 1381 LAGKLOSLDLASAAEMTCGTPPGASCSETECGGPNCRCTDEGERKCGGPGCGGLVTVAHNA 1440
Db 1381 LAGKLOSLDLASAAEMTCGTPPGASCSETECGGPNCRCTDEGERKCGGPGCGGLVTVAHNA 1440
QY 1441 WQKAMDLDQDVLASAEVEQLSKMWSEAKLRADBAKQSAEDILLKTNATKEKMDKSNEEL 1500
Db 1441 WQKAMDLDQDVLASAEVEQLSKMWSEAKLRADBAKQSAEDILLKTNATKEKMDKSNEEL 1500
QY 1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKMEPSTPQOLQNLTEDIRERVESLSQVEVI 1560
Db 1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKMEPSTPQOLQNLTEDIRERVESLSQVEVI 1560
QY 1561 LQHSAAADIARAEMLLLEAKRASKSATDVKVTADVMYKEALEEAEAKAQAQADEDI 1620
Db 1561 LQHSAAADIARAEMLLLEAKRASKSATDVKVTADVMYKEALEEAEAKAQAQADEDI 1620

QY 1621 QGTQNLTSIESETAASEETLFNASQRISELERNVEELKRKAQNSGEAEYIEKVVTYVK 1680
Db 1621 QGTQNLTSIESETAASEETLFNASQRISELERNVEELKRKAQNSGEAEYIEKVVTYVK 1680
QY 1681 QSAEDVKKTLDDGELDEKYYKKVENLIATKKTESADARRKAEMLQNEAKTLLAQANSKLQLL 1740
Db 1681 QNADDDVKKTLDDGELDEKYYKKVESLIAQKTESADARRKAELQNEAKTLLAQANSKLQLL 1740
QY 1741 KDLERKYEDNQRYLEDKAQELARLEGEVRSLLKDISOQKAVYSTCL 1786
Db 1741 EDLERKYEDNQRYLEDKAQELARLEGEVRSLLKDISOQKAVYSTCL 1786
RESULT 3
MMRTS
laminin beta-2 chain precursor - rat
N;Alternate names: laminin chain B3; S-laminin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 10-Dec-1999
C;Accession: S03539
R;Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.
Nature 338, 229-234, 1989
A;Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the neur
A;Reference number: S03539; MUID:89159410; PMID:2922051
A;Accession: S03539
A;Molecule type: mRNA
A;Residues: 1-1801 <HUN>
A;Cross-references: EMBL:X16563; NID:G57250; PIDN:CAA34561.1; PID:G57251
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C;Function:
A;Description: interact with cells and with other basement membrane proteins to promote
C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular
F;1-35/Domain: signal sequence #status predicted <SIG>
F;36-1801/Product: laminin beta-2 chain #status predicted <MAT>
F;36-285/Domain: VI <DOM5>
F;286-555/Domain: V <DOM5>
F;286-347/Domain: laminin-type EGF-like homology <LE01>
F;350-410/Domain: laminin-type EGF-like homology <LE02>
F;413-470/Domain: laminin-type EGF-like homology <LE03>
F;473-522/Domain: laminin-type EGF-like homology <LE04>
F;525-555/Domain: laminin-type EGF-like homology #status atypical <LE05>
F;556-784/Domain: IV <DOM4>
F;786-831/Domain: laminin-type EGF-like homology <LE06>
F;788-1196/Domain: III <DOM3>
F;834-877/Domain: laminin-type EGF-like homology <LE07>
F;880-927/Domain: laminin-type EGF-like homology <LE08>
F;930-986/Domain: laminin-type EGF-like homology <LE09>
F;989-1038/Domain: laminin-type EGF-like homology <LE10>
F;1041-1095/Domain: laminin-type EGF-like homology <LE11>
F;1098-1143/Domain: laminin-type EGF-like homology <LE12>
F;1146-1190/Domain: laminin-type EGF-like homology <LE13>
F;1197-1412/Domain: II <DOM2>
F;1197-1412/Region: heptad repeats
F;1413-1445/Domain: alpha <ALP>
F;1446-1801/Region: heptad repeats
F;1446-1801/Domain: I <DOM1>
F;45-50/Disulfide bonds: #status predicted
F;251,371,1088,1252,1311,1351,1502/Binding site: carbohydrate (Asn) (covalent) #status p
F;1193,1196,1800/Disulfide bonds: interchain #status predicted

Query Match 52.2%; Score 5088.5; DB 1; Length 1801;
Best Local Similarity 51.2%; Pred. No. 3.3e-186;
Matches 916; Conservative 303; Mismatches 550; Indels 21; Gaps 9;
QY 7 LAFSFLALCRARVRAQEPESY-GCAEGSCYPATGDLIGRAQLSVTSTCGLHKPEPYC 65
Db 21 LRLGLLLSVLAATLAQVPSLDVPGCSRGSCYPATGDLVGRADRLTASSTCGLHSPQPYC 80
QY 66 IVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVTTFAPNRLKIWNQSENGVENVTIQL 125
Db 81 IVSHLQDEKKCFCLDSRRPFSARDNPNSHRIQNVTTSFAPQRRTAWQSENGVPMVTIQL 140

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:26:08 ; Search time 10.1546 Seconds
(without alignments)
9158.169 Million cell updates/sec

Title: US-10-037-182-6
Perfect score: 9754
Sequence: 1 MGLQLLAFSLACRVR.....EVRLLKDISQKAVYSTCL 1786

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9754	100.0	1786	1 LMB1_HUMAN	P07942 homo sapien
2	9144	93.7	1786	1 LMB1_MOUSE	P02469 mus musculu
3	5088.5	52.2	1801	1 LMB2_RAT	P15800 rattus norv
4	5052.5	51.8	1798	1 LMB2_HUMAN	P55268 homo sapien
5	5051.5	51.8	1799	1 LMB2_MOUSE	Q61292 mus musculu
6	3846	39.4	1790	1 LMB1_DROME	P11046 drosophila
7	1762.5	18.1	1639	1 LMG1_DROME	P15215 drosophila
8	1729.5	17.7	3672	1 LML2_CAEEL	Q21313 caenorhabdi
9	1696.5	17.4	1535	1 LML1_CAEEL	Q18823 caenorhabdi
10	1676.5	17.2	1609	1 LMG1_HUMAN	P11047 homo sapien
11	1658	17.0	1607	1 LMG1_MOUSE	P02468 mus musculu
12	1645.5	16.9	3712	1 LMA_DROME	Q00174 drosophila
13	1617	16.6	3718	1 LMA5_MOUSE	Q61001 mus musculu
14	1583	16.2	303	1 LMB1_CHICK	Q01635 gallus gall
15	1569.5	16.1	3695	1 LMA5_HUMAN	O15230 homo sapien
16	1566	16.1	3110	1 LMA2_HUMAN	P24043 homo sapien
17	1559	16.0	1581	1 LMG3_MOUSE	Q910b6 mus musculu
18	1557.5	16.0	1172	1 LMB3_HUMAN	Q13751 homo sapien
19	1539	15.8	3106	1 LMA2_MOUSE	Q60675 mus musculu
20	1529.5	15.7	3075	1 LMA1_HUMAN	P25391 homo sapien
21	1515.5	15.5	1587	1 LMG3_HUMAN	Q9Y6n6 homo sapien
22	1510	15.5	3084	1 LMA1_MOUSE	P19137 mus musculu
23	1483.5	15.2	1168	1 LMB3_MOUSE	Q61087 mus musculu
24	1372	14.1	3333	1 LMA3_MOUSE	Q61789 mus musculu
25	891	9.1	1191	1 LMG2_MOUSE	Q61092 mus musculu
26	873	9.0	1193	1 LMG2_HUMAN	Q13753 homo sapien
27	695.5	7.1	604	1 NET1_HUMAN	O95631 homo sapien
28	695.5	7.1	604	1 NET1_MOUSE	O09118 mus musculu
29	692	7.1	606	1 NET1_CHICK	Q90922 gallus gall
30	666	6.8	3707	1 PGBM_MOUSE	Q05793 mus musculu
31	657	6.7	4391	1 PGBM_HUMAN	P98160 homo sapien
32	608	6.2	581	1 NET2_CHICK	Q90923 gallus gall
33	582.5	6.0	1816	1 LMA4_HUMAN	Q16363 homo sapien

34	579	5.9	612	1 UNC6_CAEEL	P34710 caenorhabdi
35	576.5	5.9	1816	1 LMA4_MOUSE	P97927 mus musculu
36	557.5	5.7	727	1 NETA_DROME	Q24567 drosophila
37	541	5.5	400	1 LMB_HIRME	Q25092 hirudo medi
38	526	5.4	3375	1 UNS2_CAEEL	Q06561 caenorhabdi
39	524.5	5.4	2556	1 NTC1_HUMAN	P46531 homo sapien
40	518.5	5.3	2524	1 NOTC_XENLA	P21783 xenopus lae
41	515.5	5.3	2319	1 NTC3_RAT	Q9r172 rattus norv
42	511	5.2	198	1 LMBV_CHICK	Q01636 gallus gall
43	506.5	5.2	2703	1 NOTC_DROME	P07207 drosophila
44	506	5.2	2531	1 NTC1_MOUSE	Q01705 mus musculu
45	505.5	5.2	2437	1 NTC1_BRARE	P46530 brachydanio

ALIGNMENTS

RESULT 1
LMB1_HUMAN
ID LMB1_HUMAN STANDARD; PRT; 1786 AA.
AC P07942;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Laminin beta-1 chain precursor (Laminin B1 chain).
GN LAMB1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90368768; PubMed=1975589;
RA Vuolteenaho R., Chow L.T., Tryggvason K.;
RT "Structure of the human laminin B1 chain gene."
RL J. Biol. Chem. 265:15611-15616(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87280097; PubMed=3611077;
RA Pikkariainen T., Eddy R., Fukushima Y., Byers M., Shows T.,
RA Pihlajaniemi T., Saraste M., Tryggvason K.;
RT "Human laminin B1 chain. A multidomain protein with gene (LAMB1)
locus in the q22 region of chromosome 7."
RL J. Biol. Chem. 262:10454-10462(1987).
RN [3]
RP SEQUENCE OF 1276-1709 FROM N.A.
RX MEDLINE=88021029; PubMed=3661559;
RA Jaye M., Modi W.S., Ricca G.A., Mudd R., Chiu I.M., O'Brien S.J.,
RA Drohan W.N.;
RT "Isolation of a cDNA clone for the human laminin-B1 chain and its
gene localization."
RL Am. J. Hum. Genet. 41:605-615(1987).
CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
is thought to mediate the attachment, migration and organization
of cells into tissues during embryonic development by interacting
with other extracellular matrix components.
CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
different polypeptide chains (alpha, beta, gamma), which are bound
to each other by disulfide bonds into a cross-shaped molecule
comprising one long and three short arms with globules at each
end. The beta-1 chain is a subunit of laminin-1 (EHS laminin),
laminin-2 (merosin), and laminin-6 (K-laminin).
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Found in the basement membranes (major
component).
CC -!- DOMAIN: The alpha-helical domains I and II are thought to interact
with other laminin chains to form a coiled coil structure.
CC -!- DOMAIN: Domains VI and IV are globular.
CC -!- SIMILARITY: Contains 1 laminin N-terminal domain.
CC -!- SIMILARITY: Contains 13 laminin EGF-like domains.
CC -!- SIMILARITY: Contains 1 laminin IV domain.

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CC -----

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DR InterPro; IPR008211; LamNT.
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DR PRINTS; PR00011; EGFLAMININ.
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DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 11.
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal; Polymorphism.
FT SIGNAL 1 21
FT CHAIN 22 1786 LAMININ BETA-1 CHAIN.
FT DOMAIN 271 334 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 335 397 LAMININ EGF-LIKE 1.
FT DOMAIN 398 457 LAMININ EGF-LIKE 2.
FT DOMAIN 458 509 LAMININ EGF-LIKE 3.
FT DOMAIN 510 540 LAMININ EGF-LIKE 4.
FT DOMAIN 541 771 LAMININ EGF-LIKE 5 (INCOMPLETE).
FT DOMAIN 773 820 LAMININ DOMAIN IV.
FT DOMAIN 821 866 LAMININ EGF-LIKE 6.
FT DOMAIN 867 916 LAMININ EGF-LIKE 7.
FT DOMAIN 917 975 LAMININ EGF-LIKE 8.
FT DOMAIN 976 1027 LAMININ EGF-LIKE 9.
FT DOMAIN 1028 1083 LAMININ EGF-LIKE 10.
FT DOMAIN 1084 1131 LAMININ EGF-LIKE 11.
FT DOMAIN 1132 1178 LAMININ EGF-LIKE 12.
FT DOMAIN 1179 1397 LAMININ EGF-LIKE 13.
FT DOMAIN 1398 1430 DOMAIN II.
FT DOMAIN 1431 1786 DOMAIN ALPHA.
FT DOMAIN 1216 1315 COILED COIL (POTENTIAL).
FT DOMAIN 1353 1388 COILED COIL (POTENTIAL).
FT DOMAIN 1442 1781 COILED COIL (POTENTIAL).
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FT DISULFID 794 803 BY SIMILARITY.
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FT DISULFID 917 933 BY SIMILARITY.
FT DISULFID 919 944 BY SIMILARITY.
FT DISULFID 946 955 BY SIMILARITY.

Query Match		100.0%;	Score 9754;	DB 1;	Length 1786;		
Best Local Similarity		100.0%;	Pred. No. 0;				
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Db	1	MGLQLLAFSLALCRARVRAQEPESYGCAGSCYPATGDLIIGRAQKLSVTSTCGLHK	60				
QY	61	PEPYCIVSHLQEDKCFICNSQDPYHETLNPDSHLIENVVTTFAPNRLKIWQSENGVEN	120				
Db	61	PEPYCIVSHLQEDKCFICNSQDPYHETLNPDSHLIENVVTTFAPNRLKIWQSENGVEN	120				
QY	121	VTIQLDLEAEFHFTHLIMTFKTRFPAAMLIERSSDFGKTGWVYRFAYDCEASFPGISTG	180				
Db	121	VTIQLDLEAEFHFTHLIMTFKTRFPAAMLIERSSDFGKTGWVYRFAYDCEASFPGISTG	180				
QY	181	PMKKVDDIIICDSRYSDIEPSTEGEVIIFRALDPAFKIEDPYPSPRIQNLIKITNLRKIFVKL	240				
Db	181	PMKKVDDIIICDSRYSDIEPSTEGEVIIFRALDPAFKIEDPYPSPRIQNLIKITNLRKIFVKL	240				
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Db	241	HTLGDNLLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGFNEEVEGMVGHCMC	300				
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Db	301	RHNTKGLNCELMDPFYHDLPRWPAEGRNSACKKNCNEHSISCHFDMAVYLATGNVSGG	360				
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Db	481	CKRLVTGQHCDCQLPEHWGLSNDLDGCRPCDCLGGALNNSCFAESGCSCRPHMIGROC	540				
QY	541	NEVEPGYYFATLDHYLYEAEANLPGVSIIVERQYIQDRIPSWTGAGFVRVPEGAYLEFF	600				
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QY	661	SRYVVLPRPVCFEKGTNYTVRLELPQYTSDDSDVESPYTLIDSLVLMPYCKSLDIFTVGG	720				
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QY	961	GYFGNPSVGGSCQPCQCHNNIDTTDPEACDKETGRCLKCLYHTEGHCQCFRFGYYGDA	1020				
Db	961	GYFGNPSVGGSCQPCQCHNNIDTTDPEACDKETGRCLKCLYHTEGHCQCFRFGYYGDA	1020				

QY	1021	LRQDCRKVCVNYLGTVQEHCHNGSDCCDKATGQCLCLPNVIGQNCDCAPNTWQLASGTG	1080				
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QY	1201	LEKAKALKISGVIGPYRETVDVSVERKVSEIKDIIAQSAAEPLKNIGNLFEAEKLIKDV	1260				
Db	1201	LEKAKALKISGVIGPYRETVDVSVERKVSEIKDIIAQSAAEPLKNIGNLFEAEKLIKDV	1260				
QY	1261	TEMMAQVEVKLSDTTSQSNSTAKELDSLQTEABSLDNTVKELAEQLFEFIKNSDIRGALDS	1320				
Db	1261	TEMMAQVEVKLSDTTSQSNSTAKELDSLQTEABSLDNTVKELAEQLFEFIKNSDIRGALDS	1320				
QY	1321	ITKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVMMERESQFKKEQEOARLLDE	1380				
Db	1321	ITKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVMMERESQFKKEQEOARLLDE	1380				
QY	1381	LAGKLQSLDLSAAAEWTCGTPPGASCSETGCGPNCRCTDEGERKCGGPGCGGLVTVAHNA	1440				
Db	1381	LAGKLQSLDLSAAAEWTCGTPPGASCSETGCGPNCRCTDEGERKCGGPGCGGLVTVAHNA	1440				
QY	1441	WQKAMDLDDVLSALAEVEQLSKMVSEAKLRADAEAKQSAEDILLKTNATKEKMDKSNEEL	1500				
Db	1441	WQKAMDLDDVLSALAEVEQLSKMVSEAKLRADAEAKQSAEDILLKTNATKEKMDKSNEEL	1500				
QY	1501	RNLIKQIRNFLTQDSADLDSIEAVANEVLKMEMPTPQQLQNLNLTEDIRERVESLSQVEVI	1560				
Db	1501	RNLIKQIRNFLTQDSADLDSIEAVANEVLKMEMPTPQQLQNLNLTEDIRERVESLSQVEVI	1560				
QY	1561	LQHSAAADIAAEMLLEAEAKRASKSATDVKYTADVMVKEALEEAAKQVAAEKAIKQADEDI	1620				
Db	1561	LQHSAAADIAAEMLLEAEAKRASKSATDVKYTADVMVKEALEEAAKQVAAEKAIKQADEDI	1620				
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Db	1741	KDLERKYEDNQRYLEDKAQELARLEGEVRSLLKDISQKVAVYSTCL	1786				

RESULT 2
LMB1_MOUSE
ID LMB1_MOUSE STANDARD; PRT; 1786 AA.
AC P02469;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Laminin beta-1 chain precursor (Laminin B1 chain).
GN LAMB1-1 OR LAMB-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87147212; PubMed=3493487;
RA Sasaki M., Kato S., Kohno K., Martin G.R., Yamada Y.;
RT "Sequence of the cDNA encoding the laminin B1 chain reveals a
multidomain protein containing cysteine-rich repeats."
RL Proc. Natl. Acad. Sci. U.S.A. 84:935-939(1987).

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RN [2]
RP SEQUENCE OF 1292-1786 FROM N.A.
RX MEDLINE=85051302; PubMed=6209134;
RA Barlow D.P., Green N.M., Kurkinen M., Hogan B.L.M.;
RT "Sequencing of laminin B chain cDNAs reveals C-terminal regions of
   coiled-coil alpha-helix."
RL EMBO J. 3:2355-2362(1984).
RN [3]
RP SEQUENCE OF 165-172; 539-547 AND 712-719.
RC STRAIN=BALB/c; TISSUE=Endothelial cells;
RX MEDLINE=97363207; PubMed=9219532;
RA Frieser M., Noeckel H., Pausch F., Roeder C., Hahn A., Deutzmann R.,
RA Sorokin L.M.;
RT "Cloning of the mouse laminin alpha 4 cDNA. Expression in a subset of
   endothelium."
RL Eur. J. Biochem. 246:727-735(1997).
CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
   is thought to mediate the attachment, migration and organization
   of cells into tissues during embryonic development by interacting
   with other extracellular matrix components.
CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
   different polypeptide chains (alpha, beta, gamma), which are bound
   to each other by disulfide bonds into a cross-shaped molecule
   comprising one long and three short arms with globules at each
   end. The beta-1 chain is a subunit of laminin-1 (EHS laminin),
   laminin-2 (merosin), and laminin-6 (K-laminin).
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Found in the basement membranes (major
   component).
CC -!- SIMILARITY: Contains 1 laminin N-terminal domain.
CC -!- SIMILARITY: Contains 13 laminin EGF-like domains.
CC -!- SIMILARITY: Contains 1 laminin IV domain.
CC -----
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CC -----
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DR InterPro; IPR008211; LamNT.
DR Pfam; PF00053; laminin_EGF; 13.
DR Pfam; PF00055; laminin_Nterm; 1.
DR PRINTS; PR00011; EGFLAMININ.
DR SMART; SM00180; EGF_Lam; 11.
DR SMART; SM00136; LamNT; 1.
DR PROSITE; PS00022; EGF_1; 9.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 11.
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
FT SIGNAL 1 21
FT CHAIN 22 1786 LAMININ BETA-1 CHAIN.
FT DOMAIN 22 270 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 271 334 LAMININ EGF-LIKE 1.
FT DOMAIN 335 397 LAMININ EGF-LIKE 2.
FT DOMAIN 398 457 LAMININ EGF-LIKE 3.
FT DOMAIN 458 509 LAMININ EGF-LIKE 4.
FT DOMAIN 510 540 LAMININ EGF-LIKE 5 (INCOMPLETE).
FT DOMAIN 541 772 LAMININ DOMAIN IV.
FT DOMAIN 773 820 LAMININ EGF-LIKE 6.
FT DOMAIN 821 866 LAMININ EGF-LIKE 7.
FT DOMAIN 867 916 LAMININ EGF-LIKE 8.
FT DOMAIN 917 975 LAMININ EGF-LIKE 9.
FT DOMAIN 976 1027 LAMININ EGF-LIKE 10.

FT DOMAIN 1028 LAMININ EGF-LIKE 11.
FT DOMAIN 1084 LAMININ EGF-LIKE 12.
FT DOMAIN 1132 LAMININ EGF-LIKE 13.
FT DOMAIN 1179 DOMAIN II.
FT DOMAIN 1398 DOMAIN ALPHA.
FT DOMAIN 1431 DOMAIN I.
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FT DOMAIN 1815 COILED COIL (POTENTIAL).
FT DOMAIN 1888 COILED COIL (POTENTIAL).
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FT DOMAIN 65222 BY SIMILARITY.
FT DOMAIN 65319 BY SIMILARITY.
FT DOMAIN 65416 BY SIMILARITY.
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FT DOMAIN 66291 BY SIMILARITY.
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FT DOMAIN 66485 BY SIMILARITY.
FT DOMAIN 66582 BY SIMILARITY.
FT DOMAIN 66679 BY SIMILARITY.
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FT DOMAIN 67067 BY SIMILARITY.
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FT DOMAIN 67261 BY SIMILARITY.
FT DOMAIN 67358 BY SIMILARITY.
FT DOMAIN 67455 BY SIMILARITY.
FT DOMAIN 67552 BY SIMILARITY.
FT DOMAIN 67649 BY SIMILARITY.
FT DOMAIN 67746 BY SIMILARITY.
FT DOMAIN 67843 BY SIMILARITY.
FT DOMAIN 67940 BY SIMILARITY.
FT DOMAIN 68037 BY SIMILARITY.
FT DOMAIN 68134 BY SIMILARITY.
FT DOMAIN 68231 BY SIMILARITY.
FT DOMAIN 68328 BY SIMILARITY.
FT DOMAIN 68425 BY SIMILARITY.
FT DOMAIN 68522 BY SIMILARITY.
FT DOMAIN 68619 BY SIMILARITY.
FT DOMAIN 68716 BY SIMILARITY.
FT DOMAIN 68813 BY SIMILARITY.
FT DOMAIN 68910 BY SIMILARITY.
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FT DOMAIN 69104 BY SIMILARITY.
FT DOMAIN 69201 BY SIMILARITY.
FT DOMAIN 69298 BY SIMILARITY.
FT DOMAIN 69395 BY SIMILARITY.
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FT DOMAIN 69977 BY SIMILARITY.
FT DOMAIN 70074 BY SIMILARITY.
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FT DOMAIN 70268 BY SIMILARITY.
FT DOMAIN 70365 BY SIMILARITY.
FT DOMAIN 70462 BY SIMILARITY.
FT DOMAIN 70559 BY SIMILARITY.
FT DOMAIN 70656 BY SIMILARITY.
FT DOMAIN 70753 BY SIMILARITY.
FT DOMAIN 70850 BY SIMILARITY.
FT DOMAIN 70947 BY SIMILARITY.
FT DOMAIN 71044 BY SIMILARITY.
FT DOMAIN 71141 BY SIMILARITY.
FT DOMAIN 71238 BY SIMILARITY.
FT DOMAIN 71335 BY SIMILARITY.
FT DOMAIN 71432 BY SIMILARITY.
FT DOMAIN 71529 BY SIMILARITY.
FT DOMAIN 71626 BY SIMILARITY.
FT DOMAIN 71723 BY SIMILARITY.
FT DOMAIN 71820 BY SIMILARITY.
FT DOMAIN
```


GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:28 ; Search time 48.4494 Seconds
(without alignments)
11631.021 Million cell updates/sec

Title: US-10-037-182-6
Perfect score: 9754
Sequence: 1 MGLQLLAFSLALCARVR.....EVRSLKDISQKAVYSTCL 1786

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6811.5	69.8	1785	13 Q8JHV7	Q8jvh7 brachydanio
2	5808	59.5	1086	4 Q8TAS6	Q8tas6 homo sapien
3	5325	54.6	1792	13 O57484	O57484 gallus gall
4	5074.5	52.0	1799	11 Q8ROY0	Q8roy0 mus musculu
5	4891	50.1	984	11 Q8K271	Q8k271 mus musculu
6	4527	46.4	911	11 Q9CRX6	Q9crx6 mus musculu
7	3832.5	39.3	1761	4 Q86XN2	Q86xn2 homo sapien
8	3797.5	38.9	1827	13 Q8JHV6	Q8jvh6 brachydanio
9	3625.5	37.2	1631	4 Q9Y6U6	Q9y6u6 homo sapien
10	2842.5	29.1	1067	5 O44565	O44565 caenorhabdi
11	2297.5	23.6	1168	5 Q967S8	Q967s8 schistocerc
12	2034	20.9	761	4 Q9UHI2	Q9uhi2 homo sapien
13	1921	19.7	1026	5 Q8SWY0	Q8swy0 drosophila
14	1847	18.9	1069	5 Q9BPS2	Q9bps2 bombyx mori
15	1729.5	17.7	3704	5 P91904	P91904 caenorhabdi
16	1684.5	17.3	1593	13 Q8JHV8	Q8jvh8 brachydanio

17	1674.5	17.2	1623	5 Q9U3U7	Q9u3u7 anopheles g
18	1641.5	16.8	3712	5 Q9VRW0	Q9vrw0 drosophila
19	1573.5	16.1	3695	4 Q8TDF8	Q8tdf8 homo sapien
20	1491.5	15.3	1168	11 Q91V90	Q91v90 mus musculu
21	1380	14.1	1007	13 Q90ZN3	Q90zn3 gallus gall
22	1307.5	13.4	3102	5 O45614	O45614 caenorhabdi
23	1217	12.5	2731	5 Q9VJT5	Q9vjt5 drosophila
24	1217	12.5	3367	5 Q9XZC9	Q9xzc9 drosophila
25	1217	12.5	3375	5 Q8IP51	Q8ip51 drosophila
26	1101.5	11.3	1546	4 Q9NS27	Q9ns27 homo sapien
27	1099.5	11.3	1546	4 O75445	O75445 homo sapien
28	1064	10.9	1486	4 O14637	O14637 homo sapien
29	1041.5	10.7	1461	11 Q9JLP3	Q9jlp3 mus musculu
30	1040	10.7	750	4 Q86TP7	Q86tp7 homo sapien
31	1001.5	10.3	616	4 Q15483	Q15483 homo sapien
32	1001	10.3	628	11 Q9J133	Q9j133 mus musculu
33	993	10.2	628	4 Q9HB63	Q9hb63 homo sapien
34	991	10.2	628	4 Q9BZP1	Q9bzip1 homo sapien
35	975	10.0	605	4 Q7Z5B6	Q7z5b6 homo sapien
36	964	9.9	1512	11 Q8K3K1	Q8k3k1 rattus norv
37	889	9.1	1190	6 Q8HZI9	Q8hzi9 equus cabal
38	880	9.0	1196	6 Q867A2	Q867a2 canis famil
39	695.5	7.1	604	11 Q924Z9	Q924z9 rattus norv
40	680	7.0	1664	5 Q9TVQ2	Q9tvq2 caenorhabdi
41	678.5	7.0	569	13 O57339	O57339 xenopus lae
42	678	7.0	602	13 O42203	O42203 brachydanio
43	675.5	6.9	529	4 Q8N2D6	Q8n2d6 homo sapien
44	675	6.9	603	13 O42140	O42140 brachydanio
45	669.5	6.9	1574	11 O88281	O88281 rattus norv

ALIGNMENTS

RESULT 1
Q8JHV7
ID Q8JHV7 PRELIMINARY; PRT; 1785 AA.
AC Q8JHV7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Laminin beta 1.
GN LAMBL.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22065263; PubMed=12070089;
RA Parsons M.J., Pollard S.M., Saude L., Feldman B., Coutinho P.,
RA Hirst E.M., Stemple D.L.;
RT "Zebrafish mutants identify an essential role for laminins in
RT notochord formation.";
RL Development 129:3137-3146(2002).
DR EMBL; AF468049; AAM61767.1; -;
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR008211; LamNT.
DR Pfam; PF00053; laminin_EGF; 13.
DR Pfam; PF00055; laminin_Nterm; 1.
DR PRINTS; PR00011; EGF_LAMININ.
DR SMART; SM00180; EGF_Lam; 13.
DR SMART; SM00136; LamNT; 1.
DR PROSITE; PS00022; EGF_1; 10.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 12.
KW Laminin EGF-like domain.
SQ SEQUENCE 1785 AA; 197279 MW; 1BD338A0B6AB9F26 CRC64;

Query Match		69.8%;	Score 6811.5;	DB 13;	Length 1785;
Best Local Similarity		67.0%;	Pred. No. 9.3e-290;		
Matches 1198;		Conservative 253;	Mismatches 328;	Indels 9;	Gaps 7;
QY	3	LLQLAFSLALCRARVRAQEPEFSYGCAEGSCYPATGDLILIGRAQKLSVTSTCGLHKPE	62		
Db	2	LLQLAALSILG--AWALADVPELGDVCTEGSCYPATGDLILIGRAQQLLATSTCGVHKPE	58		
QY	63	PYCIIVSHLQEDKCKFCICNSQDPYHETLNP-DSHLIENAVTTTAPNRLKIWWQSENGVENV	121		
Db	59	PFCIVSHLQEEKCFVCDSRQAYNETAHQVTSIENAVTTTAPNRLKIWWQSENGLENV	118		
QY	122	TIQLDLEAEFHTHLIMTFKTRPAAMLIERSSDFGKTGWVRYPAYDCEASFPGISTGP	181		
Db	119	TIQLDLEAEFHTHLIMTFKTRPAAVMIERSADFNTQVRYFAYDCESSFPSVSHGP	178		
QY	182	MKKVDDIICDSRYSDIEPSTEGEVIFFRALDPAFKIEDPYSPRIQNLKLTNLRKFVKLH	241		
Db	179	MTKVDDVICDTRYSDIEPSTEGEVIFFRVLDPAFRIEDPYSPRIQNLKLTNLRVKFTKLH	238		
QY	242	TLGDNLLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGCMCR	301		
Db	239	TLGDNLLDSRIEIKEKYYAYIYDMVVRGNCFCYGHASECAPVDGTGEAVEGMVHGCMCN	298		
QY	302	HNTKGLNCELMDPFYHDLFWRPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGV	361		
Db	299	HNTIGLNCERCQDFYHDLFWRPAEGRNTNACKKCHNHHSHSCHEDVAVYRASGNVSGV	358		
QY	362	CDDCQHNTMGRNCQCKPFYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFSTGL	421		
Db	359	CDDCQHNTMGHNCQCKPFYHQHPEKDIRDPNICEPCNCDPVGSLNGGVCDPMTDVSGL	418		
QY	422	IAGQCRKLNVEGEHCDVCKEGFYDLSSDEDPFGCKSCACNPLGTPGGNCPDSETGHCYC	481		
Db	419	ISGQCRCKPNVEGERCDQCKQGHYGL-SEDEPLGCQPCCTCNALGTPVGGSPCDTDSGNCYC	477		
QY	482	KRLVTGQHCDCQLPEHWGLSNDLDGCRPCDCLGGALNNSCFAESGQSCSRPHMIGRCQN	541		
Db	478	KRLVTGRNCDQLPQHWGLSNDMDGCRPCDCHGGAINNCCSPVSGQCQCREHMFRRCD	537		
QY	542	EVEPGYYFATLDHYLYEABEANLPGVSIYERQYQIDRIPSWTGAQFVRVPEGAYLEFFI	601		
Db	538	QVESGFYFIALDHYTYEABEAKFGPGVTVPVRNHPQDRSPTWTGIGFVNVPEGAFLEFSI	597		
QY	602	DNIPYSMEYDILIRYEPQLDHWKAVITVQRPGRIPTSRRCNGTIPDDDNQVVSLSPGS	661		
Db	598	DNIPYSMEYDILIRYEPQLPEQWEEVMTVIRPRVITADSRCAANTMPDDDNQVVSHPGS	657		
QY	662	RYVVLPRPVCFEKGTNYTVRLLELPQYTTSSDSVSPYTLIDSLVLMPYCKSLDIFTVGS	721		
Db	658	RYVVLPRPVCFEGLNYTVRLSLSLY-SALSQVSPYTLIDSLVLMPHCKNLIDIFSGSGT	716		
QY	722	-GDGVVTNSAWETFORVRCLENSRSVVKTPMTDVCRNIIIFSISALLHOTGLACECDPQGS	780		
Db	717	EGGNLVTNSAWENFORVRCLENSQAVVKTPMTDTCRNIIYFVSALLHQVKACQCDPQGS	776		
QY	781	LSSVCDPNGGQCQCRPNVVGRTNCRCAPGTGFGPSGCKPCECHLQGSVNAFCNPVTGQC	840		
Db	777	LSTVCDPSGGQCQCRPNVVRNCDRCAPATFLFXPGQCRPCDCSPESGVSYSYCHEATQC	836		
QY	841	HCFOGVYARQCDRLPGHWGPPSCQPCQCNHADDQDPVTGECNCDQYTMGHNCERCLA	900		
Db	837	ECTIAGAYGRQCDRLPGYWGFNCRPCTCNHAEQCDPQTGQCLSCRDHTGHNCERCLG	896		
QY	901	GYIGDPIIGSDHCRPCPCPDGSDSGRQFARSQYQDPVTLQACVCDPGYIGSRCDDCAS	960		
Db	897	GYIGDPIVLSGDHCRPCPCPDGSGRQFSGACYKSPDSSQVFCVNCQGYKGARCECAP	956		
QY	961	GYFGNPSEVGGSCQPCQCHNNITDTPDPEACDKETGRCLKLYHTEGEHCQCFRFGYGDA	1020		
Db	957	GYGNPHEVGGECRCPQCQNSNIDMDPESCDARTGACVKCLYHTEGESCNCRGLGYGNA	1016		
QY	1021	LRQCRKVCVNYLGTVQEHK-NGSDCQCDKATGQCLCLPNVIGQNCDCRCAPTWQLASGT	1079		

RESULT 2

Q8TAS6	Q8TAS6	PRELIMINARY;	PRT;	1086	AA.
ID	Q8TAS6				
AC	Q8TAS6;				
DT	01-JUN-2002	(TrEMBLrel. 21, Created)			
DT	01-JUN-2002	(TrEMBLrel. 21, Last sequence update)			
DT	01-JUN-2003	(TrEMBLrel. 24, Last annotation update)			
DE	Similar to laminin, beta 1 (Fragment).				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Muscle;				
RA	Strausberg R.;				
RRL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; BC026018; AAH26018.1; -				
DR	GO; GO:0005198; F:structural molecule activity; IEA.				
DR	InterPro; IPR006209; EGF like.				
DR	InterPro; IPR002049; Laminin_EGF.				

Db	1017	LTQSCRKVCVNMGTVEEMCPSPGNCNCDLTSGQCLCLPNVVGQCHDQCAPDTWNMASGK	1076
QY	1080	GCDPCNCAAHSGFSPSCNEFTGQCOCMPGFGGRTCECQELFWGDPDVECRACDCDPRGI	1139
Db	1077	GCEDCDPNHSGSSCNEIMGQCSCKPFGGRTCRECRELFWGNPEVKCHACDCDPRGI	1136
QY	1140	ETPOCDQSTGQCVCEGVGPRCDKCTRGYSGVFPDCTPCHQCFALWDVIIAELTNRTHR	1199
Db	1137	AEQOCNKVTGHCVCVEGVSGPRCDTCARGYTGEFPQECRCHQCPAEWDIIIVGDLTNQTHR	1196
QY	1200	FLEKAKALKISGVIGPYRETVDVSVERKVSEIKDILAQSPAAEPLKNIGNLFEEAEKLIKD	1259
Db	1197	LVQKNTIKATGITGYPYQATINNVENANSIRNIIAQNPAQPLTEIQGLLEQATALMAE	1256
QY	1260	VTEMAAQVEVKLSDTTSQSNSTAKELDSLQTEAESLQNTVKELAQLEFIKNSDIRGALD	1319
Db	1257	MNSNLNLTEETLSEISSDNNSTDTKLKSLKEEAQKLEQTVKDLREQVEFVKNSDIRGARA	1316
QY	1320	SITKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVMMERESQFKEKEEQEARLLD	1379
Db	1317	SVTRYEQSONAEIRANASTTDPYNLVNQSATLRTETEELMNQTKEEFNQRQDEFKULD	1376
QY	1380	ELAGKLSLDLSAAAEAMTCGTPPGA-SCSETECGGPNCRDTDEGERKCGGPGCGGLVTVAH	1438
Db	1377	NLAGQLETLDLSESEKTCGSPAGSENCADSRGGLSCVDMQSGRCKGCGEGCDGLTTLAH	1436
QY	1439	NAWQKAMDLDQDVLALAEVEQLSKMVSBAKLRADEAKQSAEDILLKTNATKEXMDKSNE	1498
Db	1437	NAWQKAKDFLEIISAMEEVDKLSKMVSBAKVKADEAKLNAQAEVLAKTNETKXRVDSNE	1496
QY	1499	ELRNLIKQIRNFLTQDSADLDSIEAVANEVLMKEMPSTPQOLQNLTEDIRERVESLSQVE	1558
Db	1497	ELRLIKQIRDFLTQDGADLESIEAVANEVLQMQMPTTTPAQLQNLTEIRERVGSLTDVE	1556
QY	1559	VILQHSAAADIARAEMLLBEAKRASKSATDVKVTDMMVKEALEEAEKAAQVAAEKAIKQADE	1618
Db	1557	DILNQSAADILRAESLLEQARKARKEASDVKSTAEVMKEALQHAERQNSVAAELKQAAV	1616
QY	1619	DIQGTQNLTSISEETAASEETLFNASQRISELERNEVELKRKAQNSGEAEYIEKVVT	1678
Db	1617	DIKGTQDLLVSESETSDSELKLSNATRRLLKLESVDALLKEKALNTSISANSTEKEAES	1676
QY	1679	VKQSAEDVKKTLDELDEKYYKVENLIAKKTESADARRKAEMLQNEAKTLIAQANSKLQ	1738
Db	1677	INALAEQLKKLDSELKDKYSTVEELITQKAEQVABAKKRAEKLQEEARNLLQASEKLQ	1736
QY	1739	LLKDLERKYNQRYLEDKAQELARLEGEVRSLLKDISQKAVYSTCL	1786
Db	1737	LLKNLEKNYDQNKLLDKANELVDLEKAVKELLQEIISHKVTYVYSTCL	1784

OM protein - protein search, using sw model

Run on: May 18, 2004, 14:25:32 ; Search time 47.8797 Seconds
(without alignments)
10415.614 Million cell updates/sec

Title: US-10-037-182-8
Perfect score: 9654
Sequence: 1 QEPFESYGAEGSCYPATG.....EVRSLLKDISQKVAVYSTCL 1765

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	9654	100.0	1765	3 AAB19798	Aab19798 Human lam
2	9654	100.0	1765	3 AAB48449	Aab48449 Human lam
3	9654	100.0	1765	5 ABB81591	Abb81591 Human lam
4	9654	100.0	1786	2 AAW50893	Aaw50893 Human lam
5	9654	100.0	1786	3 AAB16522	Aab16522 Human lam
6	9654	100.0	1786	3 AAB19797	Aab19797 Human lam
7	9654	100.0	1786	3 AAB48448	Aab48448 Human lam
8	9654	100.0	1786	4 AAB90788	Aab90788 Human she
9	9654	100.0	1786	5 ABB81590	Abb81590 Human lam
10	9638	99.8	1786	5 AAM48896	Aam48896 Laminin p
11	9618.5	99.6	1785	2 AAY15461	Aay15461 Human lam
12	9092	94.2	1786	3 AAB19799	Aab19799 Mouse lam
13	9092	94.2	1786	3 AAB48450	Aab48450 Mouse lam
14	9092	94.2	1786	5 ABB81592	Abb81592 Mouse lam
15	9035	93.6	1776	2 AAW50894	Aaw50894 Mouse lam
16	8967.5	92.9	1764	1 AAP91672	Aap91672 Primary a
17	8873	91.9	1725	3 AAB19800	Aab19800 Mouse lam
18	8873	91.9	1725	3 AAB48451	Aab48451 Mouse lam
19	8873	91.9	1725	5 ABB81593	Abb81593 Mouse lam
20	5084	52.7	1801	2 AAW50895	Aaw50895 Rat lamin
21	5084	52.7	1801	7 ADE60383	Ade60383 Rat Prote
22	5048	52.3	1798	2 AAW50896	Aaw50896 Human lam
23	5048	52.3	1798	7 ADE60385	Ade60385 Human Pro
24	5046	52.3	1799	5 AAM50359	Aam50359 Mouse lam
25	4918	50.9	1798	5 AAU84346	Aau84346 Protein L

26	4918	50.9	1798	5 AAM50360	Aam50360 Human lam
27	3881	40.2	822	5 AAM48897	Aam48897 Laminin p
28	3850.5	39.9	1788	4 ABB62995	Abb62995 Drosophil
29	3832.5	39.7	1761	2 AAY15457	Aay15457 Human lam
30	3625.5	37.6	1670	7 ADE07851	Ade07851 Novel pro
31	3076.5	31.9	1101	7 ADE28641	Ade28641 Human NOV
32	3044.5	31.5	1105	2 AAY15459	Aay15459 SEQ ID 5
33	2776	28.8	466	2 AAR07447	Aar07447 Human lam
34	2348	24.3	527	3 AAB58995	Aab58995 Breast an
35	2115	21.9	434	1 AAP60109	Aap60109 Human B1
36	1787	18.5	315	6 ABU70520	Abu70520 Human adi
37	1759	18.2	1639	4 ABB59807	Abb59807 Drosophil
38	1680.5	17.4	1609	3 AAB19801	Aab19801 Human lam
39	1680.5	17.4	1609	3 AAB48452	Aab48452 Human lam
40	1680.5	17.4	1609	5 ABB81594	Abb81594 Human lam
41	1680.5	17.4	1609	7 ADC01887	Adc01887 Human lam
42	1680.5	17.4	1617	3 AAB19803	Aab19803 Human lam
43	1677	17.4	1572	3 AAB19806	Aab19806 Mouse lam
44	1677	17.4	1572	3 AAB48455	Aab48455 Mouse lam
45	1677	17.4	1572	5 ABB81597	Abb81597 Mouse lam

ALIGNMENTS

RESULT 1
AAB19798
ID AAB19798 standard; protein; 1765 AA.
XX
AC AAB19798;
XX
DT 05-MAR-2001 (first entry)
XX
DE Human laminin 2 mature beta-1 chain.
XX
KW Laminin 2; human; nerve regeneration; angiogenic; cell adhesion;
KW degenerative muscle disorder; muscular dystrophy; cell therapy.
XX
OS Homo sapiens.
XX
PN WO200066730-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US011378.
XX
PR 30-APR-1999; 99US-0131720P.
PR 15-JUN-1999; 99US-0139198P.
PR 12-JUL-1999; 99US-0143289P.
PR 24-SEP-1999; 99US-0155945P.
XX
(UTNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
Yurchenco P;
XX
WPI; 2000-687537/67.
XX
N-PSDB; AAA88898.
XX
Purified laminin 2 protein, useful for research and therapeutic purposes
including peripheral nerve regeneration, treatment of degenerative muscle
disorders, angiogenesis regulation, and ex vivo cell therapy.
XX
Claim 5; Page 199-204; 305pp; English.
XX
The present sequence is that of the human laminin 2 beta-1 chain mature
protein. Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and
gamma-1 (100 kDa) chains. It is thought to be specifically required for
stabilizing myotubes during skeletal muscle development, and for
preventing apoptosis. Genetic defects in its structure or expression are
associated with a major type of congenital muscular dystrophy. Laminin 2
is also thought to be important in Schwann cell/basal lamina
interactions. The invention provides laminin 2 alpha-2, beta-1 and gamma-
1 chain polypeptides (see AAB19791-806) and the polynucleotides encoding

CC them (see AAA8891-906), methods for making recombinant laminin 2, cells
CC that express recombinant laminin 2, and methods for using purified
CC laminin 2 for research and therapeutic purposes including peripheral
CC nerve regeneration, treatment of degenerative muscle disorders,
CC angiogenesis regulation, promoting cell attachment and migration, ex vivo
CC cell therapy, improving the take of grafts, improving the
CC biocompatibility of medical devices and preparing improved culture
CC devices and media
XX

SQ Sequence 1765 AA;
Query Match 100.0%; Score 9654; DB 3; Length 1765;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QEPFSGYCAEGSCYPATGDLIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICNS 60
DB 1 QEPFSGYCAEGSCYPATGDLIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICNS 60
QY 61 QDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENVTIQLDLAEFFHFTLIMTFK 120
DB 61 QDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENVTIQLDLAEFFHFTLIMTFK 120
QY 121 TFRPAAMLIERSDFGKTGWVRYFAYDCEASFPFGISTGPMKKVDDIICDSRYSIEPST 180
DB 121 TFRPAAMLIERSDFGKTGWVRYFAYDCEASFPFGISTGPMKKVDDIICDSRYSIEPST 180
QY 181 EGEVIFRALDPAFKIEDPSPRIQNLKLTNRIKFKVLHTLGNLLDSRMEIREKYIYA 240
DB 181 EGEVIFRALDPAFKIEDPSPRIQNLKLTNRIKFKVLHTLGNLLDSRMEIREKYIYA 240
QY 241 VYDMVVRGNCFCYGHASECAPVDGFNEEVGVMVGHGCMCRHNTKGLNCELMDFFYHDLPW 300
DB 241 VYDMVVRGNCFCYGHASECAPVDGFNEEVGVMVGHGCMCRHNTKGLNCELMDFFYHDLPW 300
QY 301 RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGVCGDDCOHNTMGRNCEQCKPFY 360
DB 301 RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGVCGDDCOHNTMGRNCEQCKPFY 360
QY 361 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYDFSTGLIAGQCRCKLNVEGEHCDVCK 420
DB 361 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYDFSTGLIAGQCRCKLNVEGEHCDVCK 420
QY 421 EGFYDLSSDPFGCKSCACNPLGTIPGGNPNCDSETGHYCKRLVTGQHCDDQCLPEHWGLS 480
DB 421 EGFYDLSSDPFGCKSCACNPLGTIPGGNPNCDSETGHYCKRLVTGQHCDDQCLPEHWGLS 480
QY 481 NDLGCRPCDCDLGALNNSCFAESGQCSRPHMIGRQCNEVEPGYFATLDHYLYEAE 540
DB 481 NDLGCRPCDCDLGALNNSCFAESGQCSRPHMIGRQCNEVEPGYFATLDHYLYEAE 540
QY 541 ANLPGVSIVERQYIQDRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 600
DB 541 ANLPGVSIVERQYIQDRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 600
QY 601 DHWEKAVITVQRPGRIPSTSSRCGNTIPDDNQVVSLSPGSRVYVLPVPVCFEKGTNYTVR 660
DB 601 DHWEKAVITVQRPGRIPSTSSRCGNTIPDDNQVVSLSPGSRVYVLPVPVCFEKGTNYTVR 660
QY 661 LELPQYTSSDSDVESFYTLIDSLVLMPCYSKSLDIFTVGGSGDGVVNTNSAWETFORYRCLE 720
DB 661 LELPQYTSSDSDVESFYTLIDSLVLMPCYSKSLDIFTVGGSGDGVVNTNSAWETFORYRCLE 720
QY 721 NSRSVVKTPMTDVCNRIIFSISALLHOTGLACECDPQGLSSVCDPNGGQCQCRPNVVG 780
DB 721 NSRSVVKTPMTDVCNRIIFSISALLHOTGLACECDPQGLSSVCDPNGGQCQCRPNVVG 780
QY 781 TCNRCAPGTGFGPSGCKPCECHLQGSVNAPFCNPVTGQCHCFQGVYVARQCDRLPGHWGF 840
DB 781 TCNRCAPGTGFGPSGCKPCECHLQGSVNAPFCNPVTGQCHCFQGVYVARQCDRLPGHWGF 840
QY 841 PSCQPCQCNHADDCTPVTGECNQCQDYTMGNHCERCLAGYYGDPPIGSGDHCRPCPCPD 900

DB 841 PSCQPCQCNHADDCTPVTGECNQCQDYTMGNHCERCLAGYYGDPPIGSGDHCRPCPCPD 900
QY 901 GPDSGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCASCYFNGPSEVGGSCQPCQCHNN 960
DB 901 GPDSGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCASCYFNGPSEVGGSCQPCQCHNN 960
QY 961 IDTTDPEACDKETGRCLKCLYHTEGEHCQCFRFGYGDALRQDCRKCVCNLYLGTQVEHCN 1020
DB 961 IDTTDPEACDKETGRCLKCLYHTEGEHCQCFRFGYGDALRQDCRKCVCNLYLGTQVEHCN 1020
QY 1021 GSDCQCDKATGQCLCLPNVIGQNCDCRCAPTWQLASGTGCDPCNCAAHSPGSCNEFTG 1080
DB 1021 GSDCQCDKATGQCLCLPNVIGQNCDCRCAPTWQLASGTGCDPCNCAAHSPGSCNEFTG 1080
QY 1081 QCQCMFGGRTCECQELFWGDDPVECRACDCDPRGIETPQCDQSTQCQCVCEGVEGPR 1140
DB 1081 QCQCMFGGRTCECQELFWGDDPVECRACDCDPRGIETPQCDQSTQCQCVCEGVEGPR 1140
QY 1141 CDKCTRGYSGVFPDCTPCHQCFALWDVIIAELTNRTHRFLEKAKALKISGVIQPYRETVD 1200
DB 1141 CDKCTRGYSGVFPDCTPCHQCFALWDVIIAELTNRTHRFLEKAKALKISGVIQPYRETVD 1200
QY 1201 SVKRVSEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDVTEVMAQVEVKLSDTTTSQSNST 1260
DB 1201 SVKRVSEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDVTEVMAQVEVKLSDTTTSQSNST 1260
QY 1261 AKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTTE 1320
DB 1261 AKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTTE 1320
QY 1321 PNSTVEQSALMRDVEDVMMERESQFKEQEERQARLLDELAKLQSLDLSAAAEAMTCGTP 1380
DB 1321 PNSTVEQSALMRDVEDVMMERESQFKEQEERQARLLDELAKLQSLDLSAAAEAMTCGTP 1380
QY 1381 PGASCSETECGGPNCRDTEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLALAEVEQL 1440
DB 1381 PGASCSETECGGPNCRDTEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLALAEVEQL 1440
QY 1441 SKWVSEAKLRADAEAKQSAEDILLKTNATKEMDKSNEELRNLIKQIRNFLTQDSADLDSI 1500
DB 1441 SKWVSEAKLRADAEAKQSAEDILLKTNATKEMDKSNEELRNLIKQIRNFLTQDSADLDSI 1500
QY 1501 EAVANEVLKMEPSTPQQLQNLTEDIRERVESLSQVEVILQHSADIAEAEMLLEAKRA 1560
DB 1501 EAVANEVLKMEPSTPQQLQNLTEDIRERVESLSQVEVILQHSADIAEAEMLLEAKRA 1560
QY 1561 SKSATDVKVTADMVKEALEEAEAKQVAAEKAKIQADEDIQGTQNLTSIESETAAASEETL 1620
DB 1561 SKSATDVKVTADMVKEALEEAEAKQVAAEKAKIQADEDIQGTQNLTSIESETAAASEETL 1620
QY 1621 FNASQRISELERNVBELKRKAQNSGEAEVIEKVYTVKQSAEDVKKTLDGELDEKYKV 1680
DB 1621 FNASQRISELERNVBELKRKAQNSGEAEVIEKVYTVKQSAEDVKKTLDGELDEKYKV 1680
QY 1681 ENLIAKKTESADARRKAEMLQNEAKTLAQANSKLQLLKDLEKRYEDNQRYLEDKAQEL 1740
DB 1681 ENLIAKKTESADARRKAEMLQNEAKTLAQANSKLQLLKDLEKRYEDNQRYLEDKAQEL 1740
QY 1741 ARLEGEVRSLLKDISQKAVYSTCL 1765
DB 1741 ARLEGEVRSLLKDISQKAVYSTCL 1765

RESULT 2
AAB48449
ID AAB48449 standard; protein; 1765 AA.
XX
AC AAB48449;
XX
DT 02-MAR-2001 (first entry)
XX
DE Human laminin 8 polypeptide, SEQ ID NO: 16.
XX

KW Human; laminin 8; neuroprotective; angiogenic; osteopathic;
KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;
KW vascular tissue injury; neural injury; angiogenesis regulation.
XX
OS Homo sapiens.
XX
XX WO200066732-A2.
XX
XX 09-NOV-2000.
XX
XX 28-APR-2000; 2000WO-US011543.
XX
XX 30-APR-1999; 99US-0131720P.
PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.
PR 11-FEB-2000; 2000US-0182012P.
XX
PA (BIOS-) BIOSTRATUM INC.
XX
XX Kortesia J, Tryggvason K;
PI
XX
DR WPI; 2000-687539/67.
DR N-PSDB; AAC83710.
XX
XX Purified laminin 8 protein, useful for research and therapeutic purposes
PT including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.
XX
PS Claim 5; Page 163-168; 245pp; English.
XX
CC The present sequence is a laminin 8 polypeptide chain. Laminins are a
CC family of heterotrimeric glycoproteins that function via binding
CC interactions with neighbouring cell receptors and by forming laminin
CC networks. They are signalling molecules which influence cellular
CC function. Laminin 8 is useful for treating injuries to tissue of
CC mesenchymal origin, such as bone, cartilage, tendon, and ligament,
CC treating injuries to vascular tissue, promoting cell attachment and
CC migration, ex vivo cell therapy, improving the biocompatibility of
CC medical devices, and preparing improved cell culture devices and media.
CC Laminin 8 is also useful for promoting re-endothelialisation at the site
CC of vascular injuries, improving the take of grafts, improving the
CC biocompatibility of medical devices, treating neural injuries (neural
CC regeneration), regulating angiogenesis, and promoting cell attachment and
CC migration
XX
SQ Sequence 1765 AA;
Query Match 100.0%; Score 9654; DB 3; Length 1765;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QEPFSGCAEGSCYPATGDLIGRAQKLSVTSTGLHKPEPYCIIVSHLQEDKKCFICNS 60
Db 1 QEPFSGCAEGSCYPATGDLIGRAQKLSVTSTGLHKPEPYCIIVSHLQEDKKCFICNS 60
QY 61 QDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENVTIQLDLEAFPHFTHLIMTFK 120
Db 61 QDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENVTIQLDLEAFPHFTHLIMTFK 120
QY 121 TFRPAAMLIERSSDFGKTGWYRYFAYDCEASFPSTGPMKKVDDIICDSRYSDIEPST 180
Db 121 TFRPAAMLIERSSDFGKTGWYRYFAYDCEASFPSTGPMKKVDDIICDSRYSDIEPST 180
QY 181 EGEVIFRALDPAFKIEDPSPRIQNLLKITNLRKIFVKLHTLGLNLLDSRMEIREKYYA 240
Db 181 EGEVIFRALDPAFKIEDPSPRIQNLLKITNLRKIFVKLHTLGLNLLDSRMEIREKYYA 240
QY 241 VYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGHCMCRHNTKGLNCELAMDFFYHDLPW 300
Db 241 VYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGHCMCRHNTKGLNCELAMDFFYHDLPW 300
QY 301 RPAEGRNSACKKCNCHNEHSISCHFDMAVYLATGNVSGGVCDCCQHNTMGRNCEQCKPFY 360
Db

Db 301 RPAEGRNSACKKCNCHNEHSISCHFDMAVYLATGNVSGGVCDCCQHNTMGRNCEQCKPFY 360
QY 361 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSTGLIAGQCRCRKLNVGEHCDVCK 420
Db 361 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSTGLIAGQCRCRKLNVGEHCDVCK 420
QY 421 EGFYDLSSSEDPFGCKSCACNPLGTIPGGNPNCDSETGHYCKRLVTGQHCDCQLPEHWGLS 480
Db 421 EGFYDLSSSEDPFGCKSCACNPLGTIPGGNPNCDSETGHYCKRLVTGQHCDCQLPEHWGLS 480
QY 481 NDLDGCRPCDCDLGGALNNSCFAESGQCSCRPMMIGRCQNEVEPGYYFATLDHYLYEAE 540
Db 481 NDLDGCRPCDCDLGGALNNSCFAESGQCSCRPMMIGRCQNEVEPGYYFATLDHYLYEAE 540
QY 541 ANLGPGVSIVERQYIQDRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 600
Db 541 ANLGPGVSIVERQYIQDRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 600
QY 601 DHWEKAVITVQRPGRIPFSSRCGNTIPDDDNQVYSLSPGSRYYVLPVPVCFEKGNTYTVR 660
Db 601 DHWEKAVITVQRPGRIPFSSRCGNTIPDDDNQVYSLSPGSRYYVLPVPVCFEKGNTYTVR 660
QY 661 LELPQYTSSDSDESYPYTLIDSLVLMYPYCKSLDIFTVGGSGDGVVNTNSAWETQRYRCLE 720
Db 661 LELPQYTSSDSDESYPYTLIDSLVLMYPYCKSLDIFTVGGSGDGVVNTNSAWETQRYRCLE 720
QY 721 NSRSVVKTPMTDVCNRIIPFISALLHQTGLACECDPQGSLSVCDPNGGCQCQCRPNVVG 780
Db 721 NSRSVVKTPMTDVCNRIIPFISALLHQTGLACECDPQGSLSVCDPNGGCQCQCRPNVVG 780
QY 781 TCNRCAPGTFGFGPSGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDRCLPGHWGF 840
Db 781 TCNRCAPGTFGFGPSGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDRCLPGHWGF 840
QY 841 PSCQPCQCNHADDCCDPTVTECLNCQDYTMGHNCERCLAGYGDPIIGSGDHCRCPCPCPD 900
Db 841 PSCQPCQCNHADDCCDPTVTECLNCQDYTMGHNCERCLAGYGDPIIGSGDHCRCPCPCPD 900
QY 901 GPDSGRQFARSCYQDPVTIQLACVCDPGYIGSRDDCASGYFGNPNSEVGGSCQPCQCHNN 960
Db 901 GPDSGRQFARSCYQDPVTIQLACVCDPGYIGSRDDCASGYFGNPNSEVGGSCQPCQCHNN 960
QY 961 IDTTDPEACDKETGRCLKLYHTEGEHCQFCRFGYGDALRQDCRKCVCNLYGTVQEHCN 1020
Db 961 IDTTDPEACDKETGRCLKLYHTEGEHCQFCRFGYGDALRQDCRKCVCNLYGTVQEHCN 1020
QY 1021 GSDCQCDKATGQCLCLPNVIGQNCDCRCAPNTWQLASGTGCDPCNCNAHSFGPSCNEFTG 1080
Db 1021 GSDCQCDKATGQCLCLPNVIGQNCDCRCAPNTWQLASGTGCDPCNCNAHSFGPSCNEFTG 1080
QY 1081 QCQMPFGGRTCTSECQELFWGDDVECRACDCDPRGIETPQCDQSTGCVCVEGVEGPR 1140
Db 1081 QCQMPFGGRTCTSECQELFWGDDVECRACDCDPRGIETPQCDQSTGCVCVEGVEGPR 1140
QY 1141 CDKCTRGYSGVFPDCTPCHQCFALWDVIIAELTNRTHRFLEKAKALKISGVIGPYRETVD 1200
Db 1141 CDKCTRGYSGVFPDCTPCHQCFALWDVIIAELTNRTHRFLEKAKALKISGVIGPYRETVD 1200
QY 1201 SVERKVSEIKDILAQSRAEPLKNIGNLFEEAEKLIKDVTEMMAQVEVKLSDTTSQSNST 1260
Db 1201 SVERKVSEIKDILAQSRAEPLKNIGNLFEEAEKLIKDVTEMMAQVEVKLSDTTSQSNST 1260
QY 1261 AKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTTE 1320
Db 1261 AKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTTE 1320
QY 1321 PNSTVEQSALMRDRVEDVMNERESQFKEKQEEQARLLDELAKGLQSLDLSAAEMTCGTP 1380
Db 1321 PNSTVEQSALMRDRVEDVMNERESQFKEKQEEQARLLDELAKGLQSLDLSAAEMTCGTP 1380
QY 1381 PGASCSETECGGPNCRDTDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVL SALAEVEQL 1440
Db 1381 PGASCSETECGGPNCRDTDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVL SALAEVEQL 1440

QY 1441 SKMVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNEELRNLIKQIRNFLTQDSADLDSI 1500
Ddb 1441 SKMVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNEELRNLIKQIRNFLTQDSADLDSI 1500
QY 1501 EAVANEVLKXEMPSTPQQLNLTEDIRERVESLSQVEVILQHSAAADIARAEMLLEBAKRA 1560
Ddb 1501 EAVANEVLKXEMPSTPQQLNLTEDIRERVESLSQVEVILQHSAAADIARAEMLLEBAKRA 1560
QY 1561 SKSATDVKVTADMVKEALEEAEKQVAAEKAQADEDIQGTQNLTSIESETAASEETL 1620
Ddb 1561 SKSATDVKVTADMVKEALEEAEKQVAAEKAQADEDIQGTQNLTSIESETAASEETL 1620
QY 1621 FNASQRISSELRNVEELKRKAQNSGEABYIEKVVTYVKQSAEDVKKTLDGELDEKYKKV 1680
Ddb 1621 FNASQRISSELRNVEELKRKAQNSGEABYIEKVVTYVKQSAEDVKKTLDGELDEKYKKV 1680
QY 1681 ENLIAKTTESADARRKAEMLQNEAKTLLAQANSKQLLKDLEKRYEDNQRYLEDKAQEL 1740
Ddb 1681 ENLIAKTTESADARRKAEMLQNEAKTLLAQANSKQLLKDLEKRYEDNQRYLEDKAQEL 1740
QY 1741 ARLEGEVRSLLKDISQKVAVYSTCL 1765
Ddb 1741 ARLEGEVRSLLKDISQKVAVYSTCL 1765

RESULT 3
ABB81591
ID ABB81591 standard; protein; 1765 AA.
XX ABB81591;
XX 19-SEP-2002 (first entry)
XX Human laminin 10 second chain protein sequence SEQ ID NO:8.
DE Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;
KW tissue repair development; laminin; healing; vascular tissue;
KW re-endothelialisation; vascular injury; cell attachment; cell stasis;
KW proliferation; migration.
XX Homo sapiens.

XX WO200250111-A2.
XX 27-JUN-2002.
XX 21-DEC-2001; 2001WO-US051035.
XX 21-DEC-2000; 2000US-0257449P.
XX 28-MAR-2001; 2001US-0279282P.
XX 13-NOV-2001; 2001US-00279282.
XX (BIOS-) BIOSTRATUM INC.
XX Tryggvason K, Doi M, Thyboll J;
XX WPI; 2002-557650/59.
XX N-PSDB; ABQ72909.
XX New human laminin-10 proteins, useful for accelerating the healing of
XX vascular tissue, improving the biocompatibility of grafts, or for
XX promoting re-endothelialization at the site of vascular injuries.
XX Claim 9; Page 126-132; 231pp; English.
XX The present invention describes human laminin alpha 5. Also described is
XX an isolated laminin 10. Laminin 10 has vulnery activity. Laminins are
XX useful in maintaining cell/tissue phenotype as well as promoting cell
XX growth and differentiation in tissue repair development. Specifically,
XX laminin 10 can be used for accelerating the healing injuries of vascular
XX tissue, improving the biocompatibility of grafts useful for treating such
XX injuries, for promoting re-endothelialisation at the site of vascular

CC injuries, and promote cell attachment and subsequent cell stasis,
CC proliferation, differentiation, and/or migration. The present sequence
CC represents a second chain protein of laminin 10, from the present
CC invention
XX
SQ Sequence 1765 AA;
Query Match 100.0%; Score 9654; DB 5; Length 1765;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 OEPEFSYGAEGSCYPATGDLILIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICNS 60
Ddb 1 OEPEFSYGAEGSCYPATGDLILIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICNS 60
QY 61 QDPYHETLNPDSHLEIENVVTTFAFNRLKIWWQSENGVENVTIQLDLAEAFHFTLIMTFK 120
Ddb 61 QDPYHETLNPDSHLEIENVVTTFAFNRLKIWWQSENGVENVTIQLDLAEAFHFTLIMTFK 120
QY 121 TFRPAAMLIERSDDFGKTGWVYRYPAYDCEASFPGISGPMKKVDDDIICDSRYSIDIEPST 180
Ddb 121 TFRPAAMLIERSDDFGKTGWVYRYPAYDCEASFPGISGPMKKVDDDIICDSRYSIDIEPST 180
QY 181 EGEVIFRALDPAFKIEDPSPRIQNLKLTNLRIFVKLHGLDNLDSRMEIREKYYYA 240
Ddb 181 EGEVIFRALDPAFKIEDPSPRIQNLKLTNLRIFVKLHGLDNLDSRMEIREKYYYA 240
QY 241 VYDMVVRGNCFCYGHASECAPVDGENEEVEGMVHGHCMCRHNTKGLNCELMDIFYHDLPW 300
Ddb 241 VYDMVVRGNCFCYGHASECAPVDGENEEVEGMVHGHCMCRHNTKGLNCELMDIFYHDLPW 300
QY 301 RPAEGRNSACKKCNKNEHSISCHFDMAVYLATGNVSGGVDDCQHNTMGRNCEQCKPFY 360
Ddb 301 RPAEGRNSACKKCNKNEHSISCHFDMAVYLATGNVSGGVDDCQHNTMGRNCEQCKPFY 360
QY 361 YQHPERDIRDPNFCERCTCDPAGSONEGICDSYDTFSTGLIAGQCRCKLNVEGEHCDVCK 420
Ddb 361 YQHPERDIRDPNFCERCTCDPAGSONEGICDSYDTFSTGLIAGQCRCKLNVEGEHCDVCK 420
QY 421 EGFYDLSSDDPFGCKSCACNPLGTIPGGNPNCDSETGHYCKRLVTGQHCDCQLPEHWGLS 480
Ddb 421 EGFYDLSSDDPFGCKSCACNPLGTIPGGNPNCDSETGHYCKRLVTGQHCDCQLPEHWGLS 480
QY 481 NDLGCRPCDCDLGALNNSCFAESGQCSRPHMIGRQNEVEPGYFATLDHYLYEAE 540
Ddb 481 NDLGCRPCDCDLGALNNSCFAESGQCSRPHMIGRQNEVEPGYFATLDHYLYEAE 540
QY 541 ANLPGVSIIVERQYIQDRIPSWTGAFFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 600
Ddb 541 ANLPGVSIIVERQYIQDRIPSWTGAFFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 600
QY 601 DHWEKAVITVORPGRIPTSSRCGNTIPDDNQVWVSLSPGSRYVLPVPRVCFEKGNTYTVR 660
Ddb 601 DHWEKAVITVORPGRIPTSSRCGNTIPDDNQVWVSLSPGSRYVLPVPRVCFEKGNTYTVR 660
QY 661 LELPQYTSDDSDVESPYTLIDSLVLMPYCKSLDIFTVGGSGDVVTNSAWETFORYRCLE 720
Ddb 661 LELPQYTSDDSDVESPYTLIDSLVLMPYCKSLDIFTVGGSGDVVTNSAWETFORYRCLE 720
QY 721 NSRSVVKTPMTDVCRNIIFSISALIHQTGLACECDPQGSLSVCDPNGGQCQCRPNVVGR 780
Ddb 721 NSRSVVKTPMTDVCRNIIFSISALIHQTGLACECDPQGSLSVCDPNGGQCQCRPNVVGR 780
QY 781 TCNRCAPGTGFGPSGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDRCLPGHWGF 840
Ddb 781 TCNRCAPGTGFGPSGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDRCLPGHWGF 840
QY 841 PSCQPCQCNGHADDCCDPTVTECLNCDYTMGNHCERCLAGYVGDPIIGSDHCRPCPCPD 900
Ddb 841 PSCQPCQCNGHADDCCDPTVTECLNCDYTMGNHCERCLAGYVGDPIIGSDHCRPCPCPD 900
QY 901 GPDSGRQFARSCYQDPVTQLACVCDPGYIGSRCDDCASGYFGNPEVGGSCQPCQCHNN 960
Ddb 901 GPDSGRQFARSCYQDPVTQLACVCDPGYIGSRCDDCASGYFGNPEVGGSCQPCQCHNN 960

Db 901 GPDSGRQFARSCYQDPVTIQLACVDPGYIGSRCDDCASGYFGNPNSEVGGSCPCQCCHNN 960

QY 961 IDTTDPEACDKETGRCLKCLYHTEGEHCQFCRFGYGDALRQDCRKVCNLYLGTVQEHCN 1020

Db 961 IDTTDPEACDKETGRCLKCLYHTEGEHCQFCRFGYGDALRQDCRKVCNLYLGTVQEHCN 1020

QY 1021 GSDCQCDKATGQCLCLPNVIGQNCDCRCAPNTWOLASGTGCDPCNCNAAHSFGPSCNEFTG 1080

Db 1021 GSDCQCDKATGQCLCLPNVIGQNCDCRCAPNTWOLASGTGCDPCNCNAAHSFGPSCNEFTG 1080

QY 1081 QCQCMFGGGRTCSECQELFWGDPDVECRACDCDPRGIETPQCQDSTGCVCVEGVEGPR 1140

Db 1081 QCQCMFGGGRTCSECQELFWGDPDVECRACDCDPRGIETPQCQDSTGCVCVEGVEGPR 1140

QY 1141 CDKCTRGYSGVFPDCTPCHQCFALWDVIAELTNRTHRFLEKAKALKISGIVGYRETVD 1200

Db 1141 CDKCTRGYSGVFPDCTPCHQCFALWDVIAELTNRTHRFLEKAKALKISGIVGYRETVD 1200

QY 1201 SVERKVSEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDVTEMAQVEVKLSDDTTSQSNST 1260

Db 1201 SVERKVSEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDVTEMAQVEVKLSDDTTSQSNST 1260

QY 1261 AKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAERVNASITTE 1320

Db 1261 AKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAERVNASITTE 1320

QY 1321 PNSTVEQSALMRDRVEDVMVERESQFKEQEEOARLLDELAKGLQSLDLSAAEMTCGTP 1380

Db 1321 PNSTVEQSALMRDRVEDVMVERESQFKEQEEOARLLDELAKGLQSLDLSAAEMTCGTP 1380

QY 1381 PGASCSETECGGPNCRTEDEGRKCGGPGCGGLVTVAHNAWQKAMDLDQDVLASALAEVEQL 1440

Db 1381 PGASCSETECGGPNCRTEDEGRKCGGPGCGGLVTVAHNAWQKAMDLDQDVLASALAEVEQL 1440

QY 1441 SKWVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNEELRNLIKQIRNFLTQDSADLDSI 1500

Db 1441 SKWVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNEELRNLIKQIRNFLTQDSADLDSI 1500

QY 1501 EAVANEVLKMEPSTPQQLQNLTEDIRERVESLSQVEVILQHSAAADIARAEMLLLEEAKRA 1560

Db 1501 EAVANEVLKMEPSTPQQLQNLTEDIRERVESLSQVEVILQHSAAADIARAEMLLLEEAKRA 1560

QY 1561 SKSATDVKVTADMVKEALEEAEKAQVAEAEKAIKQADEDIQGTQNLTSIESETAASEETL 1620

Db 1561 SKSATDVKVTADMVKEALEEAEKAQVAEAEKAIKQADEDIQGTQNLTSIESETAASEETL 1620

QY 1621 FNASQRISELERNVVELKRKAQNSGEAEYIEKVYTVKQSAEDVKKTLDGELDEKYKKV 1680

Db 1621 FNASQRISELERNVVELKRKAQNSGEAEYIEKVYTVKQSAEDVKKTLDGELDEKYKKV 1680

QY 1681 ENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLLKDLERKYEDNQRYLEDKAQEL 1740

Db 1681 ENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLLKDLERKYEDNQRYLEDKAQEL 1740

QY 1741 ARLEGEVRSLLKDISQKVAVYSTCL 1765

Db 1741 ARLEGEVRSLLKDISQKVAVYSTCL 1765

RESULT 4

AAW50893

ID AAW50893 standard; protein; 1786 AA.

XX AC AAW50893;

DT 07-DEC-1998 (first entry)

XX DE Human laminin B1 chain.

XX KW Laminin; human; beta-amyloid; amyloidosis; Alzheimer's disease;

KW KW Down's syndrome; hereditary cerebral haemorrhage; inflammation;

KW KW malignancy; Familial Mediterranean Fever; multiple myeloma;

KW type II diabetes; prion disease; Creutzfeldt-Jacob disease; CJD;

KW Gertsmann-Straussler syndrome; kuru; scrapie; haemodialysis;

KW carpal tunnel syndrome; senile cardiac amyloid polyneuropathy;

KW Familial Amyloidotic Polyneuropathy; thyroid carcinoma; diagnosis;

XX therapy.

OS Homo sapiens.

XX WO9815179-A1.

PN 16-APR-1998.

PD 08-OCT-1997; 97WO-US018145.

XX 08-OCT-1996; 96US-0027981P.

PF (UNIW) UNIV WASHINGTON.

XX Castillo G, Snow AD;

PI WPI; 1998-240534/21.

XX Use of laminin and fragments - for developing products for use in the

DR diagnosis and treatment of amyloid disease, e.g. Alzheimer's disease or

XX CJD.

PS Claim 15; Page 86-89; 132pp; English.

XX This is the amino acid sequence of the human laminin B1 chain. The

CC primary object of the invention is to use laminin, laminin-derived

CC protein fragments and/or laminin-derived polypeptides as potent

CC inhibitors of amyloid formation, deposition, accumulation and/or

CC persistence in Alzheimer's disease and other amyloidoses. The laminin

CC products (see AAW50888-98) may include mouse or human laminin A or A1

CC chain, laminin B1 or B2 chain, laminin A2 chain (merosin), laminin G1

CC chain, the globular repeats of the laminin A1 chain and the beta-amyloid

CC binding domain of the laminin A chain. A claimed method for treating an

CC amyloid disease comprises administering a polypeptide having a

CC conformational similarity to a fragment of a laminin protein. A method

CC for diagnosing an amyloid disease involves determining levels of laminin

CC in a sample. Production of laminin or its fourth globular repeat in vivo

CC provides a method for in vivo inhibition of beta-amyloid amyloidosis. The

CC products and methods can be used for the diagnosis, prognosis, monitoring

CC and treatment of amyloidoses such as Alzheimer's disease, Down's syndrome

CC and hereditary cerebral haemorrhage with amyloidosis of the Dutch type

CC (where the specific amyloid is the beta-amyloid protein), the amyloidosis

CC associated with chronic inflammation, various forms of malignancy and

CC Familial Mediterranean Fever (AA amyloid or inflammation-association

CC amyloidosis), the amyloidosis associated with multiple myeloma and other

CC B-cell abnormalities (AL amyloid), the amyloidosis associated with type

CC II diabetes (amylin or islet amyloid), the amyloidosis associated with

CC prion diseases including Creutzfeldt-Jacob disease, Gertsmann-Straussler

CC syndrome, kuru and animal scrapie (Prp amyloid), the amyloidosis

CC associated with long-term haemodialysis and carpal tunnel syndrome (beta

CC 2-microglobulin amyloid), the amyloidosis associated with senile cardiac

CC amyloid and Familial Amyloidotic Polyneuropathy (prealbumin or

CC transthyretin amyloid), and the amyloidosis associated with endocrine

CC tumours such as medullary carcinoma of the thyroid (variant of

CC procalcitonin)

XX SQ Sequence 1786 AA;

Query Match 100.0%; Score 9654; DB 2; Length 1786;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QEPEFSYGCAGSCYPATGDLILIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICNS 60

Db 22 QEPEFSYGCAGSCYPATGDLILIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICNS 81

QY 61 QDPYHETLNPDPSHLIENVTTFAPNRLKIWWQSENGVENVTIQLDLEAEFFHFLIMTFK 120

Db 82 QDPYHETLNPDPSHLIENVTTFAPNRLKIWWQSENGVENVTIQLDLEAEFFHFLIMTFK 141

QY 121 TFRPAAMLIERSDFGKTGWVYRYFAYDCEASFPGISTGPMKKVDDIIICDSRYSIDIEPST 180
DB 142 TFRPAAMLIERSDFGKTGWVYRYFAYDCEASFPGISTGPMKKVDDIIICDSRYSIDIEPST 201
QY 181 EGEVIFRALDPARKIEDPYSPRIQNLKLTNLRIFKFKLHTLGNLLDSRMEIREKYIYA 240
DB 202 EGEVIFRALDPARKIEDPYSPRIQNLKLTNLRIFKFKLHTLGNLLDSRMEIREKYIYA 261
QY 241 VYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGCHMCRRHNTKGLNCELMDFFYHDLPW 300
DB 262 VYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGCHMCRRHNTKGLNCELMDFFYHDLPW 321
QY 301 RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGGVCDCCQHNMTGRNCEQCKPFY 360
DB 322 RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGGVCDCCQHNMTGRNCEQCKPFY 381
QY 361 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSTGLIAGQCRCKLNVEGEHCDVCK 420
DB 382 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSTGLIAGQCRCKLNVEGEHCDVCK 441
QY 421 EGFYDLSSDPFGCKSCACNPLGTIPGGNPNCDSETGHYCKRLVTGQHCDQCCLPEHWGLS 480
DB 442 EGFYDLSSDPFGCKSCACNPLGTIPGGNPNCDSETGHYCKRLVTGQHCDQCCLPEHWGLS 501
QY 481 NDLDGCRPCDCDLGGALNNSCFAESGQCSRPHMIGRQCNEVEPGYFATLDHLYEAE 540
DB 502 NDLDGCRPCDCDLGGALNNSCFAESGQCSRPHMIGRQCNEVEPGYFATLDHLYEAE 561
QY 541 ANLPGVSIIVERQYIQDIRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 600
DB 562 ANLPGVSIIVERQYIQDIRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 621
QY 601 DHWEKAVITVQRPGRIPTSRRCGNTIPDDDNQVVSLSPGSRYYVLPVPVCFEKGNTYTVR 660
DB 622 DHWEKAVITVQRPGRIPTSRRCGNTIPDDDNQVVSLSPGSRYYVLPVPVCFEKGNTYTVR 681
QY 661 LELPOYTSSDSVESPYTLIDSLVLMPYCKSLDIFTVGGSGDGVVWNSAWETFORYRCLE 720
DB 682 LELPOYTSSDSVESPYTLIDSLVLMPYCKSLDIFTVGGSGDGVVWNSAWETFORYRCLE 741
QY 721 NSRSVVKTPMTDVCNRIIFISALLHOTGLACECDPQGSLSVCDPNQGCQCRPNVVG 780
DB 742 NSRSVVKTPMTDVCNRIIFISALLHOTGLACECDPQGSLSVCDPNQGCQCRPNVVG 801
QY 781 TCNRCAPGTGFGPGSGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDRCLPGHWGF 840
DB 802 TCNRCAPGTGFGPGSGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDRCLPGHWGF 861
QY 841 PSCQPCQCNHADDCTPVTGECLNCQDVTMGHCNRCCLAGYGDPIIGSGDHCRCPCPCPD 900
DB 862 PSCQPCQCNHADDCTPVTGECLNCQDVTMGHCNRCCLAGYGDPIIGSGDHCRCPCPCPD 921
QY 901 GPDSGRQFARSCYQDPVTIQLACVCDPGYIGSRCDDCASGYFGNPFSEVSGSCQPCQCHN 960
DB 922 GPDSGRQFARSCYQDPVTIQLACVCDPGYIGSRCDDCASGYFGNPFSEVSGSCQPCQCHN 981
QY 961 IDTTDPEACDKETGRCLKCLYHTEGEHCQCFRFGYIGDALRQDCRKCVCNVLGTVOEHCN 1020
DB 982 IDTTDPEACDKETGRCLKCLYHTEGEHCQCFRFGYIGDALRQDCRKCVCNVLGTVOEHCN 1041
QY 1021 GSDCQCDKATGQCLCPNVIGQNCDCRCAPNTWQLASGTGCDPCNCAHSPGSPCNEFTG 1080
DB 1042 GSDCQCDKATGQCLCPNVIGQNCDCRCAPNTWQLASGTGCDPCNCAHSPGSPCNEFTG 1101
QY 1081 QCQCMFGFGGRTCSECELEFWGDDVECRACDCCDPRIETPQCDQSTGQCVCVEGVEGPR 1140
DB 1102 QCQCMFGFGGRTCSECELEFWGDDVECRACDCCDPRIETPQCDQSTGQCVCVEGVEGPR 1161
QY 1141 CDKCTRGSYSGVFPDCTPCHQCPCALWDVIIAELTNRTHRFLEKAKALKISGVIPIRETVD 1200
DB 1162 CDKCTRGSYSGVFPDCTPCHQCPCALWDVIIAELTNRTHRFLEKAKALKISGVIPIRETVD 1221
QY 1201 SVERKVSEIKDILAQSPAAEPLKNIKNLFEEAEKLIKDVTEMAQVEVKLSDTTSQSNST 1260

DB 1222 SVERKVSEIKDILAQSPAAEPLKNIKNLFEEAEKLIKDVTEMAQVEVKLSDTTSQSNST 1281
QY 1261 AKELDSLQTEAESLDNTVKELAEQLEFIKNDSIDIRGALDSITKYFQMSLEAEERNASTTE 1320
DB 1282 AKELDSLQTEAESLDNTVKELAEQLEFIKNDSIDIRGALDSITKYFQMSLEAEERNASTTE 1341
QY 1321 PNSTVEQSALMRDVEDVMMERESQFKEKQEEQARLLDELAKQLQSLDLSAAAEEMTCGTP 1380
DB 1342 PNSTVEQSALMRDVEDVMMERESQFKEKQEEQARLLDELAKQLQSLDLSAAAEEMTCGTP 1401
QY 1381 PGASCSETECGGNCRTDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVL SALAEVEQL 1440
DB 1402 PGASCSETECGGNCRTDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVL SALAEVEQL 1461
QY 1441 SKMVSEAKLRADAEAKQSAEDILLKTNATKBMKDKSNEELRNLIKQIRNFLTQDSADLDSI 1500
DB 1462 SKMVSEAKLRADAEAKQSAEDILLKTNATKBMKDKSNEELRNLIKQIRNFLTQDSADLDSI 1521
QY 1501 EAVANEVLKMEMSTPQQLQNLTEDIRERVESLSQVEVILQHSADIAEAEMLLLEEAKRA 1560
DB 1522 EAVANEVLKMEMSTPQQLQNLTEDIRERVESLSQVEVILQHSADIAEAEMLLLEEAKRA 1581
QY 1561 SKSATDVKVTADMVKEALEEAEAKQAQAAEKAQKQADEDIQGTQNLTSIESETAASEETL 1620
DB 1582 SKSATDVKVTADMVKEALEEAEAKQAQAAEKAQKQADEDIQGTQNLTSIESETAASEETL 1641
QY 1621 FNASQRISELERNVBELKRKAAQNSGEAEYIEKVYTVKQSAEDVKKTLDCGELDEKYYKV 1680
DB 1642 FNASQRISELERNVBELKRKAAQNSGEAEYIEKVYTVKQSAEDVKKTLDCGELDEKYYKV 1701
QY 1681 ENLIAKTEESADARRKAEMLQNEAKTLQAQNSKLQLLKDLERKYEDNQRYLEDKAQEL 1740
DB 1702 ENLIAKTEESADARRKAEMLQNEAKTLQAQNSKLQLLKDLERKYEDNQRYLEDKAQEL 1761
QY 1741 ARLEGEVRSLLKDISOKVAVYSTCL 1765
DB 1762 ARLEGEVRSLLKDISOKVAVYSTCL 1786

RESULT 5

AAB16522
ID AAB16522 standard; protein; 1786 AA.
XX
AC AAB16522;
XX
DT 27-OCT-2000 (first entry)
XX
DE Human laminin protein sequence.
XX
KW Angiogenesis-inhibiting protein receptor; angiogenesis; angiostatin;
KW endostatin; plasminogen; laminin; treatment; wound healing; solid tumour;
KW psoriasis; scleroderma; myocardial angiogenesis; Crohn's disease;
KW cerebral collateral; arteriovenous malformation; rubeosis; cancer;
KW diabetic retinopathy; arthritis; wound healing; peptic ulcer;
KW Helicobacter related disease; fracture; cat scratch fever.
XX
OS Homo sapiens.
XX
PN WO200032631-A2.
XX
PD 08-JUN-2000.
XX
PF 06-DEC-1999; 99WO-US028897.
XX
PR 04-DEC-1998; 98US-00206059.
XX
PA (ENTR-) ENTREMED INC.
XX
PI Macdonald NJ, Sim KL;
XX
DR WPI; 2000-412290/35.
XX

PT New angiogenesis-inhibiting protein receptors, useful in methods for
PT treating diseases and processes that are mediated by angiogenesis, such
PT as solid tumors, psoriasis, scleroderma and myocardial angiogenesis.
XX
PS Claim 1; Fig 6A; 100pp; English.
XX
CC This invention relates to angiogenesis-inhibiting protein receptors, and
CC the DNA sequences encoding them. Angiogenesis is the generation of new
CC blood vessels into a tissue, and normally occurs in wound healing, foetal
CC and embryonal development and the formation of the corpus luteum,
CC endometrium and placenta. Angiostatin is a protein (see AAB16450 and
CC AAA68202) involved in angiogenesis, and has an amino acid sequence
CC similar to that of a plasminogen fragment (see murine plasminogen
CC AAB16490). Angiostatin has the ability to inhibit angiogenesis.
CC Endostatin is also an angiogenesis inhibiting protein (see AAB16451 and
CC AAA68203). Sequences AAA68242 and AAB16522 represent coding and protein
CC sequences of human laminin. Laminin is an angiostatin binding protein,
CC and some of the peptides of the invention share homology with regions of
CC laminin. Peptides AAB16452-B16521 (excluding AAB16490) are the
CC angiogenesis-inhibiting protein receptor fragments and can be used in methods
CC for treating diseases and processes that are mediated by angiogenesis,
CC such as solid tumors, psoriasis, scleroderma, myocardial angiogenesis,
CC Crohn's disease, cerebral collaterals, arteriovenous malformations,
CC rubeosis, diabetic retinopathy, arthritis, wound healing, peptic ulcers,
CC Helicobacter related diseases, fractures, placental and cat scratch
CC fever. They are useful for the detection and prognosis of cancer. DNA
CC sequences A628204-A628241 encode the peptides of the invention
XX
SQ Sequence 1786 AA;
Query Match 100.0%; Score 9654; DB 3; Length 1786;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QEPFSGCAEGSCYPATGDLIGRAQKLSVTSTGLHKPEPYCIVSHLQEDKKCFICNS 60
DB 22 QEPFSGCAEGSCYPATGDLIGRAQKLSVTSTGLHKPEPYCIVSHLQEDKKCFICNS 81
QY 61 QDPYHETLNPDLSHLIENVVTFAPNRLKIWQSENGVENVTIQLDLEAEFHTLIMTFK 120
DB 82 QDPYHETLNPDLSHLIENVVTFAPNRLKIWQSENGVENVTIQLDLEAEFHTLIMTFK 141
QY 121 TFRPAAMLIERSDDFGKTGWVRYFAYDCEASFPGISTGPMKKVDDIICDSRYSDIEPST 180
DB 142 TFRPAAMLIERSDDFGKTGWVRYFAYDCEASFPGISTGPMKKVDDIICDSRYSDIEPST 201
QY 181 EGEVIFRALDPAFKIEDPSPRIQNLKLTNLRIFVKLHTLGDNLDSRMEIREKYYA 240
DB 202 EGEVIFRALDPAFKIEDPSPRIQNLKLTNLRIFVKLHTLGDNLDSRMEIREKYYA 261
QY 241 VYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGCWCRHNTKGLNCELMDFYHDLPW 300
DB 262 VYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGCWCRHNTKGLNCELMDFYHDLPW 321
QY 301 RPAEGRNSNACKKCNCHNSISCHFDMAVYLATGNVSGVGVDDCCQHNTMGRNCEQCKPFY 360
DB 322 RPAEGRNSNACKKCNCHNSISCHFDMAVYLATGNVSGVGVDDCCQHNTMGRNCEQCKPFY 381
QY 361 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFDFTGLIAGQCRCKLNVEGEHCDVCK 420
DB 382 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFDFTGLIAGQCRCKLNVEGEHCDVCK 441
QY 421 EGFYDLSSDDPFGCKSCACNPLGTIPGGNPPCDSETGHYCKRLVTGQHCDQCLPEHWGLS 480
DB 442 EGFYDLSSDDPFGCKSCACNPLGTIPGGNPPCDSETGHYCKRLVTGQHCDQCLPEHWGLS 501
QY 481 NDLGCRPCDCLGGALNNSCFBESGQCSCRPHMIGRQCNVEVEPGYYFATLDHYLYEAE 540
DB 502 NDLGCRPCDCLGGALNNSCFBESGQCSCRPHMIGRQCNVEVEPGYYFATLDHYLYEAE 561
QY 541 ANLGPVSIVERQYIQDRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 600
|||||

DB 562 ANLGPVSIVERQYIQDRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 621
QY 601 DHWEKAVITVQRPGRIPPTSSRCNGTIPDDDNQVVSLSPGSRYVVLPRPVCFEKGTNYTVR 660
DB 622 DHWEKAVITVQRPGRIPPTSSRCNGTIPDDDNQVVSLSPGSRYVVLPRPVCFEKGTNYTVR 681
QY 661 LELPOYTSSDSDVESPYTLIDSLVLMYPYCKSLDIFTVGGSGDGVVNTNSAWETFORYRCLE 720
DB 682 LELPOYTSSDSDVESPYTLIDSLVLMYPYCKSLDIFTVGGSGDGVVNTNSAWETFORYRCLE 741
QY 721 NSRSVVKTPMTDVCRNIIIFSISALLHQTGLACECDPQGSLSVCDPNGGQCQCRPNVVG 780
DB 742 NSRSVVKTPMTDVCRNIIIFSISALLHQTGLACECDPQGSLSVCDPNGGQCQCRPNVVG 801
QY 781 TCNRCAPGTFGFGSPGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDCRCLPGHMGF 840
DB 802 TCNRCAPGTFGFGSPGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDCRCLPGHMGF 861
QY 841 PSCQPCQCNHADDGCDPVTGECNLCQDYTMGHNCERCLAGYGDPIIGSGDHCRPCPCPD 900
DB 862 PSCQPCQCNHADDGCDPVTGECNLCQDYTMGHNCERCLAGYGDPIIGSGDHCRPCPCPD 921
QY 901 GPDGRQFARSCYQDPVTIQLACVCDPGYIGSRCDDCASGYFGNPNSEVGGSCQPCQCHNN 960
DB 922 GPDGRQFARSCYQDPVTIQLACVCDPGYIGSRCDDCASGYFGNPNSEVGGSCQPCQCHNN 981
QY 961 IDTTDPEACDKETGRCLKLYHTEGEHCQFCRFGYIGDALRQDCRKCVCNLYLGTVEHCN 1020
DB 982 IDTTDPEACDKETGRCLKLYHTEGEHCQFCRFGYIGDALRQDCRKCVCNLYLGTVEHCN 1041
QY 1021 GSDCQCDKATGQCLCLPNVIGQNCDCRCPNTWOLASGTGCDPCNCNAAHSFGPSCNEFTG 1080
DB 1042 GSDCQCDKATGQCLCLPNVIGQNCDCRCPNTWOLASGTGCDPCNCNAAHSFGPSCNEFTG 1101
QY 1081 QCQWFGFGGRTCTSECQELFWGDDPVECRACDCDPRGIETPCQDQSTGQCVCVEGVEGPR 1140
DB 1102 QCQWFGFGGRTCTSECQELFWGDDPVECRACDCDPRGIETPCQDQSTGQCVCVEGVEGPR 1161
QY 1141 CDKCTRGSYGVFPDCTPCHQCFALWDVIIAELTNTRHFRLEKAKALKISGVIGPYRETVD 1200
DB 1162 CDKCTRGSYGVFPDCTPCHQCFALWDVIIAELTNTRHFRLEKAKALKISGVIGPYRETVD 1221
QY 1201 SVERKVSEIKDILAQSPAEPKLNIGNLFEEAEKLIKDVTEMMAQVEVKLSDTTSQSNST 1260
DB 1222 SVERKVSEIKDILAQSPAEPKLNIGNLFEEAEKLIKDVTEMMAQVEVKLSDTTSQSNST 1281
QY 1261 AKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTTE 1320
DB 1282 AKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTTE 1341
QY 1321 PNSTVEQSALMRDRVEDVMMERESQFKEKQEQARLLDELAKGLQSLDLSAAAEIMTCCTP 1380
DB 1342 PNSTVEQSALMRDRVEDVMMERESQFKEKQEQARLLDELAKGLQSLDLSAAAEIMTCCTP 1401
QY 1381 PGASCSETECGGPNCRCTDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLSEAEVEQL 1440
DB 1402 PGASCSETECGGPNCRCTDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLSEAEVEQL 1461
QY 1441 SKMVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNEELRNLIKQIRNFLTQDSADLDSI 1500
DB 1462 SKMVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNEELRNLIKQIRNFLTQDSADLDSI 1521
QY 1501 EAVANEVLKWMEMPSTPQQLQNLTEDIRERVESLSQVEVILQHSAAADIAEAEMLLEAAKRA 1560
DB 1522 EAVANEVLKWMEMPSTPQQLQNLTEDIRERVESLSQVEVILQHSAAADIAEAEMLLEAAKRA 1581
QY 1561 SKSATDVKVTADMVKEALEEAEKAAQVAAEKAIKQADEDIQGTQNLTSIESETAASBETL 1620
DB 1582 SKSATDVKVTADMVKEALEEAEKAAQVAAEKAIKQADEDIQGTQNLTSIESETAASBETL 1641
QY 1621 FNASQRISSELERNVEELKRKAQNSGEAEYIEKVVTYVKQSAEDVKKTLTGDELDEKVKY 1680
DB 1642 FNASQRISSELERNVEELKRKAQNSGEAEYIEKVVTYVKQSAEDVKKTLTGDELDEKVKY 1701

QY 1681 ENLIAKTEESADARRKAEMLQNEAKTLIAQANSKIQLLKDLERKYEDNQRYLEDKAQEL 1740
Db 1702 ENLIAKTEESADARRKAEMLQNEAKTLIAQANSKIQLLKDLERKYEDNQRYLEDKAQEL 1761
QY 1741 ARLEGEVRSLLKDISQKVAVYSTCL 1765
Db 1762 ARLEGEVRSLLKDISQKVAVYSTCL 1786

RESULT 6
AAB19797
ID AAB19797 standard; protein; 1786 AA.
XX AAB19797;
AC AAB19797;
XX 05-MAR-2001 (first entry)
DT Human laminin 2 beta-1 chain.
DE Laminin 2; human; nerve regeneration; angiogenic; cell adhesion;
XX degenerative muscle disorder; muscular dystrophy; cell therapy.
KW Homo sapiens.
XX OS
XX FH Key Location/Qualifiers
FT Peptide 1..21
FT /label= Signal_peptide
FT Protein 22..1786
FT /label= Mature_protein
XX WO200066730-A2.
PN 09-NOV-2000.
XX 28-APR-2000; 2000WO-US011378.
PF 30-APR-1999; 99US-0131720P.
XX 15-JUN-1999; 99US-0139198P.
PR 12-JUL-1999; 99US-0143289P.
PR 24-SEP-1999; 99US-0155945P.
XX

(UTNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
Yurchenco P;
WPI; 2000-687537/67.
N-PSDB; AAA88897.
Purified laminin 2 protein, useful for research and therapeutic purposes including peripheral nerve regeneration, treatment of degenerative muscle disorders, angiogenesis regulation, and ex vivo cell therapy.
Claim 5; Page 186-191; 305pp; English.
The present sequence is that of the beta-1 chain of human laminin 2. Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1 (100 kDa) chains. It is thought to be specifically required for stabilizing myotubes during skeletal muscle development, and for preventing apoptosis. Genetic defects in its structure or expression are associated with a major type of congenital muscular dystrophy. Laminin 2 is also thought to be important in Schwann cell/basal lamina interactions. The invention provides laminin 2 alpha-2, beta-1 and gamma-1 chain polypeptides (see AAB19791-806) and the polynucleotides encoding them (see AAA88891-906), methods for making recombinant laminin 2, cells that express recombinant laminin 2, and methods for using purified laminin 2 for research and therapeutic purposes including peripheral nerve regeneration, treatment of degenerative muscle disorders, angiogenesis regulation, promoting cell attachment and migration, ex vivo cell therapy, improving the take of grafts, improving the biocompatibility of medical devices and preparing improved culture devices and media

SQ Sequence 1786 AA;
Query Match 100.0%; Score 9654; DB 3; Length 1786;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QEPEFSYGCAEGSCYPATGDLIIAGRAQKLSVTSTCGLHKPEPYCIIVSHLQEDKKCFICNS 60
Db 22 QEPEFSYGCAEGSCYPATGDLIIAGRAQKLSVTSTCGLHKPEPYCIIVSHLQEDKKCFICNS 81
QY 61 QDPYHETLNPDHSHLIENVVTTFAPNRLKIWMQSENGVENVTIQLDLEAEFHFTHLIMTFK 120
Db 82 QDPYHETLNPDHSHLIENVVTTFAPNRLKIWMQSENGVENVTIQLDLEAEFHFTHLIMTFK 141
QY 121 TFRPAAMLIERSSDFGKTGWVRYFYAYDCEASFPFGISTGPMKKVDDIICDSRYSDIEPST 180
Db 142 TFRPAAMLIERSSDFGKTGWVRYFYAYDCEASFPFGISTGPMKKVDDIICDSRYSDIEPST 201
QY 181 EGEVIFRALDPAPKIEDPYSPRIQNLLKITNLRKIFVKLHTLGNLLDSRMEIREKYAYA 240
Db 202 EGEVIFRALDPAPKIEDPYSPRIQNLLKITNLRKIFVKLHTLGNLLDSRMEIREKYAYA 261
QY 241 VYDMVVRGNCFCYGHASECAPVDGFNEVEGMVHGHCMCRHNTKGLNCELMDFYHDLWP 300
Db 262 VYDMVVRGNCFCYGHASECAPVDGFNEVEGMVHGHCMCRHNTKGLNCELMDFYHDLWP 321
QY 301 RPAEGRNSNACKKCNCHSISCHFDMAVYLATGNVSGGVCDCCQHTMTGRNCEQCKPFY 360
Db 322 RPAEGRNSNACKKCNCHSISCHFDMAVYLATGNVSGGVCDCCQHTMTGRNCEQCKPFY 381
QY 361 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSTGLIAGQCRCKLNVEGEHCDVCK 420
Db 382 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSTGLIAGQCRCKLNVEGEHCDVCK 441
QY 421 EGFYDLSSDPFGCKSCACNPLGTIPGGNPNCDSETGHYCYCKRLVTGQHCDCQLPEHWGLS 480
Db 442 EGFYDLSSDPFGCKSCACNPLGTIPGGNPNCDSETGHYCYCKRLVTGQHCDCQLPEHWGLS 501
QY 481 NDLGCRPCDCDLGGALNNSCFAESGQCSRPHMIGRQCNEVEPGYFATLDHYLYEAE 540
Db 502 NDLGCRPCDCDLGGALNNSCFAESGQCSRPHMIGRQCNEVEPGYFATLDHYLYEAE 561
QY 541 ANLPGVSIIVERQYIQDRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 600
Db 562 ANLPGVSIIVERQYIQDRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 621
QY 601 DHWEKAVITVQRPGRIPPTSSRCGNTIPDDNQVWSLSPGSRYVVLPRPVCFEKGTNYTVR 660
Db 622 DHWEKAVITVQRPGRIPPTSSRCGNTIPDDNQVWSLSPGSRYVVLPRPVCFEKGTNYTVR 681
QY 661 LELPQYTSSDSVESPYYTLIDSLVLMPYCKSLDIFTVGGSGDGVVNTNSAWETFQRYRCLE 720
Db 682 LELPQYTSSDSVESPYYTLIDSLVLMPYCKSLDIFTVGGSGDGVVNTNSAWETFQRYRCLE 741
QY 721 NSRSVVKTPMTDVCERNIIFSIALLHQITGLACECDPQGSLSVCDPNGGQCQCRPNVAVGR 780
Db 742 NSRSVVKTPMTDVCERNIIFSIALLHQITGLACECDPQGSLSVCDPNGGQCQCRPNVAVGR 801
QY 781 TCNRCAPGTGFGPSGCKPCECHLQGSVNACFNPNVTGQCHCFQGVYARQCDRCLPGHWGF 840
Db 802 TCNRCAPGTGFGPSGCKPCECHLQGSVNACFNPNVTGQCHCFQGVYARQCDRCLPGHWGF 861
QY 841 PSCQPCQCNGHADDCTPVTGECLNCQDYTMGHNCERCLAGYIGDPIIGSGDHCRPCPCPD 900
Db 862 PSCQPCQCNGHADDCTPVTGECLNCQDYTMGHNCERCLAGYIGDPIIGSGDHCRPCPCPD 921
QY 901 GPDSGRQFARSCYQDPVTLQLACVCDPGYIGSRCDDCASGYFGNPSVGGSCQPCQCHNN 960
Db 922 GPDSGRQFARSCYQDPVTLQLACVCDPGYIGSRCDDCASGYFGNPSVGGSCQPCQCHNN 981
QY 961 IDTTDPEACDKETGRCLKCLYHTEGEHCQFCRFYGGDALRQDCRKCVCNLYLGTVOEHCN 1020
Db 982 IDTTDPEACDKETGRCLKCLYHTEGEHCQFCRFYGGDALRQDCRKCVCNLYLGTVOEHCN 1041

QY	1021	GSDCQCDKATGQCICLPNVIGQNCDCRCAPNTWQLASGTGCDPCNCNAHSGFSPSCNEFTG	1080
Db	1042	GSDCQCDKATGQCICLPNVIGQNCDCRCAPNTWQLASGTGCDPCNCNAHSGFSPSCNEFTG	1101
QY	1081	QCQCMFGGRTCTSECCQELFWGDPDVECRACDCDPRGDIETPQCQDSTGQCVCVGVGEGPR	1140
Db	1102	QCQCMFGGRTCTSECCQELFWGDPDVECRACDCDPRGDIETPQCQDSTGQCVCVGVGEGPR	1161
QY	1141	CDKCTRGYSGVFPDCTPCHQCFALWDVIIAELTNRTHRFLEKAKALKISGVIGPYRETVD	1200
Db	1162	CDKCTRGYSGVFPDCTPCHQCFALWDVIIAELTNRTHRFLEKAKALKISGVIGPYRETVD	1221
QY	1201	SVERKVSEIKDILAQSPAAPLKNIGNLFEEAEKLIKDVTEMMAQVEVKLSDTTSQSNST	1260
Db	1222	SVERKVSEIKDILAQSPAAPLKNIGNLFEEAEKLIKDVTEMMAQVEVKLSDTTSQSNST	1281
QY	1261	AKELDSLQTEAESLDNTVKELAQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTTE	1320
Db	1282	AKELDSLQTEAESLDNTVKELAQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTTE	1341
QY	1321	PNSTVEQSALMRDRVEDVMERESQFKEQEQRLLDELAGKLSLDLSAAEMTCGTP	1380
Db	1342	PNSTVEQSALMRDRVEDVMERESQFKEQEQRLLDELAGKLSLDLSAAEMTCGTP	1401
QY	1381	PGASCSETECGGPNCRDTDEGERKCGGPGCGGLVTVVAHNAWQKAMDLDQDVLALAEVEQL	1440
Db	1402	PGASCSETECGGPNCRDTDEGERKCGGPGCGGLVTVVAHNAWQKAMDLDQDVLALAEVEQL	1461
QY	1441	SKMVSEAKLRADAEAKQSAEDILKTNATKEMDKSNEELRNLIKQIRNFLTQDSADLDSI	1500
Db	1462	SKMVSEAKLRADAEAKQSAEDILKTNATKEMDKSNEELRNLIKQIRNFLTQDSADLDSI	1521
QY	1501	EAVANEVLKVMEMPSTPQQLNLTEDIRERVESLSQVEVILQHSAAADIARAEMLLBEAKRA	1560
Db	1522	EAVANEVLKVMEMPSTPQQLNLTEDIRERVESLSQVEVILQHSAAADIARAEMLLBEAKRA	1581
QY	1561	SKSATDVKVTADMVKEALEEAEKAQVAEAKAIAKQADEDIQGTQNLTLTSIESETAASEETL	1620
Db	1582	SKSATDVKVTADMVKEALEEAEKAQVAEAKAIAKQADEDIQGTQNLTLTSIESETAASEETL	1641
QY	1621	FNASQRISELERNVEELKRKAQNSGEAEYIEKVVTYVKQSAEDVKKTLDGELDEKIKKV	1680
Db	1642	FNASQRISELERNVEELKRKAQNSGEAEYIEKVVTYVKQSAEDVKKTLDGELDEKIKKV	1701
QY	1681	ENLIAKTEESADARRKAEMLQNEAKTLLAQANSKLQLLKDLEKRYEDNQRYLEDKAQEL	1740
Db	1702	ENLIAKTEESADARRKAEMLQNEAKTLLAQANSKLQLLKDLEKRYEDNQRYLEDKAQEL	1761
QY	1741	ARLEGEVRSLLKDISQKAVYSTCL	1765
Db	1762	ARLEGEVRSLLKDISQKAVYSTCL	1786
RESULT 7			
ID	AAB48448		
AC	AAB48448;		
DT	02-MAR-2001	(first entry)	
XX	Human laminin 8	polypeptide, SEQ ID NO: 14.	
DE	Human;	laminin 8; neuroprotective; angiogenic; osteopathic;	
XX	antiarteriosclerotic;	glycoprotein; mesenchymal tissue injury;	
KW	vascular tissue injury;	neural injury; angiogenesis regulation.	
XX	Homo sapiens.		
OS	WO2000066732-A2.		
XX	09-NOV-2000.		
PN			
XX			
PD			

XX	28-APR-2000;	2000WO-US011543.	
PF	30-APR-1999;	99US-0131720P.	
XX	21-AUG-1999;	99US-0149738P.	
PR	24-SEP-1999;	99US-0155945P.	
PR	11-FEB-2000;	2000US-0182012P.	
XX	(BIOS-) BIOSTRATUM INC.		
PA	Kortessmaa J,	Tryggvason K;	
XX	WPI;	2000-687539/67.	
PI	N-PSDB;	AAC83709.	
XX	Purified laminin 8 protein,	useful for research and therapeutic purposes	
PT	including peripheral nerve regeneration,	treatment of degenerative muscle	
PT	disorders, angiogenesis regulation,	and ex vivo cell therapy.	
XX	Claim 5;	Page 150-155; 245pp; English.	
PS	The present sequence is a laminin 8 polypeptide chain.	Laminins are a	
XX	family of heterotrimeric glycoproteins that function via binding		
CC	interactions with neighbouring cell receptors and by forming laminin		
CC	networks. They are signalling molecules which influence cellular		
CC	function. Laminin 8 is useful for treating injuries to tissue of		
CC	mesenchymal origin, such as bone, cartilage, tendon, and ligament,		
CC	treating injuries to vascular tissue, promoting cell attachment and		
CC	migration, ex vivo cell therapy, improving the biocompatibility of		
CC	medical devices, and preparing improved cell culture devices and media.		
CC	Laminin 8 is also useful for promoting re-endothelialisation at the site		
CC	of vascular injuries, improving the take of grafts, improving the		
CC	biocompatibility of medical devices, treating neural injuries (neural		
CC	regeneration), regulating angiogenesis, and promoting cell attachment and		
CC	migration		
XX	Sequence 1786 AA;		
SQ	Query Match	100.0%;	Score 9654; DB 3; Length 1786;
	Best Local Similarity	100.0%;	Pred. No. 0;
	Matches 1765;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	QEPEFSYGCAEGSCYPATGDLIGRAQLSVTSTCGLHKPEPYCIVSHLQEDKKCFICNS	60
Db	22	QEPEFSYGCAEGSCYPATGDLIGRAQLSVTSTCGLHKPEPYCIVSHLQEDKKCFICNS	81
QY	61	QDPYHETLNPDASHLIENVTTFAPNRLKIWWQSENGVENVTIQLDLEAEFFHFLIMTFK	120
Db	82	QDPYHETLNPDASHLIENVTTFAPNRLKIWWQSENGVENVTIQLDLEAEFFHFLIMTFK	141
QY	121	TFRPAAMLIERSDDFGKTGWVRYFAYDCEASFPGISTGPMKKVDDIICDSRYSDIEPST	180
Db	142	TFRPAAMLIERSDDFGKTGWVRYFAYDCEASFPGISTGPMKKVDDIICDSRYSDIEPST	201
QY	181	EGEVIFRALDPAFKIEDPYSPRIONLLKITNLRKFKVHLHTLGDNLDSRMEIREKYIYA	240
Db	202	EGEVIFRALDPAFKIEDPYSPRIONLLKITNLRKFKVHLHTLGDNLDSRMEIREKYIYA	261
QY	241	YDMMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGHCMCRHNTKGLNCEL CMDFYHDLPW	300
Db	262	YDMMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGHCMCRHNTKGLNCEL CMDFYHDLPW	321
QY	301	RPAEGRNSNACKKCNCSISCHFDMAVYLATGNVSGGVCDCCQHNMTGRNCEQCKPFY	360
Db	322	RPAEGRNSNACKKCNCSISCHFDMAVYLATGNVSGGVCDCCQHNMTGRNCEQCKPFY	381
QY	361	YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFDSTGLIAGQCRCKLNVEGEHCDVCK	420
Db	382	YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFDSTGLIAGQCRCKLNVEGEHCDVCK	441
QY	421	EGFYDLSSSEDPFGCKSCACNPLGTPGGNPNCDSETGHCHYCKRLVTGQHCDCQLPEHWGLS	480
Db	442	EGFYDLSSSEDPFGCKSCACNPLGTPGGNPNCDSETGHCHYCKRLVTGQHCDCQLPEHWGLS	501

QY	481	NDLDGCRPCDCDLGGALNNSCFAESGCSCRPHEMICRQCNEVEPGYYFATLDHLYEABE	540
Db	502	NDLDGCRPCDCDLGGALNNSCFAESGCSCRPHEMICRQCNEVEPGYYFATLDHLYEABE	561
QY	541	ANLPGVSIVERQYIQDRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP	600
Db	562	ANLPGVSIVERQYIQDRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP	621
QY	601	DHWEKAVITVQRPGRIPSTSSRCGNTIPDDDNQVVSISPGSRYVVLPRPVCFEKGTNYTVR	660
Db	622	DHWEKAVITVQRPGRIPSTSSRCGNTIPDDDNQVVSISPGSRYVVLPRPVCFEKGTNYTVR	681
QY	661	LELPQYTSSSDVESPYTLIDSLVLMPCYCKSLDIFTVGGSGDGVWTNSAWETFORYRCLE	720
Db	682	LELPQYTSSSDVESPYTLIDSLVLMPCYCKSLDIFTVGGSGDGVWTNSAWETFORYRCLE	741
QY	721	NSRSVVKTPMTDVCERNIIFISALLHOTGLACECDPQGSLSVCDPNGGQCQCQCPNVVGR	780
Db	742	NSRSVVKTPMTDVCERNIIFISALLHOTGLACECDPQGSLSVCDPNGGQCQCQCPNVVGR	801
QY	781	TCNRCAPGTFGFGPSGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDRCLPGHWGF	840
Db	802	TCNRCAPGTFGFGPSGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDRCLPGHWGF	861
QY	841	PSCQPCQCNGHADDCPVTGECLNCQDYTMGHNCERCLAGYYGDP IIGSGDHCRPCPCPD	900
Db	862	PSCQPCQCNGHADDCPVTGECLNCQDYTMGHNCERCLAGYYGDP IIGSGDHCRPCPCPD	921
QY	901	GPDSGRQFARSCYQDPVTQLQACVCDPGYIGSRDDCASGYFGNPSVGGSCQPCQCHNN	960
Db	922	GPDSGRQFARSCYQDPVTQLQACVCDPGYIGSRDDCASGYFGNPSVGGSCQPCQCHNN	981
QY	961	IDTTDPEACDKETGRCLKCLYHTEGEHCQFCRFGYGDALRQDCKVCVNYLGTVQEHCN	1020
Db	982	IDTTDPEACDKETGRCLKCLYHTEGEHCQFCRFGYGDALRQDCKVCVNYLGTVQEHCN	1041
QY	1021	GSDCQCDKATGQCLCLPNVIGQNCDCRCAPNTWOLASGTGCDPCNCNAHSGFSPSCNEFTG	1080
Db	1042	GSDCQCDKATGQCLCLPNVIGQNCDCRCAPNTWOLASGTGCDPCNCNAHSGFSPSCNEFTG	1101
QY	1081	QCQCMPGFGGRTCECQELFWGDPDVECRACDQDPRGTETPQCDQSTGQCVCVEGEGPR	1140
Db	1102	QCQCMPGFGGRTCECQELFWGDPDVECRACDQDPRGTETPQCDQSTGQCVCVEGEGPR	1161
QY	1141	CDKCTRGYSGVFPDCTPCHQCQCFALNDVIIAELTNRTHRFLEKAKALKISGVIGPYRETVD	1200
Db	1162	CDKCTRGYSGVFPDCTPCHQCQCFALNDVIIAELTNRTHRFLEKAKALKISGVIGPYRETVD	1221
QY	1201	SVERKVSEIKDILAQSPAABPLKNIGNLFEAAEKLIKDVTEMMAQVEVKLSDTTSQSNST	1260
Db	1222	SVERKVSEIKDILAQSPAABPLKNIGNLFEAAEKLIKDVTEMMAQVEVKLSDTTSQSNST	1281
QY	1261	AKELDSLQTEAESLNTVKELAEQLEFIKNSDIRGALDLSITKYFQMSLEAEERVNASTTE	1320
Db	1282	AKELDSLQTEAESLNTVKELAEQLEFIKNSDIRGALDLSITKYFQMSLEAEERVNASTTE	1341
QY	1321	PNSTVEQSALMRDRVEDVMMERESQFKEKQEEQARLLDELQGLQSLDLSAAEMTCGTP	1380
Db	1342	PNSTVEQSALMRDRVEDVMMERESQFKEKQEEQARLLDELQGLQSLDLSAAEMTCGTP	1401
QY	1381	PGASCSETECGGPNCRDTDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLALAEVQL	1440
Db	1402	PGASCSETECGGPNCRDTDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLALAEVQL	1461
QY	1441	SKMVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNEELRNLIKQIRNFLTQDSADLDSI	1500
Db	1462	SKMVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNEELRNLIKQIRNFLTQDSADLDSI	1521
QY	1501	EAVANEVLKMEMPSTPQQLQNLTEDIRERVESLSQVEVILQHSAADIAEAMLLBEAKRA	1560
Db	1522	EAVANEVLKMEMPSTPQQLQNLTEDIRERVESLSQVEVILQHSAADIAEAMLLBEAKRA	1581

QY	1561	SKSATDVKTADVMKEALEEAEKAQVAAEKAIKQADEDIQGTQNLLTSIESETAASEETL	1620
Db	1582	SKSATDVKTADVMKEALEEAEKAQVAAEKAIKQADEDIQGTQNLLTSIESETAASEETL	1641
QY	1621	FNASORISELERNVEELKRKAAQNSGEAEYIEKVYTVVKQSAEDVKKTLDGELDEKYYKV	1680
Db	1642	FNASORISELERNVEELKRKAAQNSGEAEYIEKVYTVVKQSAEDVKKTLDGELDEKYYKV	1701
QY	1681	ENLIAKKTESADARRKAEMLQNEAKTLAQANSKLQLLKDLERKYEDNQRYLEDKAQEL	1740
Db	1702	ENLIAKKTESADARRKAEMLQNEAKTLAQANSKLQLLKDLERKYEDNQRYLEDKAQEL	1761
QY	1741	ARLEGEVRSLLKDISQKAVYSTCL	1765
Db	1762	ARLEGEVRSLLKDISQKAVYSTCL	1786

RESULT 8

AAB90788

ID AAB90788 standard; protein; 1786 AA.

AC AAB90788;

15-JUN-2001 (first entry)

Human shear stress-response protein SEQ ID NO: 76.

Human: shear stress-response protein; vascular disease; arteriosclerosis.

XX
OS
Homo sapiens.

XX PN WO200125427-A1.

XX
PD
12-APR-2001

02-OCT-2000: 2000WO-JP006840

01-OCT-1999. 99JP-00280976

XX
PA (KYOW) KYOWA HAKKO KOGYO KK.

PA (NOJI /) NOJIMA H.
PA (NOJI /) NOJIMA H.

XX
pt
Nojima H. Yoshisue H. Ota T. Kawabata A. Sakurada K;

PI Nojima H, Ioshizue H, Oobayashi M, Oga-
ki T, Sekine S, Nakamura Y, Sugano S,
Kuga T, Sugano Y, Sugano S

WPI: 2001-266308/27.

DR N-PSDB; AAH02911.

PT DNA sequences, proteins encoded by them and antibodies against them

useful in diagnosis and treatment of vascular disease caused by

PT arteriosclerosis.

PS Claim 60; Page 440-449; 678pp; Japanese.

CC The present invention provides the protein and coding sequences of a

CC number of human shear stress response proteins. These are useful in the

CC diagnosis, treatment and screening of vascular diseases caused by

CC arteriosclerosis, including heart failure, post-PTCA restenosis and

cc hypertension

SQ Sequence 1786 AA;

Query Match	Score	DB 4;	Length
100.0%	9654	DB 4;	Length 1786

Best Local Similarity 100.0%; Pred. No. 0;

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Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY	1	QEPFSGCAEGSCYPATGDLIIIGRAQKLSVTSTCGLHKPEPYCIIVSHLQEDKKCFICNS	60
DB	22	QEPFSGCAEGSCYPATGDLIIIGRAQKLSVTSTCGLHKPEPYCIIVSHLQEDKKCFICNS	81
QY	61	QDPYHETINPDSHLIENVVTTTAPNRLKIWWQSENGVENVTIQDLEAEFHFTHLIMTFK	120
DB	82	QDPYHETINPDSHLIENVVTTTAPNRLKIWWQSENGVENVTIQDLEAEFHFTHLIMTFK	141

QY	121	TFRPAAMLIERSDFGKTWGVYRYFAYDCEASFPGISTGPMKKVDDIIICDSRYSDIEPST	180
Db	142	TFRPAAMLIERSDFGKTWGVYRYFAYDCEASFPGISTGPMKKVDDIIICDSRYSDIEPST	201
QY	181	EGEVIFRALDPAFKIEDPSPRIQNLKLTNLRIKFVKLHTLGDNLDSRMEIREKYYA	240
Db	202	EGEVIFRALDPAFKIEDPSPRIQNLKLTNLRIKFVKLHTLGDNLDSRMEIREKYYA	261
QY	241	VYDMVVRGNCFCYGHASECAPVDGFNEEVGMVHGCMCRHNTKGLNCELCMDPFYHDLPW	300
Db	262	VYDMVVRGNCFCYGHASECAPVDGFNEEVGMVHGCMCRHNTKGLNCELCMDPFYHDLPW	321
QY	301	RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGGVCDCCQHNTMGRNCEQCKPFY	360
Db	322	RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGGVCDCCQHNTMGRNCEQCKPFY	381
QY	361	YQHPEERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSLGIAGQCRCKLNVEGEHCDVCK	420
Db	382	YQHPEERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSLGIAGQCRCKLNVEGEHCDVCK	441
QY	421	EGFYDLSSSEDPFGCKSCACNPLGTIPGPNPCDSETHCYCKRLVTGQHCDCQCLPEHWGLS	480
Db	442	EGFYDLSSSEDPFGCKSCACNPLGTIPGPNPCDSETHCYCKRLVTGQHCDCQCLPEHWGLS	501
QY	481	NLDGCRPCDCDLGGALNNSCPAESGCSCSRPHMIGRQCNEVEPGYYFATLDHLYEABE	540
Db	502	NLDGCRPCDCDLGGALNNSCPAESGCSCSRPHMIGRQCNEVEPGYYFATLDHLYEABE	561
QY	541	ANLPGVSVIVERQYIQDRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP	600
Db	562	ANLPGVSVIVERQYIQDRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP	621
QY	601	DHWEKAVITVQRPGRIPRTSSRCGNTIPDDNQVVSLSPGSRVYVLPVPCFEKGTNTVTR	660
Db	622	DHWEKAVITVQRPGRIPRTSSRCGNTIPDDNQVVSLSPGSRVYVLPVPCFEKGTNTVTR	681
QY	661	LELPQYTSSDSVESPYTLIDSLVLMPYCKSLDIFTVGGSGDGVVNTNSAWETFORYRCLE	720
Db	682	LELPQYTSSDSVESPYTLIDSLVLMPYCKSLDIFTVGGSGDGVVNTNSAWETFORYRCLE	741
QY	721	NSRSVVKTPMTDVCRNIIIFSISALLHOTGLACECDPQGSLSVCDPNGGQCQCRPNVVGR	780
Db	742	NSRSVVKTPMTDVCRNIIIFSISALLHOTGLACECDPQGSLSVCDPNGGQCQCRPNVVGR	801
QY	781	TCNRCAPGTFGFGSGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDRLPGHWGF	840
Db	802	TCNRCAPGTFGFGSGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDRLPGHWGF	861
QY	841	PSCQPCQCNHADDPCDPTVTECLNCQDYTMGHNCERCLAGYVGDPIIGSDHCRPCPCPD	900
Db	862	PSCQPCQCNHADDPCDPTVTECLNCQDYTMGHNCERCLAGYVGDPIIGSDHCRPCPCPD	921
QY	901	GPDSGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCASGYFGNPNSEVGGSCQPCQCHNN	960
Db	922	GPDSGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCASGYFGNPNSEVGGSCQPCQCHNN	981
QY	961	IDTTDPEACDKETGRCLKCLYHTEGEHCQCFEFGYVGDALRQDCRKCVCNVLGTVQEHCHN	1020
Db	982	IDTTDPEACDKETGRCLKCLYHTEGEHCQCFEFGYVGDALRQDCRKCVCNVLGTVQEHCHN	1041
QY	1021	GSDCQCDKATGQCLCLPNVIGONCDRCAPNTWQLASGTGCDPCNCAHSAHSGPSCNEFTG	1080
Db	1042	GSDCQCDKATGQCLCLPNVIGONCDRCAPNTWQLASGTGCDPCNCAHSAHSGPSCNEFTG	1101
QY	1081	QCQCMFGGGRTCSEQELFWGDPDVECRACDPCDPRGIETPQCDSQSTGQCVCEGVEGPR	1140
Db	1102	QCQCMFGGGRTCSEQELFWGDPDVECRACDPCDPRGIETPQCDSQSTGQCVCEGVEGPR	1161
QY	1141	CDKCTRGYSGVFPDCTPCHQCQFALWDVIIAELTNRTHRFLEKAKALKISGVIGPYRETVD	1200
Db	1162	CDKCTRGYSGVFPDCTPCHQCQFALWDVIIAELTNRTHRFLEKAKALKISGVIGPYRETVD	1221

QY	1201	SVERKVSEIKDILAQSPAAPLKNIGNLFEEAEKLIKDVTEMMAQVEVKLSDTTSQSNST	1260
Db	1222	SVERKVSEIKDILAQSPAAPLKNIGNLFEEAEKLIKDVTEMMAQVEVKLSDTTSQSNST	1281
QY	1261	AKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTTE	1320
Db	1282	AKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTTE	1341
QY	1321	PNSTVEQSALMRDRVEDVMMERESQFKEQEEOARLLDELAKGLQSLDLSAAAEVTCGTP	1380
Db	1342	PNSTVEQSALMRDRVEDVMMERESQFKEQEEOARLLDELAKGLQSLDLSAAAEVTCGTP	1401
QY	1381	PGASCSETECGGPNCRCTDEGERKCGGPGCGGLVTVVAHNAWQKAMDLDQDVL SALAEVEQL	1440
Db	1402	PGASCSETECGGPNCRCTDEGERKCGGPGCGGLVTVVAHNAWQKAMDLDQDVL SALAEVEQL	1461
QY	1441	SKMVSEAKLRADAEAKQSAEDILLKTNATKEKMDKSNEELRNLIKQIRNFLTQDSADLDSI	1500
Db	1462	SKMVSEAKLRADAEAKQSAEDILLKTNATKEKMDKSNEELRNLIKQIRNFLTQDSADLDSI	1521
QY	1501	EAVANEVLKMEMPSTPQOLQNLTEDIRERVESLSQVEVILQHSAAADIAEAEMLLEEAKRA	1560
Db	1522	EAVANEVLKMEMPSTPQOLQNLTEDIRERVESLSQVEVILQHSAAADIAEAEMLLEEAKRA	1581
QY	1561	SKSATDVKVTADVMVKEALEEAEAKQVAAEAKIKQADEDIQGTQNL LTSISETAASEETL	1620
Db	1582	SKSATDVKVTADVMVKEALEEAEAKQVAAEAKIKQADEDIQGTQNL LTSISETAASEETL	1641
QY	1621	FNASQRISELERNVEELKRKAAQNSGEAEYIEKVYTVTKQSAEDVKKTLDGELDEKYKKV	1680
Db	1642	FNASQRISELERNVEELKRKAAQNSGEAEYIEKVYTVTKQSAEDVKKTLDGELDEKYKKV	1701
QY	1681	ENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLLKDLERKYEDNQRYLEDKAQEL	1740
Db	1702	ENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLLKDLERKYEDNQRYLEDKAQEL	1761
QY	1741	ARLEGEVRSLLKDISQKVAVYSTCL	1765
Db	1762	ARLEGEVRSLLKDISQKVAVYSTCL	1786

RESULT 9
ABB81590
ID ABB81590 standard; protein; 1786 AA.
XX
AC ABB81590;
XX
DT 19-SEP-2002 (first entry)
XX
DE Human laminin 10 second chain protein sequence SEQ ID NO:6.
DE Laminin alpha 5; laminin 10; vulneryary; cell growth; differentiation;
KW tissue repair development; laminin; healing; vascular tissue;
KW re-endothelialisation; vascular injury; cell attachment; cell stasis;
KW proliferation; migration.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT Protein /label= signal
FT 22..1786
XX /label= laminin_10_second_chain
PN WO200250111-A2.
XX
PD 27-JUN-2002.
XX
PF 21-DEC-2001; 2001WO-US051035.
XX
PR 21-DEC-2000; 2000US-0257449P.
PR 28-MAR-2001; 2001US-0279282P.
PR 13-NOV-2001; 2001US-00279282.

XX (BIOS-) BIOSTRATUM INC.
PA Tryggvason K, Doi M, Thyboll J;
XX WPI; 2002-557650/59.
XX N-PSDB; ABQ72908.
DR New human laminin-10 proteins, useful for accelerating the healing of
XX vascular tissue, improving the biocompatibility of grafts, or for
XX promoting re-endothelialization at the site of vascular injuries.
PS Claim 9; Page 113-119; 231pp; English.
XX
CC The present invention describes human laminin alpha 5. Also described is
CC an isolated laminin 10. Laminin 10 has vulnerary activity. Laminins are
CC useful in maintaining cell/tissue phenotype as well as promoting cell
CC growth and differentiation in tissue repair development. Specifically,
CC laminin 10 can be used for accelerating the healing injuries of vascular
CC tissue, improving the biocompatibility of grafts useful for treating such
CC injuries, for promoting re-endothelialization at the site of vascular
CC injuries, and promote cell attachment and subsequent cell stasis,
CC proliferation, differentiation, and/or migration. The present sequence
CC represents a second chain protein of laminin 10, from the present
XX invention
SQ Sequence 1786 AA;
Query Match 100.0%; Score 9654; DB 5; Length 1786;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QEPFSGYCAEGSCYPATGDLIGRAQKLSVTSTCGLHKPEPYCIYSHLQEDKKCFICNS 60
DB 22 QEPFSGYCAEGSCYPATGDLIGRAQKLSVTSTCGLHKPEPYCIYSHLQEDKKCFICNS 81
QY 61 QDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENVTIQLDLAEFFHFTHLIMTFK 120
DB 82 QDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENVTIQLDLAEFFHFTHLIMTFK 141
QY 121 TFRPAAMLIERSDFGKTGWYRYFAYDCEASFPGISTGPMKKVDDIICDSRYSDIEST 180
DB 142 TFRPAAMLIERSDFGKTGWYRYFAYDCEASFPGISTGPMKKVDDIICDSRYSDIEST 201
QY 181 EGEVIFRALDPAFKIEDPSPRIQNLKLTNLRKFVKLHTLGDNLDSRMEIREKYIYA 240
DB 202 EGEVIFRALDPAFKIEDPSPRIQNLKLTNLRKFVKLHTLGDNLDSRMEIREKYIYA 261
QY 241 VYDMVVRGNCFCYGHASECAPVDGPNFEEVEGMVHGHCMCRHNTKGLNCELAMDYFHDLPW 300
DB 262 VYDMVVRGNCFCYGHASECAPVDGPNFEEVEGMVHGHCMCRHNTKGLNCELAMDYFHDLPW 321
QY 301 RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGGVCDCCQHNMTGRNCEQCKPFY 360
DB 322 RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGGVCDCCQHNMTGRNCEQCKPFY 381
QY 361 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFSTGLIAGQCRCKLNVEGEHCDVCK 420
DB 382 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFSTGLIAGQCRCKLNVEGEHCDVCK 441
QY 421 EGFYDLSSDPFGCKSCACNPLGTIPGGNPNCDSETGHYCKRLVTGQHCDQCLPEHWGLS 480
DB 442 EGFYDLSSDPFGCKSCACNPLGTIPGGNPNCDSETGHYCKRLVTGQHCDQCLPEHWGLS 501
QY 481 NDLGCRPCDCDLGGLNNSCPAESGQCSCRPMTGRQCNEVEPGYYFATLDHYLYEAE 540
DB 502 NDLGCRPCDCDLGGLNNSCPAESGQCSCRPMTGRQCNEVEPGYYFATLDHYLYEAE 561
QY 541 ANLPGVSIYERQYIQDRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 600
DB 562 ANLPGVSIYERQYIQDRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 621
QY 601 DHWEKAVITVQRPGRIPRTSSRCGNTIPDDDNQVVSLSPGSRYVVLPRPVCFEKGTNYTVR 660

DB 622 DHWEKAVITVQRPGRIPRTSSRCGNTIPDDDNQVVSLSPGSRYVVLPRPVCFEKGTNYTVR 681
QY 661 LELPQYTSSDSVESPYTLIDSLVMPYCKSLDIFTVGGSGDGVVNTNSAWETFORYRCLE 720
DB 682 LELPQYTSSDSVESPYTLIDSLVMPYCKSLDIFTVGGSGDGVVNTNSAWETFORYRCLE 741
QY 721 NSRSVVKTPMTDVCRNIIFISALLHQTGLACECDPQGSLSVSCDNGGQCCQCRPNVVR 780
DB 742 NSRSVVKTPMTDVCRNIIFISALLHQTGLACECDPQGSLSVSCDNGGQCCQCRPNVVR 801
QY 781 TCNRCAPGTGFGPSGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDRCLPGHWGF 840
DB 802 TCNRCAPGTGFGPSGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDRCLPGHWGF 861
QY 841 PSCQPCQCNHADDPCDVTGECNLCQDVTMGHNCERCLAGYGDPIIGSGDHCRCPCPCPD 900
DB 862 PSCQPCQCNHADDPCDVTGECNLCQDVTMGHNCERCLAGYGDPIIGSGDHCRCPCPCPD 921
QY 901 GPDSGRQFARSCYQDPVTLQACVCDPVGYSRCDCCASGYFGNPSVGVSCQPCQCHNN 960
DB 922 GPDSGRQFARSCYQDPVTLQACVCDPVGYSRCDCCASGYFGNPSVGVSCQPCQCHNN 981
QY 961 IDTTDPEACDKETGRCLKCLYHTEGHCQCFRFGYGDALRQDCRKCVCNYLGTVQEHCN 1020
DB 982 IDTTDPEACDKETGRCLKCLYHTEGHCQCFRFGYGDALRQDCRKCVCNYLGTVQEHCN 1041
QY 1021 GSDCQCDKATGQCLCLPNVIGQNCDCRCAPTWQLASGTGCDPCNCAHSPGSCNEFTG 1080
DB 1042 GSDCQCDKATGQCLCLPNVIGQNCDCRCAPTWQLASGTGCDPCNCAHSPGSCNEFTG 1101
QY 1081 QCQCMFPGGRTCEQCLFWGDPDVECRACDPRGIETPQCQDQSTGQCVCEGVGPR 1140
DB 1102 QCQCMFPGGRTCEQCLFWGDPDVECRACDPRGIETPQCQDQSTGQCVCEGVGPR 1161
QY 1141 CDKCTRGYSGVFPDCTPCHQCFALWDVIIAELTNRTHRFLEKAKALKISGIVGYRETVD 1200
DB 1162 CDKCTRGYSGVFPDCTPCHQCFALWDVIIAELTNRTHRFLEKAKALKISGIVGYRETVD 1221
QY 1201 SVERKVSEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDVTEMAQVEVKLSDDTSQSNST 1260
DB 1222 SVERKVSEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDVTEMAQVEVKLSDDTSQSNST 1281
QY 1261 AKELDSLQTEAESLNTVKELAEQLEFIFKNSDIRGALDSITKYFQMSLEAEERVNASTTE 1320
DB 1282 AKELDSLQTEAESLNTVKELAEQLEFIFKNSDIRGALDSITKYFQMSLEAEERVNASTTE 1341
QY 1321 PNSTVEQSALMRDRVEDVMERESQFKEQEQEAPRLDELAKLQSLDLSAAEMTCGTP 1380
DB 1342 PNSTVEQSALMRDRVEDVMERESQFKEQEQEAPRLDELAKLQSLDLSAAEMTCGTP 1401
QY 1381 PGASCSETECGGPNCRTEDEGERKCGGPGGLVTVAHNAWQKAMDLDQDVLALAEVEQL 1440
DB 1402 PGASCSETECGGPNCRTEDEGERKCGGPGGLVTVAHNAWQKAMDLDQDVLALAEVEQL 1461
QY 1441 SKMVSEAKLRADAEKQSAEDILLKTNATKEKMDKSNEELRNLIKQIRNFLTQDSADLDSI 1500
DB 1462 SKMVSEAKLRADAEKQSAEDILLKTNATKEKMDKSNEELRNLIKQIRNFLTQDSADLDSI 1521
QY 1501 EAVANEVLKMEMPSTPQOLQNLTEDIRERVESLSQVEVILQHSAAADIARAEMLLEAKRA 1560
DB 1522 EAVANEVLKMEMPSTPQOLQNLTEDIRERVESLSQVEVILQHSAAADIARAEMLLEAKRA 1581
QY 1561 SKSATDVKVTADMVKEALEEAEAKQAQVAAEKAIKQADEDIQGTQNLTSIESETAASEETL 1620
DB 1582 SKSATDVKVTADMVKEALEEAEAKQAQVAAEKAIKQADEDIQGTQNLTSIESETAASEETL 1641
QY 1621 FNASQRISELERNVVELKRAAQNSGEAEYIEKVYTVKQSAEDVKKTLDELDEKYYKV 1680
DB 1642 FNASQRISELERNVVELKRAAQNSGEAEYIEKVYTVKQSAEDVKKTLDELDEKYYKV 1701
QY 1681 ENLIATKTEESADARRKAEMLQNEAKTLLAQANSKLQLLKLKERKYEDNQRYLEDKAQEL 1740

Db	1702	ENLIAKTEESADARRKAEMLQNEAKTLIAQANSKLQLLDKLBERKYEDNQRYLEDKAQEL	1761
QY	1741	ARLEGEVRSLLKDISQKAVYSTCL	1765
Db	1762	ARLEGEVRSLLKDISQKAVYSTCL	1786
RESULT 10			
ID	AAM48896		
XX	AAM48896	standard; protein; 1786 AA.	
AC	AAM48896;		
XX			
DT	04-APR-2002	(first entry)	
XX			
DE	Laminin protein.		
XX			
KW	Human; angiostatin; endostatin; angiogenesis; cancer; metastasis;		
KW	psoriasis; scleroderma; Crohn's disease; corneal disease; retinopathy;		
KW	arthritis; wound healing; Helicobacter pylori; peptic ulcer;		
KW	gene therapy; angiostatin antagonist; endostatin antagonist;		
KW	antiangiogenic; cytostatic; antiarthritic; antiinflammatory;		
KW	cerebroprotective; antidiabetic; virucide; antipyretic; vulnerary;		
KW	gynaecological; cat scratch fever.		
XX			
OS	Unidentified.		
XX			
PN	WO200193897-A2.		
XX			
PD	13-DEC-2001.		
XX			
PF	04-JUN-2001; 2001WO-US017947.		
XX			
PR	02-JUN-2000; 2000US-0209065P.		
PR	08-MAY-2001; 2001US-0289387P.		
XX			
PA	(ENTR-) ENTREMED INC.		
XX			
PI	Sim KL, Macdonald NJ;		
XX			
DR	WPI; 2002-130569/17.		
DR	N-PSDB; ABA97525.		
XX			
PT	Regulating angiogenesis and treatment of angiogenesis-mediated diseases,		
PT	e.g. hemangioma, tumors or cancer, by administering a tropomyosin binding		
PT	compound or actin disrupting compound.		
XX			
PS	Example 11; Fig 6A; 95pp; English.		
XX			
CC	The present invention relates to methods of regulating angiogenesis in an		
CC	individual by administering an angiogenesis regulating composition		
CC	comprising a tropomyosin binding compound or an actin disrupting		
CC	compound. The compositions are useful for treating diseases and processes		
CC	mediated by angiogenesis including haemangioma, solid tumours, blood		
CC	bourne tumours, leukaemia, metastasis, Crohn's disease, coronary or		
CC	cerebral collaterals, arthritis, diabetic neovascularisation, macular		
CC	degeneration, wound healing, Helicobacter related diseases, ovulation,		
CC	menstruation, and cat scratch fever. The present sequence is a protein		
CC	described in the exemplification of the invention		
SQ	Sequence 1786 AA;		
Query Match			
Best Local Similarity 99.8%; Score 9638; DB 5; Length 1786;			
Matches 1763; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
QY	1	QEPEFSYGCAEGSCYPATGDLIGRAQKLSVTSTCGLHKPEPYCIIVSHLQEDKKCFICNS	60
Db	22	QEPEFSYGCAEGSCYPATGDLIGRAQKLSVTSTCGLHKPEPYCIIVSHLQEDKKCFICNS	81
QY	61	QDPVHETLNPDSHLIENVVTFAPNRLKIWWQSENGVENVTIQLDLEAEFFHFLIMTFK	120
Db	82	QDPVHETLNPDSHLIENVVTFAPNRLKIWWQSENGVENVTIQLDLEAEFFHFLIMTFK	141

QY	121	TFRPAAMLIERSSDFGKTGWVYRFAYDCEASFPGISTGPMKKVDDIICDSRYSDIEPST	180
Db	142	TFRPAAMLIERSSDFGKTGWVYRFAYDCEASFPGISTGPMKKVDDIICDSRYSDIEPST	201
QY	181	EGEVIFRALDPAFKIEDPSPRIQNLKITNLRIKFVKLHTLGNLLDSRMEIREKYAYA	240
Db	202	EGEVIFRALDPAFKIEDPSPRIQNLKITNLRIKFVKLHTLGNLLDSRMEIREKYAYA	261
QY	241	YDVMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGCMCRHNTKGLNCELCMDFYHDLPW	300
Db	262	YDVMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGCMCRHNTKGLNCELCMDFYHDLPW	321
QY	301	RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGGVCDCCOHTMTGRNCEQCKPFY	360
Db	322	RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGGVCDCCOHTMTGRNCEQCKPFY	381
QY	361	YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSTGLIAGQCRCKLNVEGEHCDVCK	420
Db	382	YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSTGLIAGQCRCKLNVEGEHCDVCK	441
QY	421	EGFYDLSSDDPFGCKSCACNPLGTIPGPNPCDSETHCYCKRLVTGQHCDQCLPEHWGLS	480
Db	442	EGFYDLSSDDPFGCKSCACNPLGTIPGPNPCDSETHCYCKRLVTGQHCDQCLPEHWGLS	501
QY	481	NLDGCRPCDDDLGGALNNSCFAESGCSCSRPHMIGRQCNEVEBPGYFATLDHYLYEAE	540
Db	502	NLDGCRPCDDDLGGALNNSCFAESGCSCSRPHMIGRQCNEVEBPGYFATLDHYLYEAE	561
QY	541	ANLPGVSIIVERQYIQDRIPSWTGAQFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP	600
Db	562	ANLPGVSIIVERQYIQDRIPSWTGAQFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP	621
QY	601	DHWEKAVITVQRPGRIPSTSSRCGNTIPDDDNQVVSLSPGSRVYVLPVPVCFEKGNTYTVR	660
Db	622	DHWEKAVITVQRPGRIPSTSSRCGNTIXDDDNQVVSLSPGSRVYVLPVPVCFEKGNTYTVR	681
QY	661	LELPQYTSDDSDVESPYTLIDSLVLMPYCKSLDIFTVGGSGDGVVNTNSAWETFQRYRCLE	720
Db	682	LELPQYTSDDSDVESPYTLIDSLVLMPYCKSLDIFTVGGSGDGVVNTNSAWETFQRYRCLE	741
QY	721	NSRSVVKTPMTDVCRNIIIFSISALHLQHTGLACECPQGSLSVSDPENGQCQCRPNVVG	780
Db	742	NSRSVVKTPMTDVCRNIIIFSISALHLQHTGLACECPQGSLSVSDPENGQCQCRPNVVG	801
QY	781	TCNRCAPGTFGFGPSGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDRLPGHWGF	840
Db	802	TCNRCAPGTFGFGPSGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDRLPGHWGF	861
QY	841	PSCQPCQCNHADDCDPVTGECNLCQDYMTHGNCERCLAGYVGDPIIGSDHCHRCPCPCPD	900
Db	862	PSCQPCQCNHADDCDPVTGECNLCQDYMTHGNCERCLAGYVGDPIIGSDHCHRCPCPCPD	921
QY	901	GPDSGRQFARSCYQDPVTTLQACVCDPFGYIGSRCDDCASGYFGNPNSEVGGSCQPCQCHNN	960
Db	922	GPDSGRQFARSCYQDPVTTLQACVCDPFGYIGSRCDDCASGYFGNPNSEVGGSCQPCQCHNN	981
QY	961	IDTTDPEACDKETGRCLKCLYHTEGEHCQFCRFGYVGDALRQDCRKCVCNVLGTVQEHCN	1020
Db	982	IDTTDPEACDKETGRCLKCLYHTEGEHCQFCRFGYVGDALRQDCRKCVCNVLGTVQEHCN	1041
QY	1021	GSDCCQDKATGQCLCLPNVIGQNCDCRCAPTWQLASGTGCDPCNCAHSGFSPSCNEFTG	1080
Db	1042	GSDCCQDKATGQCLCLPNVIGQNCDCRCAPTWQLASGTGCDPCNCAHSGFSPSCNEFTG	1101
QY	1081	QCQWFGFGGRTCECQELFWGDDVECRACDCDPRGIETPQCDQSTGQCVCVEGEGPR	1140
Db	1102	QCQWFGFGGRTCECQELFWGDDVECRACDCDPRGIETPQCDQSTGQCVCVEGEGPR	1161
QY	1141	CDKCTRGYSGVFPDCTPCHQCFALWDVIIAELTNRTHRFLEKAKALKISGVIQYRETVD	1200
Db	1162	CDKCTRGYSGVFPDCTPCHQCFALWDVIIAELTNRTHRFLEKAKALKISGVIQYRETVD	1221

QY 1201 SVERKVSEIKDILAQSPAAPLKNIGNLFEEAEKLIKDVTEMAQVEVKLSDTTQSQNST 1260
Dd 1222 SVERKVSEIKDILAQSPAAPLKNIGNLFEEAEKLIKDVTEMAQVEVKLSDTTQSQNST 1281

QY 1261 AKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTTE 1320
Dd 1282 AKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTTE 1341

QY 1321 PNSTVEQSALMRDRVEDVMMERESQFKEQEBEQARLLDELAKLQSLDLSAAAEMTCTGTP 1380
Dd 1342 PNSTVEQSALMRDRVEDVMMERESQFKEQEBEQARLLDELAKLQSLDLSAAAEMTCTGTP 1401

QY 1381 PGASCSETECGGNCRTEDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLALAEVEQL 1440
Dd 1402 PGASCSETECGGNCRTEDEGERKCGGPGCGGGLVTVAHNAWQKAMDLDQDVLALAEVEQL 1461

QY 1441 SKMVSEAKLRADAEAKQSAEDILLKTNATKEKMDKSNEELRNLIKQIRNFLTQDSADLDSI 1500
Dd 1462 SKMVSEAKLRADAEAKQSAEDILLKTNATKEKMDKSNEELRNLIKQIRNFLTQDSADLDSI 1521

QY 1501 EAVANEVLKMEPSTPQQLQNLTEDIRERVESLSQVEVILQHSAAADIARAEMLLLEEAKRA 1560
Dd 1522 EAVANEVLKMEPSTPQQLQNLTEDIRERVESLSQVEVILQHSAAADIARAEMLLLEEAKRA 1581

QY 1561 SKSATDVKVTADMVKEALEEAEAKQAQAAEKAQADEDIQGTQNLNLTSESETAASEETL 1620
Dd 1582 SKSATDVKVTADMVKEALEEAEAKQAQAAEKAQADEDIQGTQNLNLTSESETAASEETL 1641

QY 1621 FNASQRISELERNVEELKRKAQNSGEAEYIEBKVVYTVKQSAEDVKKTLDGELDEKYYKV 1680
Dd 1642 FNASQRISELERNVEELKRKAQNSGEAEYIEBKVVYTVKQSAEDVKKTLDGELDEKYYKV 1701

QY 1681 ENLIAKKTESADARRKAEMLQNEAKTLLAQANSKIQLLKOLERKYEDNQRYLEDKAQEL 1740
Dd 1702 ENLIAKKTESADARRKAEMLQNEAKTLLAQANSKIQLLKOLERKYEDNQRYLEDKAQEL 1761

QY 1741 ARLEGEVRSLKDISQKAVVYSTCL 1765
Dd 1762 ARLEGEVRSLKDISQKAVVYSTCL 1786

RESULT 11
AAAY15461

ID AAY15461 standard; protein; 1785 AA.

AC AAY15461;

DT 26-JUL-1999 (first entry)

DE Human laminin beta 1 subunit.

KW Laminin 12; alpha 2; beta 1; gamma 3; subunit; nerve regeneration;
KW connective tissue adhesion; tissue repair; wound; nerve growth;
KW laminin beta 1 subunit.

OS Homo sapiens.

PN WO9919348-A1.

XX 22-APR-1999.

PF 08-OCT-1998; 98WO-US021391.

XX 10-OCT-1997; 97US-0061609P.

PR (GEHO) GEN HOSPITAL CORP.

XX Burgeson RE, Champliaud M, Olson P, Koch M, Brunken W;

XX WPI; 1999-326542/27.

DR N-PSDB; AAX59769.

XX Purified laminin 12 useful for promoting tissue repair and promoting

PT nerve growth.
XX
PS Disclosure; Fig 4; 86pp; English.
XX

CC The specification describes laminin 12 which includes an alpha 2, beta 1
CC and gamma 3 subunit. Laminin is a connective tissue adhesion molecule.
CC Laminin is useful for promoting tissue repair due to wounds and to
CC promote nerve growth or regeneration. The present sequence represents
CC human laminin beta 1 subunit

XX
SQ Sequence 1785 AA;

Query Match 99.6%; Score 9618.5; DB 2; Length 1785;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1762; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 QEPFSGYCAEGSCYPATGDLILIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICNS 60
Dd 22 QEPFSGYCAEGSCYPATGDLILIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKQFICNS 81

Qy 61 QDPYHETLNPDSHLIENVVTTFAPNRLKIWQSENGVENVTIQLDLEAEFHFTHLIMTFK 120
Dd 82 QDPYHETLNPDSHLIENVVTTFAPNRLKIWQSENGVENVTIQLDLEAEFHFTHLIMTFK 141

Qy 121 TFRPAAMLIERSDFGKTGWVRYFYAYDCEASFPFGISTGPMKKVDDIICDSRYSDIEPST 180
Dd 142 TFRPAAMLIERSDFGKTGWVRYFYAYDCEASFPFGISTGPMKKVDDIICDSRYSDIEPST 201

Qy 181 EGEVIFRALDPAFKIEDPYSPRIQNLLKITNLRIKFVKLHTLGNLLDSRMEIREKYYA 240
Dd 202 EGEVIFRALDPAFKIEDPYSPRIQNLLKITNLRIKFVKLHTLGNLLDSRMEIREKYYA 261

Qy 241 VYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGHCMCRHNTKGLNCELMDFFYHDLWP 300
Dd 262 VYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGHCMCRHNTKGLNCELMDFFYHDLWP 321

Qy 301 RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGVCGDDCQHTMTGRNCEQCKPFY 360
Dd 322 RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGVCGDDCQHTMTGRNCEQCKPFY 381

Qy 361 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSTGLIAGQCCKLNVEGEHCDVCK 420
Dd 382 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSTGLIAGQCCKLNVEGEHCDVCK 441

Qy 421 EGFYDLSSDPFGCKSCACNPLGTIPGGNCPDSETHCYCKRLVTGQHCDCQLPEHWGLS 480
Dd 442 EGFYDLSSDPFGCKSCACNPLGTIPGGNCPDSETHCYCKRLVTGQHCDCQLPEHWGLS 501

Qy 481 NDLDGCRPCDCDLGGALNNSCFAESGQSCSRPHMIGRQCNEVEPGYVFATLDHYLYEAE 540
Dd 502 NDLDGCRPCDCDLGGALNNSCFAESGQSCSRPHMIGRQCNEVEPGYVFATLDHYLYEAE 561

Qy 541 ANLPGVSIIVERQYIQDRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 600
Dd 562 ANLPGVSIIVERQYIQDRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 621

Qy 601 DHWEKAVITVQRPGRIPTSRRCGNTIPDDDNQVVSLSPGSRVYVLPVPVCFEKGNTYTVR 660
Dd 622 DHWEKAVITVQRPGRIPTSRRCGNTIPDDDNQVVSLSPGSRVYVLPVPVCFEKGNTYTVR 681

Qy 661 LELPQYTSSDSVESPYTLIDSLVLMPCYCKSLDIFTVGGSGDGVVNTNSAWETFORYRCLE 720
Dd 682 LELPQYTSSDSVESPYTLIDSLVLMPCYCKSLDIFTVGGSGDGVVNTNSAWETFORYRCLE 741

Qy 721 NSRSVVKTPMTDVCENIIFISALLHOTGLACECDPQGSLSVSCDPPNGSQCCQCRPNVWGR 780
Dd 742 NSRSVVKTPMTDVCENIIFISALLHOTGLACECDPQGSLSVSCDPPNGSQCCQCRPNVWGR 801

Qy 781 TCNRCAPGTFGFGPSGCKPCECHLQGSVNAPNPNVTGQCHCFQGVYARQCDRCLPGHWGF 840
Dd 802 TCNRCAPGTFGFGPSGCKPCECHLQGSVNAPNPNVTGQCHCFQGVYARQCDRCLPGHWGF 861

Qy 841 PSCQPCQCNHADDCTPVTGECNLCQDYTMGNCERCLAGYYGDPPIIGSGDHCRPCPCPD 900

Db	862	PSQPCQCNHGADDCDPVTGECNCDQYTMGHCNCRCLAGYGDPIIGSGDHRPCPCPD	921
Qy	901	GPDSGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCASGYFGNPNSEVGGSCQPCQCHNN	960
Db	922	GPDSGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCASGYFGNPNSEVGGSCQPCQCHNN	981
Qy	961	IDTDPACDKETGRCLKCLYHTEGEHCQCFRFGYGDALRQDCRKCVCNKLGTVEHCN	1020
Db	982	IDTDPACDKETGRCLKCLYHTEGEHCQCFRFGYGDALRQDCRKCVCNKLGTVEHCN	1041
Qy	1021	GSDCQCDKATGQCLCLPNVIGNCDRCAPNTWQLASGTGCDPCNCAHSPGSPCNEFTG	1080
Db	1042	GSDCQCDKATGQCLCLPNVIGNCDRCAPNTWQLASGTGCDPCNCAHSPGSPCNEFTG	1101
Qy	1081	QCQMPGFGGRTCTSECCQELFWGDPDVECRACDCDPRGIETPQCQDSTGQCVCEGVEGPR	1140
Db	1102	QCQMPGFGGRTCTSECCQELFWGDPDVECRACDCDPRGIETPQCQDSTGQCVCEGVEGPR	1161
Qy	1141	CDKTRGYSGVFPDCTPCHQCQFALWDVIIAELTNRTHRFLEKAKALKISGVIGPYRETVD	1200
Db	1162	CDKTRGYSGVFPDCTPCHQCQFALWDVIIAELTNRTHRFLEKAKALKISGVIGPYRETVD	1221
Qy	1201	SVERKVSSEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDVTEMMAQVEVKLSDTTSQSNST	1260
Db	1222	SVERKVSSEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDVTEMMAQVEVKLSDTTSQSNST	1281
Qy	1261	AKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTTE	1320
Db	1282	AKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTTE	1341
Qy	1321	PNSTVEQSALMRDRVEDVMMERE-SQFKEKOEQARLLDELAKGLQSLDLSAAAEWTCGT	1379
Db	1342	PNSTVEQSALMRDRVEDVMMERE-SQFKEKOEQARLLDELAKGLQSLDLSAAAEWTCGT	1401
Qy	1380	PPGASCSETECGGPNCRTEDEGERKCGGPGGGLVTVAHNAWQKAMDLDQDVLALAEVEQ	1439
Db	1402	PPGASCSETECGGPNCRTEDEGERKCGGPGGGLVTVAHNAWQKAMDLDQDVLALAEVEQ	1461
Qy	1440	LSKMVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNBEELRNLIKQIRNFLTQDSADLDS	1499
Db	1462	LSKMVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNBEELRNLIKQIRNFLTQDSADLDS	1521
Qy	1500	IEAVANEVLKMEPSTPQQLNLTEDIRERVESLSQVEVILQHSAAADIARAEMLLEAKR	1559
Db	1522	IEAVANEVLKMEPSTPQQLNLTEDIRERVESLSQVEVILQHSAAADIARAEMLLEAKR	1581
Qy	1560	ASKSATDVKVTADMVKEALEEAEKAQVAAEKAQKQADEDIQGTQNLTSIESETAASEET	1619
Db	1582	ASKSATDVKVTADMVKEALEEAEKAQVAAEKAQKQADEDIQGTQNLTSIESETAASEET	1641
Qy	1620	LFNASORISELERNVEELKRKAQNSGEAEYIEKVVTYVKQSAEDVKTLDGELDEKYYK	1679
Db	1642	LFNASORISELERNVEELKRKAQNSGEAEYIEKVVTYVKQSAEDVKTLDGELDEKYYK	1701
Qy	1680	VENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLLKDLERKYEDNQRYLEDKAQE	1739
Db	1702	VENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLLKDLERKYEDNQRYLEDKAQE	1761
Qy	1740	LARLEGEVRSLLKDISQKVAVYST	1763
Db	1762	LARLEGEVRSLLKDISQKVAVYST	1785

RESULT 12
AAB19799
ID AAB19799 standard; protein; 1786 AA.

XX AAB19799;

AC AAB19799;

XX 05-MAR-2001 (first entry)

XX Mouse laminin 2 beta-1 chain.

XX	Laminin 2; mouse; nerve regeneration; angiogenic; cell adhesion; degenerative muscle disorder; muscular dystrophy; cell therapy.
KW	Mus musculus.
XX	
OS	
XX	
XX	Key Location/Qualifiers
FT	Peptide 1..21
FT	/label= signal_peptide
FT	Protein 22..1786
FT	/label= Mature_protein
XX	WO200066730-A2.
PN	
XX	
PD	09-NOV-2000.
XX	
XX	28-APR-2000; 2000WO-US011378.
PF	
XX	
XX	30-APR-1999; 99US-0131720P.
PR	15-JUN-1999; 99US-0139198P.
PR	12-JUL-1999; 99US-0143289P.
PR	24-SEP-1999; 99US-0155945P.
XX	
PA	(UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX	
XX	Yurchenco P;
PI	
XX	
DR	WPI; 2000-687537/67.
DR	N-PSDB; AAA88899.
XX	
PT	Purified laminin 2 protein, useful for research and therapeutic purposes including peripheral nerve regeneration, treatment of degenerative muscle disorders, angiogenesis regulation, and ex vivo cell therapy.
PT	
XX	
PS	Claim 5; Page 212-218; 305pp; English.
XX	
CC	The present sequence is that of the beta-1 chain of mouse laminin 2.
CC	Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1 (100 kDa) chains. It is thought to be specifically required for stabilizing myotubes during skeletal muscle development, and for preventing apoptosis. Genetic defects in human laminin 2 structure or expression are associated with a major type of congenital muscular dystrophy. Laminin 2 is also thought to be important in Schwann cell/basal lamina interactions. The invention provides laminin 2 alpha-2, beta-1 and gamma-1 chain polypeptides (see AAB19791-806) and the polynucleotides encoding them (see AAA88891-906), methods for making recombinant laminin 2, cells that express recombinant laminin 2, and methods for using purified laminin 2 for research and therapeutic purposes including peripheral nerve regeneration, treatment of degenerative muscle disorders, angiogenesis regulation, promoting cell attachment and migration, ex vivo cell therapy, improving the take of grafts, improving the biocompatibility of medical devices and preparing improved culture devices and media
XX	
SQ	Sequence 1786 AA;

Query Match 94.2%; Score 9092; DB 3; Length 1786;
Best Local Similarity 93.0%; Pred. No. 0;
Matches 1642; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

Qy	1	QEPEFSYGCAGSCYPATGDLILIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICNS	60
Db	22	QEPEFSYGCAGSCYPATGDLILIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICDS	81
Qy	61	QDPYHETLNPDShLIENVVTTTFAPNRLKIWWQSENGVENVTIQLDLEAEFFHFLIMTFK	120
Db	82	RDPYHETLNPDShLIENVVTTTFAPNRLKIWWQSENGVENVTIQLDLEAEFFHFLIMTFK	141
Qy	121	TFRPAAMLIERSDDFGKTGWVTRFYAYDCEASFPGISTGPMKKVDDIICDSRYSDIEPST	180
Db	142	TFRPAAMLIERSDDFGKTGWVTRFYAYDCESSFPFGISTGPMKKVDDIICDSRYSDIEPST	201
Qy	181	EGEVIFRALDPAFKIEDPYSPIQNLLKITNLRKFVKLHTLGDNLDSRMEIREKYVA	240

Db 202 EGEVIFRALDPAPKIEDPSPRIQNLLKTNLRIFKVLGHTLGNLLDSRMEIREKYIYA 261
QY 241 VYDMVVRGNCFCYGHASECAPVDGFNEEVGMVHGHCMCRHNTKGLNCELMDFFYHDLPW 300
Db 262 VYDMVVRGNCFCYGHASECAPVDGVNEEVGMVHGHCMCRHNTKGLNCELMDFFYHDLPW 321
QY 301 RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGVCDCCOHNMTGRNCEQCKPFY 360
Db 322 RPAEGRNSNACKKNCNEHSCHFDMAVFLATGNVSGVCDCCOHNMTGRNCEQCKPFY 381
QY 361 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYDFSTGLIAGQCRCCKLNVEGEHCDVCK 420
Db 382 FQHPERDIRDPNLCBPCTCDPAGSENGGICDGYTDFSVGLIAGQCRCCKLHVEGERCDVCK 441
QY 421 EGFYDLSSDPFGCKSCACNPLGTIPGGNPNCDSETGHYCKRVLVTGQHCDQCCLPEHWGLS 480
Db 442 EGFYDLSEAEDPYGCKSCACNPLGTIPGGNPNCDSETGYCYCKRLVTGQRCDQCCLPQHWGLS 501
QY 481 NDLGCRPCDCDLGGALNNSCFAESGQCSCRPHMIGRQCNEVEPGYFATLDHYLYEAE 540
Db 502 NDLGCRPCDCDLGGALNNSCSEDSGQCCLPHMIGRQCNEVESGYFTTLDHYLYEAE 561
QY 541 ANLPGVSVIVERQYIQDRIPSWTGAFFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 600
Db 562 ANLPGVVVVERQYIQDRIPSWTGPGRVVRVPEGAYLEFFIDNIPYSMEYEILIRYEPQLP 621
QY 601 DHWEKAVITVQRPGRIPSTSSRCNTIPDDDNQVVSLSPGSRVYVLPVPVCFEKGNTYTVR 660
Db 622 DHWEKAVITVQRPGRIPASSRCNTVPDDDNQVVSLSPGSRVYVLPVPVCFEKGNTYTVR 681
QY 661 LELPOYTSSDSVESPYTILDSLVLMPYCKSLDIFTVGGSGDGVVTVNSAWETFORYRCLE 720
Db 682 LELPOYTASGDSVESPYTIFDSLVLMPYCKSLDIFTVGGSGDGEVTVNSAWETFORYRCLE 741
QY 721 NSRSVVKTPMTDVCNRIIFSISALLHOTGLACECDPQGSLSVSCDPPNGCQCQCRPNVVG 780
Db 742 NSRSVVKTPMTDVCNRIIFSISALIHOTGLACECDPQGSLSVSCDPPNGCQCQCRPNVVG 801
QY 781 TCNRCAPGTGFGPGSGCKPCECHLQGSVNACFPVTVGQCHCFQGVYARQCDRCLPGHWGF 840
Db 802 TCNRCAPGTGFGPGNGCKPCDCHLQGSASAFCDALTGQCHCFQGIYARQCDRCLPGYWG 861
QY 841 PSCQPCQCNHADDCTPVTGECCLNCQDVTMGHNCERCLAGYGDPIIGSGDHCRPCPCPD 900
Db 862 PSCQPCQCNHALDCTVTGECCLSCQDVTYTGHNCRCLAGYGDPIIGSGDHCRPCPCPD 921
QY 901 GPDSGRQFARSCYQDPVTIQLACVCDPVGYSRCDPCASGYFGNPSFVSGSCQPCQCHN 960
Db 922 GPDSGRQFARSCYQDPVTIQLACVCDPVGYSRCDPCASGFFGNPSDFGSCQPCQCHN 981
QY 961 IDTTDPEACDKETGRCLKLYHTEGEHCQFCRFGYGDALRQDCRKCVCNLYLGTVQEHCN 1020
Db 982 IDTTDPEACDKDTGRCLKLYHTEGDHCQLCQGYGDALRQDCRKCVCNLYLGTVQEHCN 1041
QY 1021 GSDCQCDKATGQCLCLPNVIGQNCDCRCAPNTWQLASGTGCDPCNCAHSGFSPSCNEFTG 1080
Db 1042 GSDCHCDKATGQCSCLPNVIGQNCDCRCAPNTWQLASGTGCGPCNCAHSGFSPSCNEFTG 1101
QY 1081 QCQCMFGFGGRTCSECELFWDGPDVECRACDCDPRGIETPQCDQSTGQCVCVGEVGP 1140
Db 1102 QCQCMFGFGGRTCSECELFWDGPDVECRACDCDPRGIETPQCDQSTGQCVCVGEVGP 1161
QY 1141 CDKCTRGYSGVFPDCTPCHQCPCALWDVIAELTNRTHRFLEKAKALKISGVTGPYRETVD 1200
Db 1162 CDKCTRGYSGVFPDCTPCHQCPCALWDVIAELTNRTHRFLEKAKALKISGVTGPYRETVD 1221
QY 1201 SVERKVSEIKDILAQSPAAEPLKNIGNLFEAEKLIKDVTEMAQVEVKLSDTTSQSNST 1260
Db 1222 SVEKKVNEIKDILAQSPAAEPLKNIGILFEAEKLIKDVTEKMAQVEVKLTDTASQSNST 1281
QY 1261 AKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTTE 1320

Db 1282 AGELGALQAEASLDKTVKELAEQLEFIKNSDIQGALDSITKYFQMSLEAEKRVNASTTD 1341
QY 1321 PNSTVEQSALMRDRVEDVMMERESQFKEKEQBEQARLLDELAKLQSLDLSAAAEMTCTGP 1380
Db 1342 PNSTVEQSALTRDRVEDLMLERESPFKEQEEQARLLDELAKLQSLDLSAAAEQMTCTGP 1401
QY 1381 PGASCSETECGGNCRTDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLASAEVEQL 1440
Db 1402 PGADCSSECGGNCRTDEGEKKCGGPGCGGLVTVAHSAWQKAMDFDRDVLASAEVEQL 1461
QY 1441 SKMVSEAKLRADAKQSAEDILLKTNATKEKMDKSNELRNLIKQIRNFLTQDSADLDSI 1500
Db 1462 SKMVSEAKVRADAKQNAQDVLKTNATKEKVDKSNEDLRNLIKQIRNFLTQDSADLDSI 1521
QY 1501 EAVANEVLKMEMBPTPQQLQNLTEDIRERVESLSQVEVILQHSADIARAEMLLLEEAKRA 1560
Db 1522 EAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVILQSSAADIARAEMLLLEEAKRA 1581
QY 1561 SKSATDVKVTADMVKEALEEAEKAQVAAEKAQKQADEDIQGTQNLTSIESETAASEETL 1620
Db 1582 SKSATDVKVTADMVKEALEEAEKAQVAAEKAQKQADEDIQGTQNLTSIESETAASEETL 1641
QY 1621 FNASQRISELERNVHELKRKAQNSGEAEYIEKVYTVKQSAEDVVKTLTGDELDEKYKKV 1680
Db 1642 TNASQRIKSLERNVEELKRKAQNSGEAEYIEKVYTVKQNAADDVVKTLTGDELDEKYKKV 1701
QY 1681 ENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLLKDLERKYEDNQRYLEDKAQEL 1740
Db 1702 ESLIAQKTESADARRKAELLQNEAKTLLAQANSKLQLEDLERKYEDNQRYLEDKAQEL 1761
QY 1741 ARLEGEVRSLLKDISQKAVVYSTCL 1765
Db 1762 VRLEGEVRSLLKDISQKAVVYSTCL 1786

RESULT 13
AAB48450
ID AAB48450 standard; protein; 1786 AA.
XX AAB48450;
AC
XX
DT 02-MAR-2001 (first entry)
XX
DE Mouse laminin 8 polypeptide, SEQ ID NO: 18.
XX
KW Mouse; laminin 8; neuroprotective; angiogenic; osteopathic;
KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;
KW vascular tissue injury; neural injury; angiogenesis regulation.
OS Mus musculus.
XX
PN WO200066732-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US011543.
XX
PR 30-APR-1999; 99US-0131720P.
PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.
PR 11-FEB-2000; 2000US-0182012P.
XX
PA (BIOS-) BIOSSTRATUM INC.
XX
PI Kortessmaa J, Tryggvason K;
XX
DR WPI; 2000-687539/67.
DR N-PSDB; AAC83711.
XX
PT Purified laminin 8 protein, useful for research and therapeutic purposes
PT including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.
XX

ID ABB81592 standard; protein; 1786 AA.
XX AC ABB81592;
AC
DT 19-SEP-2002 (first entry)
XX DE Mouse laminin 10 second chain protein sequence SEQ ID NO:10.
XX KW Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;
KW tissue repair development; laminin; healing; vascular tissue;
KW re-endothelialisation; vascular injury; cell attachment; cell stasis;
XX proliferation; migration.
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT /label= signal
FT Protein 22..1786
FT /label= laminin_10_second_chain
PN WO200250111-A2.
XX
PD 27-JUN-2002.
XX
PF 21-DEC-2001; 2001WO-US051035.
XX
PR 21-DEC-2000; 2000US-0257449P.
PR 28-MAR-2001; 2001US-0279282P.
PR 13-NOV-2001; 2001US-00279282.
XX
PA (BIOS-) BIOSTRATUM INC.
XX
PI Tryggvason K, Doi M, Thyboll J;
XX
DR WPI; 2002-557650/59.
DR N-PSDB; ABQ72910.
XX
PT New human laminin-10 proteins, useful for accelerating the healing of
PT vascular tissue, improving the biocompatibility of grafts, or for
PT promoting re-endothelialization at the site of vascular injuries.
XX
PS Claim 9; Page 140-145; 231pp; English.
XX
CC The present invention describes human laminin alpha 5. Also described is
CC an isolated laminin 10. Laminin 10 has vulnery activity. Laminins are
CC useful in maintaining cell/tissue phenotype as well as promoting cell
CC growth and differentiation in tissue repair development. Specifically,
CC laminin 10 can be used for accelerating the healing injuries of vascular
CC tissue, improving the biocompatibility of grafts useful for treating such
CC injuries, for promoting re-endothelialisation at the site of vascular
CC injuries, and promote cell attachment and subsequent cell stasis,
CC proliferation, differentiation, and/or migration. The present sequence
CC encodes a second chain protein of laminin 10, from the present invention
XX
SQ Sequence 1786 AA;
Query Match 94.2%; Score 9092; DB 5; Length 1786;
Best Local Similarity 93.0%; Pred. No. 0;
Matches 1642; Conservative 71; Mismatches 52; Indels 0; Gaps 0;
QY 1 QEPEFSYGCAEGSCYPATGDLIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICNS 60
DB 22 QEPEFSYGCAEGSCYPATGDLIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICDS 81
QY 61 QDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENVTIQLDLEAFHFTHLIMTFK 120
DB 82 RDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENVTIQLDLEAFHFTHLIMTFK 141
QY 121 TFRPAAMLIERSDFGKTGWVRYFAYDCEASPPGISTGPMKKVDDIICDSRYSDIEPST 180
DB 142 TFRPAAMLIERSDFGKTGWVRYFAYDCEASPPGISTGPMKKVDDIICDSRYSDIEPST 201

QY 181 EGEVIFRALDPAFKIEDPSPRIQNLLKITNLRIFVKLHTLGDNLDSRMEIREKYYA 240
DB 202 EGEVIFRALDPAFKIEDPSPRIQNLLKITNLRIFVKLHTLGDNLDSRMEIREKYYA 261
QY 241 VYDMVVRGNCFCYGHASECAPVDGFNEVEGMVHGHCMCRHNTKGLNCELMDYFHDLPW 300
DB 262 VYDMVVRGNCFCYGHASECAPVDGFNEVEGMVHGHCMCRHNTKGLNCELMDYFHDLPW 321
QY 301 RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGVCDQCQHNMTGRNCEQCKPFY 360
DB 322 RPAEGRNSNACKKNCNEHSSSCHFDMAVYLATGNVSGVCDQCQHNMTGRNCEQCKPFY 381
QY 361 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFSTGLIAGQCRCRKLNVGEHCDVCK 420
DB 382 FQHPERDIRDPNLCPEPCTCDPAGSENGGICDGYTDFSVGLIAGQCRCRKLHVEGERCDVCK 441
QY 421 EGFYDLSSSEDPFGCKSCACNPLGTIPGPNPCDSETHCYCKRLVTGQHCDCQLPEHWGLS 480
DB 442 EGFYDLSEADPYGCKSCACNPLGTIPGPNPCDSETHCYCKRLVTGQHCDCQLPEHWGLS 501
QY 481 NDLDGCRPCDCDLGGALNNSCFAESGQSCSRPHMIGRQCNEVEPGYVFATLDHYLYEAE 540
DB 502 NDLDGCRPCDCDLGGALNNSCSEDSGQSCSLPHMIGRQCNEVESGYFTTLDHYLYEAE 561
QY 541 ANLPGVSIIVERQYIQDRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 600
DB 562 ANLPGVSVVVERQYIQDRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 621
QY 601 DHWEKAVITVQRPGRIPTSRRCGNTIPDDDNQVVSLSPGSRYVVLPRPVCFEKGNTYTVR 660
DB 622 DHWEKAVITVQRPGRIPASSRCGNTVPDDDNQVVSLSPGSRYVVLPRPVCFEKGNTYTVR 681
QY 661 LELPQYTSDDSDVESPYTLIDSLVMPYCKSLDIFTVGGSGDGVVVTNSAWETFYRYRCLE 720
DB 682 LELPQYTSAGSDVESPYTFIDSLVMPYCKSLDIFTVGGSGDGEVTNSAWETFYRYRCLE 741
QY 721 NSRSVVKTPMTDVCRNIIFISALLHQTLGACECDPQGSLSVSCDPNGGQCCRPNVVGR 780
DB 742 NSRSVVKTPMTDVCRNIIFISALIHQTLGACECDPQGSLSVSCDPNGGQCCRPNVVGR 801
QY 781 TCNRCAPGTGFGPGSGCKPCECHLQGSVNAFNPNVTGQCHCFQGVYARQCDRLPGHWGF 840
DB 802 TCNRCAPGTGFGPGNGCKPCDCHLQGSASAFCDAITGQCHCFQGIYARQCDRLPGYWG 861
QY 841 PSCQPCQCNHADDCCDPTVTECLNCQDYTMHNCERCLAGYGDPIIGSGDHCRPCPCPD 900
DB 862 PSCQPCQCNHADDCCDPTVTECLSCQDYTMHNCERCLAGYGDPIIGSGDHCRPCPCPD 921
QY 901 GDSGRQFARSCYQDPVTIQLACVCDPGYIGSRCDCCASGYFGNPNSEVGGSCQPCQCHNN 960
DB 922 GDSGRQFARSCYQDPVTIQLACVCDPGYIGSRCDCCASGFFGNPNSEVGGSCQPCQCHNN 981
QY 961 IDTTDPEACDKETGRCLKLYHTEGEHCQCFRFGYGDALRQDCRKCVCNVLGTVQEHCN 1020
DB 982 IDTTDPEACDKETGRCLKLYHTEGEHCQCFRFGYGDALRQDCRKCVCNVLGTVQEHCN 1041
QY 1021 GSDCQCDKATGQCLCLPNVIGQNCDCRCPNTWQLASGTGCDPCNCAHSAHSGPSCNEFTG 1080
DB 1042 GSDCHCDKATGQCSCLPNVIGQNCDCRCPNTWQLASGTGCGPCNCAHSAHSGPSCNEFTG 1101
QY 1081 QCQCMFGGRTCSCEQLFWGDDPVECRACDCCDPRGIETPQCDQSTGQCVCVEGEGPR 1140
DB 1102 QCQCMFGGRTCSCEQLFWGDDPVECRACDCCDPRGIETPQCDQSTGQCVCVEGEGPR 1161
QY 1141 CDKTRGYSGVFPDCTPCHQCFALWDVIIAELTNRTHRFLEKAKALKISGVIGPYRETVD 1200
DB 1162 CDKTRGYSGVFPDCTPCHQCFALWDVIAELTNRTHRFLEKAKALKISGVIGPYRETVD 1221
QY 1201 SVERKVVSEIKDILAQSPAABPLKNIGNLFEEAEKLIKDVTEMAQVEVKLSDTTSQSNST 1260
DB 1222 SVEKKVNEIKDILAQSPAABPLKNIGNILFEEAEKLIKDVTEKMAQVEVKLTDTSQSNST 1281
QY 1261 AKELDSLQTEAESLDNTVKELAEQLEFINKNSDIRGALDSITKYFQMSLEAEERNASTTE 1320

Db 1282 AGELGALQAAESLDKTVKELAEQLEFIKNDSIQGALDSITKYFQMSLEAEKRVNASTTD 1341
QY 1321 PNSTVEQSALMRDVEDVMMERESQFKEQEQEARLLDELAKLQSLDLSAAAEAMTCGTP 1380
Db 1342 PNSTVEQSALTRDVEDLMLERESPFKEQEQEARLLDELAKLQSLDLSAAAAQMTGTP 1401
QY 1381 PGASCSETECGPNCRTDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVL SALAEVEQL 1440
Db 1402 PGADCSSECGPNCRTDEGEKKCGGPGCGGLVTVAHSAWQKAMD FDRDVL SALAEVEQL 1461
QY 1441 SKMVSEAKLRADAQKQSAEDILLKTNATKEMDKMSNEELRNLIKQIRNFLTQDSADLDSI 1500
Db 1462 SKMVSEAKVRADAQKQNAQDVLLKTNATKEKVDKSNEDLRNLIKQIRNFLTQDSADLDSI 1521
QY 1501 EAVANEVLKVMMPSTPQQLNLTEDIRERVESLSQVEVILQHSAAADIARAEMLLEEAkra 1560
Db 1522 EAVANEVLKSGNASTPQQLNLTEDIRERVETLSQVEVILQQAADIARAEL LLEEAkra 1581
QY 1561 SKSATDVKVTADMVKEALEEAQVAEAKAIKQADEDIQGTQNL LTSIESETAASEETL 1620
Db 1582 SKSATDVKVTADMVKEALEEAQVAEAKAIKQADEDIQGTQNL LTSIESETAASEETL 1641
QY 1621 FNASQRISLELERNVEELKRKAQNSGAEYIEKVVTYVKQSAEDVKKTL DGE LDEKVKV 1680
Db 1642 TNASQRISKLERNVEELKRKAQNSGAEYIEKVVS VKQNA DDVKKTL DGE LDEKVKV 1701
QY 1681 ENLIAKKTESADARRKAEMLQNEAKTLAQANSKLQLLKD LERKYVEDNQRYLEDKAQEL 1740
Db 1702 ESLIAQKTESADARRKAELLQNEAKTLAQANSKLQLLED LERKYVEDNQRYLEDKAQEL 1761
QY 1741 ARLEGEVRSLLKDISQKVAVYSTCL 1765
Db 1762 VRLEGEVRSLLKDISQKVAVYSTCL 1786

RESULT 15

AAW50894
ID AAW50894 standard; protein; 1776 AA.

XX AC AAW50894;

DT 07-DEC-1998 (first entry)

DE Mouse laminin B1 chain.

XX Laminin; mouse; beta-amyloid; amyloidosis; Alzheimer's disease;
KW Down's syndrome; hereditary cerebral haemorrhage; inflammation;
KW malignancy; Familial Mediterranean Fever; multiple myeloma;
KW type II diabetes; prion disease; Creutzfeldt-Jacob disease; CJD;
KW Gertstmann-Straussler syndrome; kuru; scrapie; haemodialysis;
KW carpal tunnel syndrome; senile cardiac amyloid polynuropathy;
KW Familial Amyloidotic Polynuropathy; thyroid carcinoma; diagnosis;
KW therapy.

XX Mus sp.

OS WO9815179-A1.

XX 16-APR-1998.

XX 08-OCT-1997; 97WO-US018145.

XX 08-OCT-1996; 96US-0027981P.

XX (UNIW) UNIV WASHINGTON.

XX Castillo G, Snow AD;

XX WPI; 1998-240534/21.

XX Use of laminin and fragments - for developing products for use in the
PT diagnosis and treatment of amyloid disease, e.g. Alzheimer's disease or

PT CJD.

XX Claim 15; Page 90-93; 132pp; English.

XX This is the amino acid sequence of the mouse laminin B1 chain. The
PS primary object of the invention is to use laminin, laminin-derived
CC protein fragments and/or laminin-derived polypeptides as potent
CC inhibitors of amyloid formation, deposition, accumulation and/or
CC persistence in Alzheimer's disease and other amyloidoses. The laminin
CC products (see AAW50888-98) may include mouse or human laminin A or A1
CC chain, laminin B1 or B2 chain, laminin A2 chain (merosin), laminin G1
CC chain, the globular repeats of the laminin A1 chain and the beta-amyloid
CC binding domain of the laminin A chain. A claimed method for treating an
CC amyloid disease comprises administering a polypeptide having a
CC conformational similarity to a fragment of a laminin protein. A method
CC for diagnosing an amyloid disease involves determining levels of laminin
CC in a sample. Production of laminin or its fourth globular repeat in vivo
CC provides a method for in vivo inhibition of beta-amyloid amyloidosis. The
CC products and methods can be used for the diagnosis, prognosis, monitoring
CC and treatment of amyloidoses such as Alzheimer's disease, Down's syndrome
CC and hereditary cerebral haemorrhage with amyloidosis of the Dutch type
CC (where the specific amyloid is the beta-amyloid protein), the amyloidosis
CC associated with chronic inflammation, various forms of malignancy and
CC Familial Mediterranean Fever (AA amyloid or inflammation-association
CC amyloidosis), the amyloidosis associated with multiple myeloma and other
CC B-cell abnormalities (AL amyloid), the amyloidosis associated with type
CC II diabetes (amylin or islet amyloid), the amyloidosis associated with
CC prion diseases including Creutzfeldt-Jacob disease, Gertstmann-Straussler
CC syndrome, kuru and animal scrapie (PrP amyloid), the amyloidosis
CC associated with long-term haemodialysis and carpal tunnel syndrome (beta
CC 2-microglobulin amyloid), the amyloidosis associated with senile cardiac
CC amyloid and Familial Amyloidotic Polynuropathy (prealbumin or
CC transthyretin amyloid), and the amyloidosis associated with endocrine
CC tumours such as medullary carcinoma of the thyroid (variant of
CC procalcitonin)

XX SQ Sequence 1776 AA;

Query Match 93.6%; Score 9035; DB 2; Length 1776;

Best Local Similarity 92.9%; Pred. No. 0;

Matches 1634; Conservative 69; Mismatches 52; Indels 4; Gaps 1;

QY 1 QEPEFSYGCAEGSCYPATGDL LIGRAQKLSVTSTCGLHKPEPYCI VSHLQEDKKCFICNS 60

Db 22 QEPEFSYGCAEGSCYPATGDL LIGRAQKLSVTSTCGLHKPEPYCI VSHLQEDKKCFICDS 81

QY 61 QDPYHETLNPDSHLIENVTTFAPNRLKI WQSENGVENVTIQDLEAEFFH THTLIMTFK 120

Db 82 RDPYHETLNPDSHLIENVTTFAPNRLKI WQSENGVENVTIQDLEAEFFH THTLIMTFK 141

QY 121 TFRPAAMLIERSSDFGKTGWVRYFAYDCEASFPGISTGPMKKVDDI ICDSRYSDIEPST 180

Db 142 TFRPAAMLIERSSDFGKTGWVRYFAYDCESSFPFISTGPMKKVDDI ICDSRYSDIEPST 201

QY 181 EGEVIFRALDPAPFKIEDPSPRIQNLKITNLRIKFVKLHTLGNLLDSRMEIREKYYA 240

Db 202 EGEVIFRALDPAPFKIEDPSPRIQNLKITNLRIKFVKLHTLGNLLDSRMEIREKYYA 261

QY 241 VYDMVVRGNCFCYGHASECAPVDGFNEEVEGWVHGCMCRHNTKGLNCELCMDFYHDLPW 300

Db 262 VYDMVVRGNCFCYGHASECAPVDGVNNEEVEGWVHGCMCRHNTKGLNCELCMDFYHDLPW 321

QY 301 RPAEGRNSNACKKCNCHSISCHFDMAVYLATGNVSGGVCCDQOHTMGRNCEQCKPFY 360

Db 322 RPAEGRNSNACKKCNCHSISCHFDMAVFLATGNVSGGVCCDQOHTMGRNCEQCKPFY 381

QY 361 YQHPERDIRDNFCERCTCDPAGSQNEGICDSYTFDSTGLIAGQCRCKLNVEGEHCDVCK 420

Db 382 FQHPERDIRDNFCERCTCDPAGSENGGICDGYTFDVSGLIAGQCRCKLHVEGERCDVCK 441

QY 421 EGFYDLSSDDPFPGCKSCACNPLGTIPGGNPCDSETHCYCKRLVTGQHCDQCLPEHWGLS 480

Db 442 EGFYDLSEADPFYGCKSCACNPLGTIPGGNPCDSETHCYCKRLVTGQRCDQCLPQHWGLS 501

QY	481	NDLDGCRPCDCDLGGALNNSCFAESGQCSGRPHMIGRQCNEVEPGYYFATLDHYLYEAE	540
Db	502	NDLDGCRPCDCDLGGALNNSCSEDSGQCSCLPHMIGRQCNEVESGYFTTLDHYIYEAE	561
QY	541	ANLPGVSVIVERQYIQDRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP	600
Db	562	ANLPGVVVVERQYIQDRIPSWTGPGRVVRVPEGAYLEFFIDNIPYSMEYELLIRYEPQLP	621
QY	601	DHWEKAVITVQRGRIPSTSSRCGNTIPDDDNQVVSLSPGSRYYVVLPRPVCFEKGNTYTVR	660
Db	622	DHWEKAVITVQRPGKIPASSRCGNTVPDDDNQVVSLSPGSRYYVVLPRPVCFEKGMMYTVR	681
QY	661	LPLPQYTSSDSVESPYTLIDSLVLMPYCKSLDIFTVGGSGDGVVTVNSAWETFORYRCLE	720
Db	682	LPLPQYTASGDSVESPYTFIDSLVLMPYCKSLDIFTVGGSGDGEVTVNSAWETFORYRCLE	741
QY	721	NSRSVVKTPMTDVCRNIIIFSISALLHOTGLACEDPQGSLSVCDPNGGQCQCRPNVVGR	780
Db	742	NSRSVVKTPMTDVCRNIIIFSISALIHOTGLACEDPQGSLSVCDPNGGQCQCRPNVVGR	801
QY	781	TCNRCAPGTFGFGSGCKPCECHLQGSVNFCNPVTGQCHCFQGVYARQCDRCLPGHWGF	840
Db	802	TCNRCAPGTFGFGPGCKPCDCHLQGSASAFDAITGQCHCFQGIYARQCDRCLPGYWG	861
QY	841	PSCQPCQCNHADDPCVTGECNQCDDYTMGHNCERCLAGYYGDPPIIGSGDHCRPCPCPD	900
Db	862	PSCQPCQCNHADDCTVTGECNQCDDYTMGHNCERCLAGYYGDPPIIGSGDHCRPCPCPD	921
QY	901	GPDSGRQFARSCYQDPVTQLACVCDPGYIGSRCDPCASGYFGNPSVGGSCQPCQCHN	960
Db	922	GPDSGRQFARSCYQDPVTQLACVCDPGYIGSRCDPCASGFFGNPSDFGSGCQPCQCHN	981
QY	961	IDTTDPEACDKETGRCLKCLYHTEGEHCQFCRFGYYGDLALQDCRKCVCNYLGTVQEHCN	1020
Db	982	IDTTDPEACDKETGRCLKCLYHTEGDHCQLCQYGYGDLALQDCRKCVCNYLGTVKEHCN	1041
QY	1021	GSDCQCDKATGQCLCLPNVIGONCDRCAPNTWQLASGTGCDPCNCAHSGFSGSCNEFTG	1080
Db	1042	GSDCHCDKATGQCSCLPNVIGONCDRCAPNTWQLASGTGCGPCNCAHSGFSGSCNEFTG	1101
QY	1081	QCQCMGFGGRTCEQBELFWGDDPVECRACDCEPRGIETPCDQSTGQCVCVEGVEGPR	1140
Db	1102	QCQCMGFGGRTCEQBELFWGDDPVECRACDCEPRGIETPCDQSTGQCVCVEGVEGPR	1161
QY	1141	CDKCTRGYSGVFPDCTPCHQCFALWDVIIAELTNTRHREFLEKAKALKISGVIGPYRETVD	1200
Db	1162	CDKCTRGYSGVFPDCTPCHQCFALWDIIIGELTNTRHREFLEKAKALKISGVIGPYRETVD	1221
QY	1201	SVERKVSEIKDILAQSPAABPLKNIGNLFEEAEKLIKDVTEMMQAVEVKLSDTTSQSNT	1260
Db	1222	SVEKKVNEIKDILAQSPAABPLKNIGILFEEAEKLIKDVTEKMAQVEVKLTDTSQSNT	1281
QY	1261	AKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKIFQMSLEAEERYVNASTTE	1320
Db	1282	AGELGALQAEAESLDKTVKELAEQLEFIKNSDIQALDSDITKIFQMSLEAEKRYVNASTTD	1341
QY	1321	PNSTVEQSALMRDRVEDVNMERESQFKEQEEQARLLDELAKGLQSLDLSAAAEWTCGTP	1380
Db	1342	PNSTVEQSALTRDRVEDLMLERESPFKEQEEQARLLDELAKGLQSLDLSAAAEWTCGTP	1401
QY	1381	PGASCSETECGGPNCRDTEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLSSALABVEQL	1440
Db	1402	PGADCSSECECGGPNCRDTEGEKKCGGPGCGGLVTVAHSAWQKAMDFDRDVLSSALABVEQL	1461
QY	1441	SKMVSEAKLRADAEAKQSAEDILLKTNATKEKMDKSNELRNLIKQIRNFLTQDSADLDSI	1500
Db	1462	SKMVSEAKVRADAEAKQNAQDVLKTNATKEKVKDKSNEDLRNLIKQIRNFLTQDSADLDSI	1521
QY	1501	EAVANEVLKWEPPSTPQQLQNLTDIERERVESLSQVEVILQHSAAADIAEAEMLEBAKRA	1560
Db	1522	EAVANEVLKSGNASTPQQLQNLTDIERERVETLSQVEVILQHSAAADIAEAELLEBAKRA	1581

QY	1561	SKSATDVKVYTD	MDMVEALEEAEKAIQ	DAEDIIQGT	QNLLTSIESETA	AAASEETL	1620
Db	1582	SKSATDVKVYTD	MDMVEALEEAEKAIQ	DAEDIIQGT	QNLLTSIESETA	AAASEETL	1641
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Db	1698	ESLIAKKTESAD	ARRKAEMLQNEAKTLL	AQANSKIQLLKDLER	KYEDNQRYLEDKA	QAE	1757
QY	1741	ARLEGEVRSLLK	DISQKVA	1759			
Db	1758	VRLEGEVRSLLK	DISQKVA	1776			

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Job time : 53.9797 secs

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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:30:58 ; Search time 13.3519 Seconds
(without alignments)
6824.493 Million cell updates/sec

Title: US-10-037-182-8
Perfect score: 9654
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	9654	100.0	1765	4 US-09-562-702A-16	Sequence 16, Appl
2	9654	100.0	1765	4 US-09-561-818A-16	Sequence 16, Appl
3	9654	100.0	1786	4 US-09-562-702A-14	Sequence 14, Appl
4	9654	100.0	1786	4 US-09-561-818A-14	Sequence 14, Appl
5	9654	100.0	1786	4 US-09-561-709B-9	Sequence 9, Appl
6	9092	94.2	1786	4 US-09-562-702A-18	Sequence 18, Appl
7	9092	94.2	1786	4 US-09-561-818A-18	Sequence 18, Appl
8	8873	91.9	1725	4 US-09-562-702A-20	Sequence 20, Appl
9	8873	91.9	1725	4 US-09-561-818A-20	Sequence 20, Appl
10	6051.5	62.7	1196	1 US-08-144-121-4	Sequence 4, Appl
11	6051.5	62.7	1196	2 US-08-735-893-4	Sequence 4, Appl
12	5046	52.3	1799	4 US-09-845-583A-6	Sequence 6, Appl
13	4923	51.0	1798	4 US-09-561-709B-11	Sequence 11, Appl
14	4918	50.9	1798	4 US-09-845-583A-8	Sequence 8, Appl
15	3832.5	39.7	1761	4 US-09-561-709B-1	Sequence 1, Appl
16	3076.5	31.9	1101	4 US-09-561-709B-5	Sequence 5, Appl
17	2940.5	30.5	1342	4 US-09-561-709B-13	Sequence 13, Appl
18	1680.5	17.4	1609	4 US-09-562-702A-22	Sequence 22, Appl
19	1680.5	17.4	1609	4 US-09-561-818A-22	Sequence 22, Appl
20	1680.5	17.4	1617	4 US-09-562-702A-26	Sequence 26, Appl
21	1677	17.4	1572	4 US-09-562-702A-32	Sequence 32, Appl
22	1677	17.4	1572	4 US-09-561-818A-28	Sequence 28, Appl
23	1677	17.4	1605	4 US-09-562-702A-30	Sequence 30, Appl
24	1677	17.4	1605	4 US-09-561-818A-26	Sequence 26, Appl
25	1673	17.3	279	1 US-08-152-019A-29	Sequence 29, Appl
26	1673	17.3	1576	4 US-09-562-702A-24	Sequence 24, Appl
27	1673	17.3	1576	4 US-09-561-818A-24	Sequence 24, Appl

28	1673	17.3	1584	4 US-09-562-702A-28	Sequence 28, Appl
29	1667	17.3	278	2 US-08-460-309-13	Sequence 13, Appl
30	1667	17.3	278	2 US-08-125-077-13	Sequence 13, Appl
31	1605	16.6	3635	4 US-09-845-583A-2	Sequence 2, Appl
32	1565	16.2	3111	2 US-08-460-309-4	Sequence 4, Appl
33	1565	16.2	3111	2 US-08-125-077-4	Sequence 4, Appl
34	1559.5	16.2	3088	4 US-09-562-702A-8	Sequence 8, Appl
35	1559.5	16.2	3089	4 US-09-562-702A-4	Sequence 4, Appl
36	1559.5	16.2	3110	4 US-09-562-702A-2	Sequence 2, Appl
37	1559.5	16.2	3110	4 US-09-562-702A-6	Sequence 6, Appl
38	1559.5	16.2	3110	4 US-09-561-709B-7	Sequence 7, Appl
39	1553.5	16.1	1172	4 US-09-919-172-16	Sequence 16, Appl
40	1538.5	15.9	1170	4 US-09-561-709B-12	Sequence 12, Appl
41	1535.5	15.9	3106	4 US-09-562-702A-10	Sequence 10, Appl
42	1534.5	15.9	3084	4 US-09-562-702A-12	Sequence 12, Appl
43	1529	15.8	3075	2 US-08-460-309-5	Sequence 5, Appl
44	1529	15.8	3075	2 US-08-125-077-5	Sequence 5, Appl
45	1515.5	15.7	1587	4 US-09-845-583A-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-562-702A-16
; Sequence 16, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 1765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-16

Query Match 100.0%; Score 9654; DB 4; Length 1765;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	61	QDPYHETLNPDSHLIENVV	TFAPNRLKIWQSENGVENVTIQLDLEAEFHTLIMTFK	120
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DB 361 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDSTGLIAGQCRCKLNVEGEHCHDVCK 420
QY 421 EGFYDLSSDPFGCKSCACNPLGTIPGPNPCDSETGHCYCKRLVTGQCHCDQCLPEHWGLS 480
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DB 1501 EAVANEVLKMEPSTPQQLONLTEDIRERVESLSQVEVILQHSAAADIARAEMLLEAKRA 1560
QY 1561 SKSATDVKVTADMVKEALEEAEKAQVAAEKAQADEDIQGTQNLTSIESETAASEETL 1620
DB 1561 SKSATDVKVTADMVKEALEEAEKAQVAAEKAQADEDIQGTQNLTSIESETAASEETL 1620
QY 1621 FNASQRISELERNVVELKRAAQAQNSGEAEYIEKVYVTVKQSAEDVKKTLDGELDEKYYKV 1680
DB 1621 FNASQRISELERNVVELKRAAQAQNSGEAEYIEKVYVTVKQSAEDVKKTLDGELDEKYYKV 1680
QY 1681 ENLIACKTEESADARRKAEMLONEAKTLLAQANSKLOLLKDLERKYEDNQRYLEDKAQEL 1740
DB 1681 ENLIACKTEESADARRKAEMLONEAKTLLAQANSKLOLLKDLERKYEDNQRYLEDKAQEL 1740
QY 1741 ARLEGEVRSLLKDISQKVAVYSTCL 1765
DB 1741 ARLEGEVRSLLKDISQKVAVYSTCL 1765
RESULT 2
US-09-561-818A-16
; Sequence 16, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortessmaa, Jarkko
; APPLICANT: Tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 1765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-818A-16
Query Match 100.0%; Score 9654; DB 4; Length 1765;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QEPFESYGAEGSCYCPATGDLIGRAQKLSVTSTCGLHKPEYICVSHLQEDKKCFICNS 60
DB 1 QEPFESYGAEGSCYCPATGDLIGRAQKLSVTSTCGLHKPEYICVSHLQEDKKCFICNS 60
QY 61 QDPYHETLNPDNPSHLEIENVVTTAPNRLKIWMQSENGVENVTIQLDLEAEFFHFLIMTFK 120
DB 61 QDPYHETLNPDNPSHLEIENVVTTAPNRLKIWMQSENGVENVTIQLDLEAEFFHFLIMTFK 120
QY 121 TFRPAAMLIERSSDPGKTGWVRYFYAYDCEASFPGISTGPMKKVDDIICDSRYSDIERST 180
DB 121 TFRPAAMLIERSSDPGKTGWVRYFYAYDCEASFPGISTGPMKKVDDIICDSRYSDIERST 180
QY 181 EGEVIFRALDPAPFKIEDPSPRIQNLKITNLRIKFVKLHTLGDNLDSRMEIREKYYVA 240
DB 181 EGEVIFRALDPAPFKIEDPSPRIQNLKITNLRIKFVKLHTLGDNLDSRMEIREKYYVA 240
QY 241 VYDMVVRGNCFCYGHASECAPVDGNEVEVEGMVHGHCMCRHNTKGLNCELMDFFYHDLPLW 300
DB 241 VYDMVVRGNCFCYGHASECAPVDGNEVEVEGMVHGHCMCRHNTKGLNCELMDFFYHDLPLW 300
QY 301 RPAEGRNSACKKCNNEHSISCHFDMAVYLATGNVSGVCGDDCOHNTMGRNCEQCKPFY 360

Db 301 RPAEGRNSACKKNCNEHSISCHFDMAVYLATGNVSGVCDCCOHNMTGRNCEQCKPFY 360
QY 361 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDSTGLIAGQCCKLNVEGEHCDVCK 420
Db 361 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDSTGLIAGQCCKLNVEGEHCDVCK 420
QY 421 EGFYDLSSDPFGCKSCACNPLGTIPGPNPCDSETHCYCKRLVTGHCDDQCLPEHWGLS 480
Db 421 EGFYDLSSDPFGCKSCACNPLGTIPGPNPCDSETHCYCKRLVTGHCDDQCLPEHWGLS 480
QY 481 NDLDGCRPCDCLGGALNNSCFAESGQCSRPHMIGRQCNEVEPGYYPATLDHYLYEABE 540
Db 481 NDLDGCRPCDCLGGALNNSCFAESGQCSRPHMIGRQCNEVEPGYYPATLDHYLYEABE 540
QY 541 ANLPGVSIIVERQYIQDRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 600
Db 541 ANLPGVSIIVERQYIQDRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 600
QY 601 DHWEKAVITVQRPGRIPPTSSRCNGTIPDDDNQVVSLSPGSRYVVLPRPVCFEKGTNYTVR 660
Db 601 DHWEKAVITVQRPGRIPPTSSRCNGTIPDDDNQVVSLSPGSRYVVLPRPVCFEKGTNYTVR 660
QY 661 LELPOYTSSDSVESPYTLIDSLVMPYCKSLDIFTVGGSGDGVVNTNSAWETFORYRCLE 720
Db 661 LELPOYTSSDSVESPYTLIDSLVMPYCKSLDIFTVGGSGDGVVNTNSAWETFORYRCLE 720
QY 721 NSRSVVKTPMTDVCNRIIPFISALLHOTGLACECDPQGSLSVCDPNGGQCQCRPNVVG 780
Db 721 NSRSVVKTPMTDVCNRIIPFISALLHOTGLACECDPQGSLSVCDPNGGQCQCRPNVVG 780
QY 781 TCNRCAPGTFGFGPSGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDCRLPGHWGF 840
Db 781 TCNRCAPGTFGFGPSGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDCRLPGHWGF 840
QY 841 PSQPCQCNHADDPCDPTVTECLNCQDVTMGNHCERCLAGYGDPIIGSGDHCRPCPCPD 900
Db 841 PSQPCQCNHADDPCDPTVTECLNCQDVTMGNHCERCLAGYGDPIIGSGDHCRPCPCPD 900
QY 901 GPDSCRQFARSCYQDPVTILOACVCDPQYIGSRCCDPCAGYFNGPSEVGGSCQPCQCHNN 960
Db 901 GPDSCRQFARSCYQDPVTILOACVCDPQYIGSRCCDPCAGYFNGPSEVGGSCQPCQCHNN 960
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Db 1021 GSDCQCDKATGQCLCLPNVIGONCDRCAPNTWQLASGTGCDPCNCAHSGFSCNEFTG 1080
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Db 1081 QCQCMFGFGGRTCECQELFWGDPDVECRACDCDPRGIEPTQCDQSTGQCVCVEGVEGPR 1140
QY 1141 CDKCTRGSYGVFPDCTPCHQCQFALWDVIAELTNRTHRFLEKAKALKISGVIGRETVD 1200
Db 1141 CDKCTRGSYGVFPDCTPCHQCQFALWDVIAELTNRTHRFLEKAKALKISGVIGRETVD 1200
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Db 1201 SVERKVSEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDVTEMMAQVEVKLSDTTSQSNST 1260
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Db 1261 AKELDSLOTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTTE 1320
QY 1321 PNSTVEQSALMRDRVEDVMMERESQFKEQEEQARLLDELAKGLQSLDLSAAAEFTCGTP 1380
Db 1321 PNSTVEQSALMRDRVEDVMMERESQFKEQEEQARLLDELAKGLQSLDLSAAAEFTCGTP 1380
QY 1381 PGASCSETECGGNCRDTDEGERKCGGPGCGGLVTVAHNWQKAMDLDQDVLALAEVEQL 1440
Db 1381 PGASCSETECGGNCRDTDEGERKCGGPGCGGLVTVAHNWQKAMDLDQDVLALAEVEQL 1440

QY 1441 SKMVSEAKLRADAEAKQSAEDILLKTNATKQKDKSNEELRNLIKQIRNFLTQDSADLDSI 1500
Db 1441 SKMVSEAKLRADAEAKQSAEDILLKTNATKQKDKSNEELRNLIKQIRNFLTQDSADLDSI 1500
QY 1501 EAVANEVLKMEMPSTPQOLQNLTEDIRERVESLSQVEVILQHSAAADIARAEMLLBEAKRA 1560
Db 1501 EAVANEVLKMEMPSTPQOLQNLTEDIRERVESLSQVEVILQHSAAADIARAEMLLBEAKRA 1560
QY 1561 SKSATDVKVTADMVKEALEEAEAKQAQAAEKAQADEDIQGTQNLNLTSSIESETAASEETL 1620
Db 1561 SKSATDVKVTADMVKEALEEAEAKQAQAAEKAQADEDIQGTQNLNLTSSIESETAASEETL 1620
QY 1621 FNASQRISELERNEVEELKRAAQNSEAEYIEKVYTVVKQSAEDVKKTLTDLGELDEKYYKV 1680
Db 1621 FNASQRISELERNEVEELKRAAQNSEAEYIEKVYTVVKQSAEDVKKTLTDLGELDEKYYKV 1680
QY 1681 ENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLLKDLERKYEDNQRYLEDKAQEL 1740
Db 1681 ENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLLKDLERKYEDNQRYLEDKAQEL 1740
QY 1741 ARLEGEVRSLLKDISQKVAVYSTCL 1765
Db 1741 ARLEGEVRSLLKDISQKVAVYSTCL 1765

RESULT 3
US-09-562-702A-14
; Sequence 14, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-14

Query Match 100.0%; Score 9654; DB 4; Length 1786;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QEPEFSYGCAEGSCYPATGDDLIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICNS 60
Db 22 QEPEFSYGCAEGSCYPATGDDLIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICNS 81
QY 61 QDPYHETLNPDASHLIENVVTTFAPNRLKIWWQSENGVENVTIQDLLEAEFFHFLIMTFK 120
Db 82 QDPYHETLNPDASHLIENVVTTFAPNRLKIWWQSENGVENVTIQDLLEAEFFHFLIMTFK 141
QY 121 TFRPAAMLIERSSDFGKTGWGVYRYPAYDCEASFPGISTGPMKKVDDIICDSRYSDIEPST 180
Db 142 TFRPAAMLIERSSDFGKTGWGVYRYPAYDCEASFPGISTGPMKKVDDIICDSRYSDIEPST 201
QY 181 EGEVIFRALDPAPFKIEDPSPRIQNLKITNLRIFKFKLHGLGDNLLDSRMEIREKYYVA 240
Db 202 EGEVIFRALDPAPFKIEDPSPRIQNLKITNLRIFKFKLHGLGDNLLDSRMEIREKYYVA 261
QY 241 VYDMVVRGNCFCYGHASECAPVDGFEVEEVEGMVHGCMCRHNTKGLNCCLCMDFYHDLPW 300

Db 262 VYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVTHGCMCRHNTKGLNCELMDFFYHDLPW 321
Qy 301 RPAEGRNSACKKNCNEHSISCHFDMAVYLATNVSGVCDCCOHNMTGRNCEQCKPFY 360
Db 322 RPAEGRNSACKKNCNEHSISCHFDMAVYLATNVSGVCDCCOHNMTGRNCEQCKPFY 381
Qy 361 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSTYDFSTGLIAGQCRCRKLNVGEHCDVCK 420
Db 382 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSTYDFSTGLIAGQCRCRKLNVGEHCDVCK 441
Qy 421 EGFYDLSSDEDFGCKSCACNPLGTIPGGNPNCDSETHCYCKRLVTGQHCDQCLPEHWGLS 480
Db 442 EGFYDLSSDEDFGCKSCACNPLGTIPGGNPNCDSETHCYCKRLVTGQHCDQCLPEHWGLS 501
Qy 481 NDLDGCRPCDCDLGGALNNSCPAESGQCSCRPHEMIGRCQNEVEPGYYFATLDHLYEAE 540
Db 502 NDLDGCRPCDCDLGGALNNSCPAESGQCSCRPHEMIGRCQNEVEPGYYFATLDHLYEAE 561
Qy 541 ANLGPVGSIVERQYIQDRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 600
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Qy 601 DHWEKAVITVQRPGRIPTSRRCGNTIPDDDNQVVSLSPGSRYYVLPVPVCFEKGNTYTVR 660
Db 622 DHWEKAVITVQRPGRIPTSRRCGNTIPDDDNQVVSLSPGSRYYVLPVPVCFEKGNTYTVR 681
Qy 661 LELPQYTSSDSVESPYTLIDSLVMPYCKSLDIFTVGGSGDGVVWNSAWETFORYRCLE 720
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Qy 721 NSRSVVKTPMTDVCNRNIIFISALLHQTGLACECDPQSSLSSVCDPNNGCQCQCRPNVVG 780
Db 742 NSRSVVKTPMTDVCNRNIIFISALLHQTGLACECDPQSSLSSVCDPNNGCQCQCRPNVVG 801
Qy 781 TCNRCAPGTGFGPSGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDRLPGHWGF 840
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Db 862 PSCQPCQCNHADDPCDPTVTECLNCQDYTMGHNCERCLAGYGDPIIGSGDHCRPCPCPD 921
Qy 901 GPDSGRQFARSCYQDPVTQLACVCDPGYIGSRCDPCASGYFGNPSVGGSCQPCQCHNN 960
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Qy 961 IDTTDEACDKETGRCLKCLYHTEGEHCQCFRFGYIGDALRQDRCRKCVCNVLGTVQEHCN 1020
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Qy 1201 SVERKVSEIKDILAQSPAAPLKNIGNLFEEAEKLIKDVTEMAQVEVKLSDTTSQSNST 1260
Db 1222 SVERKVSEIKDILAQSPAAPLKNIGNLFEEAEKLIKDVTEMAQVEVKLSDTTSQSNST 1281
Qy 1261 AKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTTE 1320
Db 1282 AKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTTE 1341
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Db 1342 PNSTVEQSALMRDRVEDVMMERESQFKEQEQAARLLDELAKGLQSLDLSAAABMTCGTP 1401
Qy 1381 PGASCSETECGGPNCRITDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLASAEVEQL 1440
Db 1402 PGASCSETECGGPNCRITDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLASAEVEQL 1461
Qy 1441 SKMVSEAKLRADAEAKQSAEDILLKTNATKEKMDKSNEELRNLIKQIRNFLTQDSADLDSI 1500
Db 1462 SKMVSEAKLRADAEAKQSAEDILLKTNATKEKMDKSNEELRNLIKQIRNFLTQDSADLDSI 1521
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Db 1522 EAVANEVLKMEPSTPQOLQNLTEDIRERVESLSQVEVILQHSAAADIARAEMLLEAAKRA 1581
Qy 1561 SKSATDVKVTADMVKEALEEAEAKQAQAAEKAIAKQADEDIQGTQNLTSIESETAASEETL 1620
Db 1582 SKSATDVKVTADMVKEALEEAEAKQAQAAEKAIAKQADEDIQGTQNLTSIESETAASEETL 1641
Qy 1621 FNASQRISELERNVEELKRKAAQNSGEAEYIEKVYVTVKQSAEDVKKTLDGELDEKYYKKV 1680
Db 1642 FNASQRISELERNVEELKRKAAQNSGEAEYIEKVYVTVKQSAEDVKKTLDGELDEKYYKKV 1701
Qy 1681 ENLIAKTEESADARRKAEMLQNEAKTLLAQANSKLQLLKDLERKYEDNQRYLEDKAQEL 1740
Db 1702 ENLIAKTEESADARRKAEMLQNEAKTLLAQANSKLQLLKDLERKYEDNQRYLEDKAQEL 1761
Qy 1741 ARLEGEVRSLLKDISQKVAVYSTCL 1765
Db 1762 ARLEGEVRSLLKDISQKVAVYSTCL 1786

RESULT 4

US-09-561-818A-14
; Sequence 14, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortessmaa, Jarrko
; APPLICANT: Tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-818A-14

Query Match 100.0%; Score 9654; DB 4; Length 1786;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QEPEFSYGCAEGSCYPATGDLILIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICNS 60
Db 22 QEPEFSYGCAEGSCYPATGDLILIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICNS 81
Qy 61 QDPYHETLNPDASHLIENVVVTFAPNRLKIWWQSENGVENVTIQLDLEAEFFHFLIMTFK 120
Db 82 QDPYHETLNPDASHLIENVVVTFAPNRLKIWWQSENGVENVTIQLDLEAEFFHFLIMTFK 141
Qy 121 TFRPAAMLIERSSDFGKTGWYRYFAYDCEASFPGISTGPMKKVDDIICDSRYSIDIEPST 180
Db 142 TFRPAAMLIERSSDFGKTGWYRYFAYDCEASFPGISTGPMKKVDDIICDSRYSIDIEPST 201
Qy 181 EGEVIFRALDPAFKIEDPSPRIQNLKLTNLRIKFVKLHTLGDNLDSRMEIREKYIYA 240
Db 202 EGEVIFRALDPAFKIEDPSPRIQNLKLTNLRIKFVKLHTLGDNLDSRMEIREKYIYA 261
Qy 241 VYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVTHGCMCRHNTKGLNCELMDFFYHDLPW 300
Db 262 VYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVTHGCMCRHNTKGLNCELMDFFYHDLPW 321

QY 301 RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGGVCDCCQHNMTGRNCEQCKPFY 360
Db 322 RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGGVCDCCQHNMTGRNCEQCKPFY 381
QY 361 YQHPERDIRPNFCERCTCDPAGSQNEGICDSYTFSTGLIAGQCRCCKLVNVEGEHCDVCK 420
Db 382 YQHPERDIRPNFCERCTCDPAGSQNEGICDSYTFSTGLIAGQCRCCKLVNVEGEHCDVCK 441
QY 421 EGFYDLSSDDPFGCKSCACNPLGTIPGGNPCDSETHCYCKRLVTGQHCDQCLPEHWGLS 480
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QY 481 NDLDGCRPCDCLGGALNNSCFAESGQCSCRPHMIGRCQNEVEPGYYFATLDHLYEABE 540
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QY 541 ANLGPVGSIVERQYIQDIRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 600
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Db 622 DHWEKAVITVORPGRIPTSSRCGNTIPDDDNQVVSLSPGSRYVWLPRPVCFEKGTNYTVR 681
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QY 781 TCNRCAPGTFGFGPSGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCRCRCLPGHWGF 840
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QY 841 PSCQPCQCNHGADDCDPTVTEGCLNCQDVTMGHNCERCILAGYVGDPIIGSGDHCRPCPCPD 900
Db 862 PSCQPCQCNHGADDCDPTVTEGCLNCQDVTMGHNCERCILAGYVGDPIIGSGDHCRPCPCPD 921
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QY 961 IDTTDEACDKETGRCLKCLYHTEGEHCQFCRFGYYGDBALRQDCRCKVCNLYLGTVQEHCN 1020
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Db 1222 SVERKVSBEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDVTEMMAQVEVKLSDTTSQSNS 1281
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Db 1282 AKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTTE 1341
QY 1321 PNSTVEQSALMRDRVEDVMMERESQFKEQEEQARLLDELAKGLQSLDLSAAAEWTCGTP 1380
Db 1342 PNSTVEQSALMRDRVEDVMMERESQFKEQEEQARLLDELAKGLQSLDLSAAAEWTCGTP 1401

QY 1381 PGASCSETECGGPNCRDTDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVL SALAEVEQL 1440
Db 1402 PGASCSETECGGPNCRDTDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVL SALAEVEQL 1461
QY 1441 SKMVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNEELRNLIKQIRNFLTQDSADLDSI 1500
Db 1462 SKMVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNEELRNLIKQIRNFLTQDSADLDSI 1521
QY 1501 EAVANEVLKMEMPSTPQQLQNLTEDIRERVESLSQVEVILQHSAAADIARAEMLLEEAKRA 1560
Db 1522 EAVANEVLKMEMPSTPQQLQNLTEDIRERVESLSQVEVILQHSAAADIARAEMLLEEAKRA 1581
QY 1561 SKSATDVKVTADMVKEALEEAEKAQVAAEKAIKQADEDIQCTQNLLTSIESETAASEETL 1620
Db 1582 SKSATDVKVTADMVKEALEEAEKAQVAAEKAIKQADEDIQCTQNLLTSIESETAASEETL 1641
QY 1621 FNASQRISELERNVEELKRKAQNSGEAEYIEKVVTYVKQSAEDVKKTLDGELDEKYYKV 1680
Db 1642 FNASQRISELERNVEELKRKAQNSGEAEYIEKVVTYVKQSAEDVKKTLDGELDEKYYKV 1701
QY 1681 ENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLLKD LERKYEDNQRYLEDKAQEL 1740
Db 1702 ENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLLKD LERKYEDNQRYLEDKAQEL 1761
QY 1741 ARLEGEVRSLLKDISQKAVYSTCL 1765
Db 1762 ARLEGEVRSLLKDISQKAVYSTCL 1786

RESULT 5
US-09-561-709B-9
; Sequence 9, Application US/09561709B
; Patent No. 6682911
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Champiaud, Marie-France
; APPLICANT: Olson, Pamela
; APPLICANT: Koch, Manuel
; APPLICANT: Brunken, William
; TITLE OF INVENTION: LAMININS AND USES THEREOF
; FILE REFERENCE: 10287-060001
; CURRENT APPLICATION NUMBER: US/09/561,709B
; CURRENT FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 09/168,949
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: US 60/061,609
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-709B-9

Query Match 100.0%; Score 9654; DB 4; Length 1786;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QEPEFSYGCAEGSCYPATGDLILIGRAQKLSVTSTCGLHKPEPPIVSHLOEDKKCFICNS 60
Db 22 QEPEFSYGCAEGSCYPATGDLILIGRAQKLSVTSTCGLHKPEPPIVSHLOEDKKCFICNS 81
QY 61 QDPYHETLNPDSHLIENVTTFAPNRLKIWWQSENGVENVTIQLDLEAEFFHFTHLIMTFK 120
Db 82 QDPYHETLNPDSHLIENVTTFAPNRLKIWWQSENGVENVTIQLDLEAEFFHFTHLIMTFK 141
QY 121 TFRPAAMLIERSDDFGKTGWGVRYPAYDCEASFPGISTGPMKKVDDIICDSRYSDIEPST 180
Db 142 TFRPAAMLIERSDDFGKTGWGVRYPAYDCEASFPGISTGPMKKVDDIICDSRYSDIEPST 201
QY 181 EGEVIFRALDPAPKIEDPYSPRIQNLLKITNLRIFVKLHTLGDNLDSRMEIREKYYVA 240

Db 202 EGEVIFRALDPAFKIEDPSPRIQNLKLTNLRKIFVKLHTLGDNLDSRMEIREKYYA 261
QY 241 VYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGHCMCRHNTKGLNCELMDFFYHDLPW 300
Db 262 VYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGHCMCRHNTKGLNCELMDFFYHDLPW 321
QY 301 RPAEGRNSACKKNCNEHSISCHFDMAVYLATGNVSGVCDQCQHTMTGRNCEOCKPFY 360
Db 322 RPAEGRNSACKKNCNEHSISCHFDMAVYLATGNVSGVCDQCQHTMTGRNCEOCKPFY 381
QY 361 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYDFSTGLIAGQCRCKLNVEGHCDCVK 420
Db 382 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYDFSTGLIAGQCRCKLNVEGHCDCVK 441
QY 421 EGFYDLSSDDPFGCKSCACNPLGTIPGNGPCDSETHCYCKRLVTGQHCDCQCLPEHWGLS 480
Db 442 EGFYDLSSDDPFGCKSCACNPLGTIPGNGPCDSETHCYCKRLVTGQHCDCQCLPEHWGLS 501
QY 481 NDLDGCRPCDCLGGALNNSCFAESGQSCRPHEMIGRQCNEVEPGYFFATLDHYLYEAE 540
Db 502 NDLDGCRPCDCLGGALNNSCFAESGQSCRPHEMIGRQCNEVEPGYFFATLDHYLYEAE 561
QY 541 ANLPGVSVIVERQYIQRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 600
Db 562 ANLPGVSVIVERQYIQRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 621
QY 601 DHWEKAVITVORPGRIPTSRRCNGTIPDDDNQVWSLSPGSRVYVLPVPVCFEKGNTYTVR 660
Db 622 DHWEKAVITVORPGRIPTSRRCNGTIPDDDNQVWSLSPGSRVYVLPVPVCFEKGNTYTVR 681
QY 661 LELPQYTSDDSVESPYTLIDSLVLMPYCKSLDIFTVSGSGDGVVNTNSAWETFORYRCLE 720
Db 682 LELPQYTSDDSVESPYTLIDSLVLMPYCKSLDIFTVSGSGDGVVNTNSAWETFORYRCLE 741
QY 721 NSRSVVKTPMTDVCERNIIFISALLHQTGLACECDPQGSLSVSCDPPNGGQCCQCRPNVVG 780
Db 742 NSRSVVKTPMTDVCERNIIFISALLHQTGLACECDPQGSLSVSCDPPNGGQCCQCRPNVVG 801
QY 781 TCNRCAPGTFGPGSGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDRLPGHWGF 840
Db 802 TCNRCAPGTFGPGSGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDRLPGHWGF 861
QY 841 PSCQPCQCNHADDCCDPTVTECLNCQDYTMGNHCERCLAGYGDPIIGSGDHCRPCPCPD 900
Db 862 PSCQPCQCNHADDCCDPTVTECLNCQDYTMGNHCERCLAGYGDPIIGSGDHCRPCPCPD 921
QY 901 GPDSGRQFARSCYQDPVTLQACVCDPFGYIGSRCDCCASGYFGNPSFVGGSCQPCQCHNN 960
Db 922 GPDSGRQFARSCYQDPVTLQACVCDPFGYIGSRCDCCASGYFGNPSFVGGSCQPCQCHNN 981
QY 961 IDTTDPEACDKETGRCLKLYHTEGHCQFCRFGYIGDALRQDCRCKVCNVLGTQVQHCN 1020
Db 982 IDTTDPEACDKETGRCLKLYHTEGHCQFCRFGYIGDALRQDCRCKVCNVLGTQVQHCN 1041
QY 1021 GSDCQCDKATGQCLCLPNVIGQNCDCRCPNTWQLASGTGCDPCNCAHSPGSCNEFTG 1080
Db 1042 GSDCQCDKATGQCLCLPNVIGQNCDCRCPNTWQLASGTGCDPCNCAHSPGSCNEFTG 1101
QY 1081 QCQCMFPGFGRTCECQELFWGDDVECRACDCDPRGIETPQCDQSTGQCVCEGVEGPR 1140
Db 1102 QCQCMFPGFGRTCECQELFWGDDVECRACDCDPRGIETPQCDQSTGQCVCEGVEGPR 1161
QY 1141 CDKCTRGYSVFPDCTPCHQCFALWDVIAELTNTRHFLKAKALKISGVIGPYRETVD 1200
Db 1162 CDKCTRGYSVFPDCTPCHQCFALWDVIAELTNTRHFLKAKALKISGVIGPYRETVD 1221
QY 1201 SVERKVSEIKDILAQSPAAEPLKNIGNLFEAEKLIKDVTEMAQVEVKLSDTTSQSNST 1260
Db 1222 SVERKVSEIKDILAQSPAAEPLKNIGNLFEAEKLIKDVTEMAQVEVKLSDTTSQSNST 1281
QY 1261 AKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEABERNVASTTE 1320
Db 1282 AKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEABERNVASTTE 1341

QY 1321 PNSTVEQSALMRDRVEDVMERESQFKEKQEQEARLLDELAKLQSLDLSAAAEAMTCGTP 1380
Db 1342 PNSTVEQSALMRDRVEDVMERESQFKEKQEQEARLLDELAKLQSLDLSAAAEAMTCGTP 1401
QY 1381 PGASCSETECGGPNCRDTEGERKCGGPGCGGLVTVAHNAWKAMDLDQDVLASAEVEQL 1440
Db 1402 PGASCSETECGGPNCRDTEGERKCGGPGCGGLVTVAHNAWKAMDLDQDVLASAEVEQL 1461
QY 1441 SKMVSEAKLRADAEKQSAEDILLKTNATKEMDKSNEELRNLIKQIRNFLTQDSADLDSI 1500
Db 1462 SKMVSEAKLRADAEKQSAEDILLKTNATKEMDKSNEELRNLIKQIRNFLTQDSADLDSI 1521
QY 1501 EAVANEVLKMEMPSPTQOLONLTEDIRERVESLSQVEVILQHSADIAEAEMLLEAKRA 1560
Db 1522 EAVANEVLKMEMPSPTQOLONLTEDIRERVESLSQVEVILQHSADIAEAEMLLEAKRA 1581
QY 1561 SKSATDVKVTADVMKEALEEAEKAAQVAAEKAKQADEDIQGTQNLTSIESETAASEETL 1620
Db 1582 SKSATDVKVTADVMKEALEEAEKAAQVAAEKAKQADEDIQGTQNLTSIESETAASEETL 1641
QY 1621 FNASQRISELERNVBELKRAAQAQNSGEAEYIEKVYTVKQSAEDVKKTLDGELDEKYYKV 1680
Db 1642 FNASQRISELERNVBELKRAAQAQNSGEAEYIEKVYTVKQSAEDVKKTLDGELDEKYYKV 1701
QY 1681 ENLIAKKTESADARRKAEMLONEAKTLLAQANSKLOLLKDLERKYEDNORYLEDKAQEL 1740
Db 1702 ENLIAKKTESADARRKAEMLONEAKTLLAQANSKLOLLKDLERKYEDNORYLEDKAQEL 1761
QY 1741 ARLEGEVRSLLKDISQKAVVYSTCL 1765
Db 1762 ARLEGEVRSLLKDISQKAVVYSTCL 1786

RESULT 6
US-09-562-702A-18
; Sequence 18, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-562-702A-18

Query Match 94.2%; Score 9092; DB 4; Length 1786;
Best Local Similarity 93.0%; Pred. No. 0;
Matches 1642; Conservative 71; Mismatches 52; Indels 0; Gaps 0;
QY 1 QEPFSGYCAEGSCYCPATGDLGIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICNS 60
Db 22 QEPFSGYCAEGSCYCPATGDLGIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICNS 81
QY 61 QDPYHETLNPDHSHLIENVVTTAPNRLKIWQSENGVENVTIQLDLEAEFHTLIMTFK 120
Db 82 RDPYHETLNPDHSHLIENVVTTAPNRLKIWQSENGVENVTIQLDLEAEFHTLIMTFK 141
QY 121 TFRPAAMLIERSDDFGKTGWGVYRFAVYDCEASFPGISTGPMKKVDDIICDSRYSDIEPST 180

Db 142 TFRPAAMLIERSDFGKTGWYRYFAYDCESSFPGISTGPMKKVDDIICDSRYSDIEPST 201
QY 181 EGEVIFRALDPAFKIEDPYSPIQNLLKITNLRKFVKLHTLGDNLDSRMEIREKYIYA 240
Db 202 EGEVIFRALDPAFKIEDPYSPIQNLLKITNLRKFVKLHTLGDNLDSRMEIREKYIYA 261
QY 241 VYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGCMCRHNTKGLNCELMDPFYHDLPW 300
Db 262 VYDMVVRGNCFCYGHASECAPVDGWNEEVEGMVHGCMCRHNTKGLNCELMDPFYHDLPW 321
QY 301 RPAEGNSNACKKCNNEHSISCHPDMVAVYLATGNVSGGVCDDCQHNTMGRNCEOCKPFY 360
Db 322 RPAEGNSNACKKCNNEHSSSCHPDMVAVFLATGNVSGGVCDDCQHNTMGRNCEOCKPFY 381
QY 361 YQHPERDIRDPNFCERCTCDPAGSONEGICDSYTDFTSTGLIAGQCRCKLNVEGEHCDVCK 420
Db 382 FQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGLIAGQCRCKLHVEGERCDVCK 441
QY 421 EGFYDLSSDPFGCKSCACNPLGTTIPGPNPCDSETHCYCKRLVTGQHCDQCCLPEHWGLS 480
Db 442 EGFYDLSSDPFGCKSCACNPLGTTIPGPNPCDSETHCYCKRLVTGQHCDQCCLPEHWGLS 501
QY 481 NDLDGCRPCDCLGGALNNSCFAESQCSRPHMIGRQCNVEPBGYYFATLDHLYEABE 540
Db 502 NDLDGCRPCDCLGGALNNSCSEDSQCSCLPHMIGRQCNVEPBGYYFATLDHLYEABE 561
QY 541 ANLGPVSVIVERQYIQRIPSWTGAQFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 600
Db 562 ANLGPVSVIVERQYIQRIPSWTGAQFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 621
QY 601 DHWEKAVITVQRPGRIPRTSSRCGNTIPDDNQVVSLSPGSRVYVLPVRPVCFEKGTNTYVR 660
Db 622 DHWEKAVITVQRPGRIPRTSSRCGNTIPDDNQVVSLSPGSRVYVLPVRPVCFEKGTNTYVR 681
QY 661 LELPOYTSSDSVESPYTLIDSLVMPYCKSLDIFTVGGSGDGVVNTNSAWETFORVRCLE 720
Db 682 LELPOYTASGDSVESPYTFIDSLVMPYCKSLDIFTVGGSGDGVVNTNSAWETFORVRCLE 741
QY 721 NSRSVVKTPMTDVCNRIIFSISALHHTGLACECDPQGSLSVCDPNGGQCQCRPNVVG 780
Db 742 NSRSVVKTPMTDVCNRIIFSISALHHTGLACECDPQGSLSVCDPNGGQCQCRPNVVG 801
QY 781 TCNRCAPGTGFGSPGCKPCECHLOGSVNAFCNPVTGQCHCFQGYVYARQCDRCLPGHWGF 840
Db 802 TCNRCAPGTGFGSPGCKPCKDCHLOGSASAFDAITGQCHCFQGYVYARQCDRCLPGHWGF 861
QY 841 PSCQPCQCNHADDPCDVTGECLNCQDVTMGNHCERCLAGYGPDIIGSGDHCRPCPCPD 900
Db 862 PSCQPCQCNHADDPCDVTGECLNCQDVTMGNHCERCLAGYGPDIIGSGDHCRPCPCPD 921
QY 901 GPDGSRQFARSCYQDPVTLQACVCDPGYIGSRCDCCASGYFGNPSSEVGGSCQPCQCHNN 960
Db 922 GPDGSRQFARSCYQDPVTLQACVCDPGYIGSRCDCCASGYFGNPSSEVGGSCQPCQCHNN 981
QY 961 IDTTDPEACDKETGRCLKCLYHTEGEHCQCFRFGYGDALRQDCRKCVCNLYLGTVQEHCN 1020
Db 982 IDTTDPEACDKETGRCLKCLYHTEGEHCQCFRFGYGDALRQDCRKCVCNLYLGTVQEHCN 1041
QY 1021 GSDCQCDKATGQCLCLPNVIGQNCDCRCAPNWTQLASGTGCDPCNCAHSAHSPGSCNEFTG 1080
Db 1042 GSDCHCDKATGQCSCLPNVIGQNCDCRCAPNWTQLASGTGCDPCNCAHSAHSPGSCNEFTG 1101
QY 1081 QCQCMFGGGRTCSEQELFWGDPDVECRACDPRGIETPQCDSGTGQCVCEVEGPR 1140
Db 1102 QCQCMFGGGRTCSEQELFWGDPDVECRACDPRGIETPQCDSGTGQCVCEVEGPR 1161
QY 1141 CDKCTRGYSGVFPDCTPCHQCFALWDVIAELTNRTHRFLEKAKALKISGVIGPYRETVD 1200
Db 1162 CDKCTRGYSGVFPDCTPCHQCFALWDVIAELTNRTHRFLEKAKALKISGVIGPYRETVD 1221
QY 1201 SVERKVSEIKDILAQSPAAEPLKNIGNLFEABEKLKDVTEMAQVEVKLSDTTSQSNSI 1260

Db 1222 SVEKKVNEIKDILAQSPAAEPLKNIGNILFEEAEKLTQDVTEKMAQVEVKLTDTASQSNST 1281
QY 1261 AKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTTE 1320
Db 1282 AGELGALQAEAESLDNTVKELAEQLEFIKNSDIQGALDSITKYFQMSLEAEKRNVASTTD 1341
QY 1321 PNSTVEQSALMRDRVEDVMERESQFKEQEQAARLLDELAKLQSLDLSAAAEVMTCTGP 1380
Db 1342 PNSTVEQSALTRDRVEDLMLERESPFKEQEQAARLLDELAKLQSLDLSAAAEVMTCTGP 1401
QY 1381 PGASCSETECGGPNCRRTDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLASAEVEQL 1440
Db 1402 PGADCSESECGGPNCRRTDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLASAEVEQL 1461
QY 1441 SKMVSEAKLRADAEAKQSAEDIIKLTNATKEKMDKSNEELRNLIKQIRNFLTQDSADLDSI 1500
Db 1462 SKMVSEAKVRADAEAKQNAQDVLLKTNATKEKVDKSNEDLRNLIKQIRNFLTQDSADLDSI 1521
QY 1501 EAVANEVLKMEMPTPQQLQNLTEDIRERVESLSQVEVILQHSAAADIAEAEMLLEEAKRA 1560
Db 1522 EAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVILQHSAAADIAEAEMLLEEAKRA 1581
QY 1561 SKSATDVKVTADVMKEALEEAEAKQVAAEAKAIKQADEDIQGTQNLITSIESETAASEETL 1620
Db 1582 SKSATDVKVTADVMKEALEEAEAKQVAAEAKAIKQADEDIQGTQNLITSIESETAASEETL 1641
QY 1621 FNASQRISELERNEVELKRKAQNSGEAEYIEKVYTVKQSAEDVKKTLTGDELDEKYYKV 1680
Db 1642 TNASQRISELERNEVELKRKAQNSGEAEYIEKVYTVKQSAEDVKKTLTGDELDEKYYKV 1701
QY 1681 ENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLOLLKDLERKYEDNQRYLEDKAQEL 1740
Db 1702 ESLIAQKTESADARRKAEMLQNEAKTLLAQANSKLOLLKDLERKYEDNQRYLEDKAQEL 1761
QY 1741 ARLEGEVRSLLKDISQKAVYSTCL 1765
Db 1762 VRLEGEVRSLLKDISQKAVYSTCL 1786

RESULT 7

US-09-561-818A-18
; Sequence 18, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortessmaa, Jarrko
; APPLICANT: Tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 18
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-561-818A-18

Query Match 94.2%; Score 9092; DB 4; Length 1786;
Best Local Similarity 93.0%; Pred. No. 0;
Matches 1642; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

QY 1 QEPFESYGCAGSCYPATGDLILIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICNS 60
Db 22 QEPFESYGCAGSCYPATGDLILIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICNS 81
QY 61 QDPYHETLNPDSHLIENVVTTTFAPNRLKIWQSENGVENVTIQLDLEAEFFHFTLIMTFK 120
Db 82 RDPYHETLNPDSHLIENVVTTTFAPNRLKIWQSENGVENVTIQLDLEAEFFHFTLIMTFK 141
QY 121 TFRPAAMLIERSDFGKTGWYRYFAYDCEASFPGISTGPMKKVDDIICDSRYSDIEPST 180
Db 142 TFRPAAMLIERSDFGKTGWYRYFAYDCEASFPGISTGPMKKVDDIICDSRYSDIEPST 201

QY 181 EGEVIFRALDPFAFKIEDPSPRIQNLKLTNLRKIFVKLHTLGNLLDSRMEIREKYVA 240
Db 202 EGEVIFRALDPFAFKIEDPSPRIQNLKLTNLRKIFVKLHTLGNLLDSRMEIREKYVA 261
QY 241 VYDMVVRGNCFCYGHASECAPVDGFNEVEGVMVGHCMCRNHTKGLNCELMDYHDLPW 300
Db 262 VYDMVVRGNCFCYGHASECAPVDGVNEVEGVMVGHCMCRNHTKGLNCELMDYHDLPW 321
QY 301 RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGVCDQCQHTMGRNCEQCKPFY 360
Db 322 RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGVCDQCQHTMGRNCEQCKPFY 381
QY 361 YQHPERDIRPNFCERCTCDPAGSQNEGICDSYTDSTGLIAGQCRCKLNVEGEHCDVCK 420
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QY 421 EGFYDLSSDPFGCKSCACNPLGTIPGNGPCDSETHGYCKRLVTHQCHDQCLPHEWGLS 480
Db 442 EGFYDLSSDPFGCKSCACNPLGTIPGNGPCDSETHGYCKRLVTHQCHDQCLPHEWGLS 501
QY 481 NDLGCRPCDCLGALNNSCFAESGQSCRPHEMIGRQCNEVEPGYFYATLDHYLYEABE 540
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QY 541 ANLPGVSIYERQYQDRIPSWTGTAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 600
Db 562 ANLPGVSIYERQYQDRIPSWTGTAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 621
QY 601 DHWEKAVITVQRPGRIPSTSSRCNGTIPDDNQVLSLPGSRVYVLPVPVCFEKNYTVR 660
Db 622 DHWEKAVITVQRPGRIPSTSSRCNGTIPDDNQVLSLPGSRVYVLPVPVCFEKNYTVR 681
QY 661 LELPQYTSDDSVESPYTLIDSLVLMYCKSLDIFTVGGSDGVVNTNSAWETFORYRCLE 720
Db 682 LELPQYTSDDSVESPYTLIDSLVLMYCKSLDIFTVGGSDGVVNTNSAWETFORYRCLE 741
QY 721 NSRSVVKTPMTDVCNRIIFSISALHGTGLACEDCPQGSLSVCDPNGGQCCQCRPNVWGR 780
Db 742 NSRSVVKTPMTDVCNRIIFSISALHGTGLACEDCPQGSLSVCDPNGGQCCQCRPNVWGR 801
QY 781 TCNRCAPGTGFGPGSGCKPCCECHLOGSVNAFCNPVTGQCHCFQGVYARQCDRLPGHWGF 840
Db 802 TCNRCAPGTGFGPGSGCKPCCECHLOGSVNAFCNPVTGQCHCFQGVYARQCDRLPGHWGF 861
QY 841 PSCQPCQNGHADDCTVTECLNCDQYTMGNHCERCLAGYGDPIIGSGDHCRPCPCPD 900
Db 862 PSCQPCQNGHADDCTVTECLNCDQYTMGNHCERCLAGYGDPIIGSGDHCRPCPCPD 921
QY 901 GPDGRQFARSCYQDPVTLQACVCDPFIYIGSRCDCCASGFGNPSVGVSCQPCQCHN 960
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QY 961 IDTTDPEACDKETGRCLKCLYHTEGHCQFCRFGYGGDALRQDCRKCVCNYLGTVQEHCN 1020
Db 982 IDTTDPEACDKETGRCLKCLYHTEGHCQFCRFGYGGDALRQDCRKCVCNYLGTVQEHCN 1041
QY 1021 GSDCQCDKATGQCLCLPNVIGQNCRCAPNTWQLASGTGCDPCNCAHSPGSCNEFTG 1080
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QY 1081 QCQCMFGGRTCECQELFWGDPDVECRACDPCDPRGIETPQCDQSTGQCVCEGVEGPR 1140
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Db 1222 SVERKVSSEIKDILAQSPAAEPLKNIGLNFEEAEKLIKDVTEMAQVEVKLSDDTTSQSNST 1281

QY 1261 AKELDSLQTEAESLNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTTE 1320
Db 1282 AGELGALQAEAESLNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTTD 1341
QY 1321 PNSTVEQSALMRDRVEDVNMERESQFKKQEQEQARLLDELAKGLQSLDLSAAAEVTCGTP 1380
Db 1342 PNSTVEQSALMRDRVEDVNMERESQFKKQEQEQARLLDELAKGLQSLDLSAAAEVTCGTP 1401
QY 1381 PGASCSETECGGPNCRCTDEGERKCGGPGCGGLVTVVAHNAWQKAMDLDQDVLASAEVEQL 1440
Db 1402 PGASCSETECGGPNCRCTDEGERKCGGPGCGGGLVTVVAHNAWQKAMDLDQDVLASAEVEQL 1461
QY 1441 SKMVSEAKLRADEAKQSAEDILLKTNATKEMKDSNEELRNLIKQIRNFLTQDSADLDSI 1500
Db 1462 SKMVSEAKLRADEAKQSAEDILLKTNATKEMKDSNEELRNLIKQIRNFLTQDSADLDSI 1521
QY 1501 EAVANEVLKMEMPTPOQLQNLTEDIRERVESLSQVEVILQHSADIARAEMLLLEEAKRA 1560
Db 1522 EAVANEVLKMEMPTPOQLQNLTEDIRERVESLSQVEVILQHSADIARAEMLLLEEAKRA 1581
QY 1561 SKSATDVKTADVMKBALEAEAKQAQAAEKAQKQADEDIQGTQNLTSIESETAASEETL 1620
Db 1582 SKSATDVKTADVMKBALEAEAKQAQAAEKAQKQADEDIQGTQNLTSIESETAASEETL 1641
QY 1621 FNASQRISELERNEVEELKRAAQAQNSGEAEVIEKVYTVKQSAEDVVKTLDDGELDEKYYKV 1680
Db 1642 FNASQRISELERNEVEELKRAAQAQNSGEAEVIEKVYTVKQSAEDVVKTLDDGELDEKYYKV 1701
QY 1681 ENLIAKKTEESADARRKAEMLQNEAKTLLAQANSKLOLLKDLERKVEDNQRYLEDKAQEL 1740
Db 1702 ENLIAKKTEESADARRKAEMLQNEAKTLLAQANSKLOLLKDLERKVEDNQRYLEDKAQEL 1761
QY 1741 ARLEGEVRSLLKDISQKAVYVSTCL 1765
Db 1762 ARLEGEVRSLLKDISQKAVYVSTCL 1786

RESULT 8

US-09-562-702A-20
; Sequence 20, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 20
; LENGTH: 1725
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-562-702A-20

Query Match 91.9%; Score 8873; DB 4; Length 1725;
Best Local Similarity 92.9%; Pred. No. 0;
Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

QY 41 EPYCIIVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVTTFAPNRLKIWWQSENGVENV 100
Db 1 EPYCIIVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVTTFAPNRLKIWWQSENGVENV 60
QY 101 TIQLDLAEAFHFTHLIMTFKTRPAAMLIERSDDFGKTGWVRYFAYDCEASFPGISTGP 160

Db 61 TIQLDLAEAFHFTLIMTFKTRPAAMLIERSSDFGTWGVRYFYAYDCSSPPISTGP 120
Qy 161 MKKYDDIIICDSRYSDIEPSTEGEVIIFRALDPAFKIEDPSPRIQNLKITNLRIKFKVLH 220
Db 121 MKKYDDIIICDSRYSDIEPSTEGEVIIFRALDPAFKIEDPSPRIQNLKITNLRIKFKVLH 180
Qy 221 TLGNLLDSRMEIREKYYAVYAVDMVVRGNCFCYCHASECAPVDGFNEEVEGMVHGCMCR 280
Db 181 TLGNLLDSRMEIREKYYAVYAVDMVVRGNCFCYCHASECAPVDGVNEEVEGMVHGCMCR 240
Qy 281 HNTKGLNCELMDFYHDLPLWRPAEGRNSNACKKNCNNEHSISCHFDMAVYLATGNVSGGV 340
Db 241 HNTKGLNCELMDFYHDLPLWRPAEGRNSNACKKNCNNEHSISCHFDMAVFLATGNVSGGV 300
Qy 341 CDDCHNTMGRNCEQCKPFYFQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFSTGL 400
Db 301 CDNCHNTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 360
Qy 401 IAGQCRCKLNVEGEHCDVCKEGFYDLSSDDPFGCKSCACNPLGTIPGGNPNCDSEIGHCYC 460
Db 361 IAGQCRCKLHVEGERCDVCKEGFYDLSSAEDPYGCKSCACNPLGTIPGGNPNCDSEIGHCYC 420
Qy 461 KRLVTGHCDDQCLPQHWGLSNDLDGCRPCDCDLGGALNNSCFAESGCSCRPMTGRQCN 520
Db 421 KRLVTGRCDDQCLPQHWGLSNDLDGCRPCDCDLGGALNNSCSEDSGCSCCLPMTGRQCN 480
Qy 521 EPEGYFATLDHLYEABEANLPGVSVIVERQYIQDRIPSWTGAQFVRVPEGAYLEFFI 580
Db 481 EVESGYFTLDHYIYEABEANLPGVVVERQYIQDRIPSWTGGFVRVPEGAYLEFFI 540
Qy 581 DNIPYSMEYDILIRYEPQLPDHWEKAVITVORPGRIPTSRRCGNTIPDDDNQVVSLSPGS 640
Db 541 DNIPYSMEYELIRYEPQLPDHWEKAVITVORPGKIPASSRCGNTVPDDDNQVVSLSPGS 600
Qy 641 RYVVLPRPVCPEKGTNYTVRLELPQYTSSDSDVESPYTLDSLVLMPYCKSLDIFTVGS 700
Db 601 RYVVLPRPVCPEKGMNYTVRLELPQYTASGSDVESPYTFIDSLVLMPYCKSLDIFTVGS 660
Qy 701 GDGVVITNSAWETFYRRCLENSRSVVKTPMTDVCNIIIFSIALHQTGLACECDPQGS 760
Db 661 GDGEVITNSAWETFYRRCLENSRSVVKTPMTDVCNIIIFSIALIHQTGLACECDPQGS 720
Qy 761 SSVCDPNGGQCCRPNVVGRTCNRCAPGTFFGPGSGCKPCECHLQGSVNAFCNVTGQCH 820
Db 721 SSVCDPNGGQCCRPNVVGRTCNRCAPGTFFGPGNGKPCDCHLQGSASAFDAITGQCH 780
Qy 821 CFQGVYARQCDRLPGHWGFPSCQPCQCNHADDGDPVTGECINQCQDYTMGHNCERCIAG 880
Db 781 CFQGIYARQCDRLPGYWGFPSCQPCQCNHADDGDPVTGECINQCQDYTTGHNCERCIAG 840
Qy 881 YGDPPIIGSGHCRPCPCPDGPDGSGRQFARSCYQDPVTQLACVCDPQYIGSRCDDCASG 940
Db 841 YGDPPIIGSGHCRPCPCPDGPDGSGRQFARSCYQDPVTQLACVCDPQYIGSRCDDCASG 900
Qy 941 YFGNPSEVGGSCQPCQCHNIDTTPDPEACDKETGRCLKCLYHTEGEHCQFCRFGYVGDAL 1000
Db 901 FFGNPSDFGSGCQPCQCHNIDTTPDPEACDKETGRCLKCLYHTEGDHCLCQYGYVGDAL 960
Qy 1001 RQDCKRCVCNLYGTQVEHCNGSDCQCDKATGQCLCLPNVIGQNCDCRCAPNTWOLASGTGC 1060
Db 961 RQDCKRCVCNLYGTVEHCNGSDCHCDKATGQCSCLPNVIGQNCDCRCAPNTWOLASGTGC 1020
Qy 1061 DPCNCNAAHSFGPSCNEFTGQCQCMPFGGRTCSQCQLFWGPDVECRACDCDPRGIET 1120
Db 1021 GPCNCNAAHSFGPSCNEFTGQCQCMPFGGRTCSQCQLFWGPDVECRACDCDPRGIET 1080
Qy 1121 PQCDQSTGQVCVEGVGPRCDKCTRGYSGVFPDCTPCHQCQFALWDVIIAELTNRTHFEL 1180
Db 1081 PQCDQSTGQVCVEGVGPRCDKCTRGYSGVFPDCTPCHQCQFALWDIIIGELTNRTHFEL 1140
Qy 1181 EKAKALKISGVIGPYRETVDSEVERKVSIEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDV 1240
Db 1141 EKAKALKISGVIGPYRETVDSEKVVNEIKDILAQSPAAEPLKNIGILFEEAEKLIKDV 1200

Qy 1241 EMAQVEVKLSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSI 1300
Db 1201 EKMAQVEVKLTDTSQSNSTAGELGALQAEASLDKTVKELAEQLEFIKNSDIQGALDSI 1260
Qy 1301 TKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVMMERESQFKEKQEEQARLLDEL 1360
Db 1261 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMERESPFKEQEEQARLLDEL 1320
Qy 1361 AGKQLSLDLASAAEMTCGTPPGASCSETGCGGNCRCTDEGERKCGGPGGLVTVAHNAW 1420
Db 1321 AGKQLSLDLASAAQMTCTGTPPGADCSESECGGNCRCTDEGEKCGGPGGLVTVAHSAW 1380
Qy 1421 QKAMDLDQDVLASALAEVEQLSKMVEAKLRADEAKQSAEDILLKTNATKEKMDKSNEELR 1480
Db 1381 QKAMDFDRDVLASALAEVEQLSKMVEAKVRADAKQNAQDVLKTNATKEKVDKSNEDLR 1440
Qy 1481 NLIKQIRNFELTQDSADLDSIEAVANEVLKMEPSTPQQLQNLTLTDIRERVESLSQVEVIL 1540
Db 1441 NLIKQIRNFELTSADLDSIEAVANEVLKSGNSTPQQLQNLTLTDIRERVETLSQVEVIL 1500
Qy 1541 QHSAADIAEAEMLLLEAKRASKSATDVKTADVMVKEALEEAEKAQVAAEKAIKQADEDIQ 1600
Db 1501 QQSAADIAEAELLLLEAKRASKSATDVKTADVMVKEALEEAEKAQVAAEKAIKQADEDIQ 1560
Qy 1601 GTQNLTSIESETAASEETLFNASQRISELERNVVEELKRKAAQNSGEAEYIEKVYTVKQ 1660
Db 1561 GTQNLTSIESETAASEETLFNASQRISELERNVVEELKRKAAQNSGEAEYIEKVYTVKQ 1620
Qy 1661 SAEDVKKTLDELDEKYYKKVENLIAKKTESADARRKAEMLQNEAKTLQAANSKLQLLK 1720
Db 1621 NADDVKKTLDELDEKYYKKVESLIAQKTESADARRKAELLQNEAKTLQAANSKLQLLK 1680
Qy 1721 DLERKYEDNQRYLEDKAQELARLEGEVRSLLKDISQKAVYSTCL 1765
Db 1681 DLERKYEDNQRYLEDKAQELVRLEGEVRSLLKDISQKAVYSTCL 1725

RESULT 9

US-09-561-818A-20
; Sequence 20, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortessmaa, Jari
; APPLICANT: Tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 1725
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-561-818A-20

Query Match 91.9%; Score 8873; DB 4; Length 1725;
Best Local Similarity 92.9%; Pred. No. 0;
Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;
Qy 41 EPYCIVSHLQEDKCKFCICNSQDPYHETLNPDSHLIENAVTTTAPNRLKIWMQSENGVENV 100
Db 1 EPYCIVSHLQEDKCKFCICDSRDPYHETLNPDSHLIENAVTTTAPNRLKIWMQSENGVENV 60
Qy 101 TIQLDLAEAFHFTLIMTFKTRPAAMLIERSSDFGTWGVRYFYAYDCSSPPISTGP 160
Db 61 TIQLDLAEAFHFTLIMTFKTRPAAMLIERSSDFGTWGVRYFYAYDCSSPPISTGP 120
Qy 161 MKKVDDIIICDSRYSDIEPSTEGEVIIFRALDPAFKIEDPSPRIQNLKITNLRIKFKVLH 220
Db 121 MKKVDDIIICDSRYSDIEPSTEGEVIIFRALDPAFKIEDPSPRIQNLKITNLRIKFKVLH 180

QY 221 TLGDNLLDSRMEIREKYYYAYVDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGCMCR 280
Db 181 TLGDNLLDSRMEIREKYYYAYVDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMCR 240
QY 281 HNTKGLNCEL CMDFYHDL PWRPAEGRNSNACKKCNNEHSISCHFDMAVYLATGNVSGGV 340
Db 241 HNTKGLNCEL CMDFYHDL PWRPAEGRNSNACKKCNNEHSISCHFDMAVYLATGNVSGGV 300
QY 341 CDDCQHNMTGRNCEQCKPFYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSTGL 400
Db 301 CDNCQHNMTGRNCEQCKPFYQHPERDIRDPNLCEPCTCDPAGSENGICDGYTDFSVGL 360
QY 401 IAGQCRCKLNVEGEHCDVCKEGFYDLSSDDPFGCKSCACNPLGTIPGPNPCDSETHCYC 460
Db 361 IAGQCRCKLNVEGERCDVCKEGFYDLSSDDPFGCKSCACNPLGTIPGPNPCDSETHCYC 420
QY 461 KRLVTGQHCDQCLPEHWGLSNDLDCRPPCDCLGGALNNSCFABSGQSCSRPHMIGRQCN 520
Db 421 KRLVTGQRCDQCLPEHWGLSNDLDCRPPCDCLGGALNNSCSEDSGQSCSLPHMIGRQCN 480
QY 521 EVEPGYFATLDHYLYEABEANLPGVSIIVERQYIQDRIPSWTGA GFVRVPEGAYLEFFI 580
Db 481 EVESGYFTTLDHYIYEABEANLPGVSVVERQYIQDRIPSWTGP GFVRVPEGAYLEFFI 540
QY 581 DNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPTRSCGNTIPDDDNQVVSLSPGS 640
Db 541 DNIPYSMEYELLIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTVPDDDNQVVSLSPGS 600
QY 641 RYVVLPRPVCFEKGNTYTVRLELPOYTSSDSDESPTLIDSLVLMPCYCKSLDIFTVGG 700
Db 601 RYVVLPRPVCFEKGMYTVRLELPQYTAGSDVESPTFTIDSLVLMPCYCKSLDIFTVGG 660
QY 701 GDGVVNTSAWETFQRYRCLENSRSVVKTPMTDVCNIIIFSISALLHQTGLACECDPQGS 760
Db 661 GDGEVNTSAWETFQRYRCLENSRSVVKTPMTDVCNIIIFSISALLHQTGLACECDPQGS 720
QY 761 SSVCDPNNGGQCRPNVVGRTNCRNCAFGTFGFGSPGCKPCCEHLQGSVNAFCNPVTGQCH 820
Db 721 SSVCDPNNGGQCRPNVVGRTNCRNCAFGTFGFGSPGCKPCCEHLQGSASAFCDAITGQCH 780
QY 821 CFQGVYARQCDRCLPGHWGFPSCQPCQNGHADDCTPVTGELNCQDYTMGHNCERCLAG 880
Db 781 CFQGIYARQCDRCLPGYWGFPSCQPCQNGHALDCTVTGELCLSCQDYTTGHNCERCLAG 840
QY 881 YGDPPIIGSDGHCRCPCPDGPDGSDGRQPARSCYQDPVTLQACVCDPGYIGSRCDDCASG 940
Db 841 YGDPPIIGSDGHCRCPCPDGPDGSDGRQPARSCYQDPVTLQACVCDPGYIGSRCDDCASG 900
QY 941 YFGNPSVGGSCQPCQCHNNDITDPEACDKETGRCLKCLVHTEGEHCQCFRFGYVGDAL 1000
Db 901 FFGNPSDFGSGCQPCQCHNNDITDPEACDKETGRCLKCLVHTEGDHCLCQGYVGDAL 960
QY 1001 RQDCRKVCVNYLGTVEHCNGSDCQCDKATGQCLCLPNVIGQNCDCRCAPNTWQLASGTGC 1060
Db 961 RQDCRKVCVNYLGTVEHCNGSDCHCDKATGQCSCLPNVIGQNCDCRCAPNTWQLASGTGC 1020
QY 1061 DPCNCAHSGFSPSCNEFTGQCQCMPEFGGRTCECOELFWGDPDVECRACDCDPRGIET 1120
Db 1021 GPCNCAHSGFSPSCNEFTGQCQCMPEFGGRTCECOELFWGDPDVECRACDCDPRGIET 1080
QY 1121 PQCDQSTGQCVCEGVGPRCDKCTRGSYSGVFPDCTPCHQCFALWDVILIAELTNRTHRFL 1180
Db 1081 PQCDQSTGQCVCEGVGPRCDKCTRGSYSGVFPDCTPCHQCFALWDVILIAELTNRTHRFL 1140
QY 1181 EKAKALKISGVIGPYRETVDSEVERKVSEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDV 1240
Db 1141 EKAKALKISGVIGPYRETVDSEVERKVSEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDV 1200
QY 1241 EMMAQVEVKLSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFFIKNSDIRGALDSI 1300
Db 1201 EKMAQVEVKLTDTSQSNSTAGELGALQAEABSLDKTVKELAEQLEFFIKNSDIQGALDSI 1260
QY 1301 TKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVMMERESQFKEQEEQARLLDEL 1360

RESULT 10
US-08-144-121-4
; Sequence 4, Application US/08144121
; Patent No. 5610031
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert E.
; APPLICANT: Wagman, David W.
; TITLE OF INVENTION: BIK CHAIN OF LAMININ AND METHODS OF USE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: United States
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/144,121
; FILING DATE: 27-OCT-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: (MGH-0780.0) MGP-021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1196 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Domain

LOCATION: 1..250
FEATURE:
NAME/KEY: Domain
LOCATION: 251..437
FEATURE:
NAME/KEY: Domain
LOCATION: 438..807
FEATURE:
NAME/KEY: Domain
LOCATION: 808..840
FEATURE:
NAME/KEY: Domain
LOCATION: 841..1196
US-08-144-121-4
Query Match
Best Local Similarity
Matches 1195; Conservative 0; Mismatches 0; Indels 571; Gaps 2;
1 OEPEFSYGCAEGSCYPATGDLIGRAQKLSVTS-TCGLHKPEPYCIIVSHLQEDKKCFICN 59
1 OEPEFSYGCAEGSCYPATGDLIGRAQKLSVTS-TCGLHKPEPYCIIVSHLQEDKKCFICN 60
60 SODPYHETLNPDASHLIENAVTTTFAPNRLKIWMQSENGVENVTIQDLLEAEFFHTHLIMTF 119
61 SODPYHETLNPDASHLIENAVTTTFAPNRLKIWMQSENGVENVTIQDLLEAEFFHTHLIMTF 120
120 KTFRPAAMLIERSSDFGKTGWYRYFYAYDCEASFPGISTGPMKKVDDIICDSRYSIDIEPS 179
121 KTFRPAAMLIERSSDFGKTGWYRYFYAYDCEASFPGISTGPMKKVDDIICDSRYSIDIEPS 180
180 TEGEVIFRALDPAFKIEDPYSPIQNLLKITNLRKIFVKLHTLGDNLLDSRMEIREKYYY 239
181 TEGEVIFRALDPAFKIEDPYSPIQNLLKITNLRKIFVKLHTLGDNLLDSRMEIREKYYY 240
240 AVYDMVVRGNCFCYCHASECAPVDGFNEEVEGMVHCHMCRRNTKGLNCELCMDFFYHDLF 299
241 AVYDMVVRGNCFCYCHASECAPVDGFNEEVEGMVHCHMCRRNTKGLNCELCMDFFYHDLF 300
300 WRPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGGVCDCCQHTMGRNCEQCKPF 359
301 WRPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGGVCDCCQHTMGRNCEQCKPF 360
360 YYQHPERDIRDNPCERCTCDPAGSQNEGICDSYTDFTSTGLIAGQCRCKLNVEGHCDCVC 419
361 YYQHPERDIRDNPCERCTCDPAGSQNEGICDSYTDFTSTGLIAGQCRCKLNVEGHCDCVC 420
420 KEGFYDLSSDPFGCKSCACNPLGTIPGPNPCDSETHCYCKRLVTGQHCDQCLPEHWGL 479
421 KEGFYDLSSDPFGCKS----- 437
480 SNDLDGCRPCDCLGALNNSCFAESGQCSRPHMIGRQCNEVEPGYFATLDHYLYEAE 539
438 ----- 437
540 EANLPGVSIVERQYIQDRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQL 599
438 ----- 437
600 PDHWEKAVITVQRPGRIPTSRRCGTIPDDDNQVVSLSPGSRVYVLP RPVCFEKGTNYTV 659
438 ----- 437
660 RLELPQYTSSDSVESPYTLLDSLVLMPYCKSLDIFTVGGSGDVVTNSAWETFORYRCL 719
438 ----- 437
720 ENSRSVVKTPMTDVCRNIIFSIALLHOTGLACECDPQGSLSVCDPENGQCQCRPNVVG 779
438 ----- 437
780 RTCNRCAPGTFGFGPSGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDRCLPGHWG 839

438 ----- 437
840 FPSCQPCQCNHGHADDCDPTVTECLNCQDYTMGHNCRCLAGYGDPIIGSGDHCRCPCP 899
438 ----- 437
900 DGPDSGRQFARSCYQDPVTLQLACVCDPGYIGSRCDDCASGYFGNPSVGGSCPCQCHN 959
438 ----- 437
960 NIDTTDPEACDKETGRCLKCLYHTEGHCQCFRFGYGDALRQDRCKVCNVLGTVQEH 1019
438 ----- 437
1020 NGSDCQCDKATGQCLCLPNVIGONCDRCAPNTWQLASGTGCDPCNCAHSGFSPSCNEFT 1079
451 NGSDCQCDKATGQCLCLPNVIGONCDRCAPNTWQLASGTGCDPCNCAHSGFSPSCNEFT 510
1080 GQCQCMPPGFGGRTSCQELFWGDPDVECRACDCDPRGIETPCDQSTGQCVCEGVEGP 1139
511 GQCQCMPPGFGGRTSCQELFWGDPDVECRACDCDPRGIETPCDQSTGQCVCEGVEGP 570
1140 RCDKCTRGYSVGFPPDCTPCHQCFALWDVIAELTNRTHRFLEKAKALKISGVIPIRET 1199
571 RCDKCTRGYSVGFPPDCTPCHQCFALWDVIAELTNRTHRFLEKAKALKISGVIPIRET 630
1200 DSVERKVSEIKDILAQSPAAEPLKNIGNLFEAEKLIKDVTEMAQVEVKLSDDTTSQNS 1259
631 DSVERKVSEIKDILAQSPAAEPLKNIGNLFEAEKLIKDVTEMAQVEVKLSDDTTSQNS 690
1260 TAKELDSLQTEAESLDNTVKELAEQLEFKNDSIRGALDSITKYFQMSLEAEERVNASTT 1319
691 TAKELDSLQTEAESLDNTVKELAEQLEFKNDSIRGALDSITKYFQMSLEAEERVNASTT 750
1320 EPNSTVEQSALMRDRVEDVMMERESQFKEQEEOARLLDELAKLQSLDLSAAAEEMTCGT 1379
751 EPNSTVEQSALMRDRVEDVMMERESQFKEQEEOARLLDELAKLQSLDLSAAAEEMTCGT 810
1380 PPGASCSETECGGNCRDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVL SALAEVEQ 1439
811 PPGASCSETECGGNCRDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVL SALAEVEQ 870
1440 LSKMVSEAKLRADAKQSAEDILLKTNATKEKMDKSNEELRNLIKQIRNFLTQDSADLDS 1499
871 LSKMVSEAKLRADAKQSAEDILLKTNATKEKMDKSNEELRNLIKQIRNFLTQDSADLDS 930
1500 IEAVANEVLKMEPSTPQQLQNLTERIRVESLSQVEVILQHSADIAEAEMLEAEKR 1559
931 IEAVANEVLKMEPSTPQQLQNLTERIRVESLSQVEVILQHSADIAEAEMLEAEKR 990
1560 ASKSATDVKVTADVMVKEALEEAEKAQVAAEKAIKQADEDIQGTQNLTSIESETAASEET 1619
991 ASKSATDVKVTADVMVKEALEEAEKAQVAAEKAIKQADEDIQGTQNLTSIESETAASEET 1050
1620 LFNASQRISELERNVBELKRAAQNSGEAEYIEKVYTVTKQSAEDVKKTLTGELDEKYYK 1679
1051 LFNASQRISELERNVBELKRAAQNSGEAEYIEKVYTVTKQSAEDVKKTLTGELDEKYYK 1110
1680 VENLIAKTEESADARRKAEMLQNEAKTLTLLAQANSKLQLLKDLERKYEDNQRYLEDKAQE 1739
1111 VENLIAKTEESADARRKAEMLQNEAKTLTLLAQANSKLQLLKDLERKYEDNQRYLEDKAQE 1170
1740 LARLEGEVRSLLKDISQKAVVYSTCL 1765
1171 LARLEGEVRSLLKDISQKAVVYSTCL 1196

RESULT 11
US-08-735-893-4
; Sequence 4, Application US/08735893
; Patent No. 5914317
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert E.

APPLICANT: Wagman, David W.
TITLE OF INVENTION: B1k CHAIN OF LAMININ AND METHODS OF USE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: BOSTON
STATE: Massachusetts
COUNTRY: United States
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/735,893
FILING DATE: 18-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/144,121
FILING DATE: 27-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: (MGH-0780.1) MGP-021DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1196 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Domain
LOCATION: 1..250
NAME/KEY: Domain
LOCATION: 251..437
FEATURE:
NAME/KEY: Domain
LOCATION: 438..807
FEATURE:
NAME/KEY: Domain
LOCATION: 808..840
FEATURE:
NAME/KEY: Domain
LOCATION: 841..1196
US-08-735-893-4

Query Match 62.7%; Score 6051.5; DB 2; Length 1196;
Best Local Similarity 67.7%; Pred. No. 0;
Matches 1195; Conservative 0; Mismatches 0; Indels 571; Gaps 2;
QY 1 QPEFSYGCAGSCYPATGDLIGRAQKLSVTS-TCGLHKPEPYCIIVSHLQEDKCFICN 59
Db 1 QPEFSYGCAGSCYPATGDLIGRAQKLSVTS-TCGLHKPEPYCIIVSHLQEDKCFICN 60
QY 60 SQDPYHETLNPDHSHLIENVTTFAPNRLKIWQSENGVENVTIQLDLAEFFHFLIMTF 119
Db 61 SQDPYHETLNPDHSHLIENVTTFAPNRLKIWQSENGVENVTIQLDLAEFFHFLIMTF 120
QY 120 KTFRPAAMLIERSDFGKTGWYRYFAYDCEASFPGISGPMKKVDDIIICDSRYSDIEPS 179
Db 121 KTFRPAAMLIERSDFGKTGWYRYFAYDCEASFPGISGPMKKVDDIIICDSRYSDIEPS 180
QY 180 TEGEVIFRALDPAFKIEDPSPRIQNLKITNLRIKFVKLHGLTGLDNLDSRMEIREKYYY 239
Db 181 TEGEVIFRALDPAFKIEDPSPRIQNLKITNLRIKFVKLHGLTGLDNLDSRMEIREKYYY 240

QY 240 AVYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGCMCRHNTKGLNCELQWDFYHDL 299
Db 241 AVYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGCMCRHNTKGLNCELQWDFYHDL 300
QY 300 WRPAEGRNSNACKKCNNEHSISCHFDMAVYLATGNVSGGVCDCCQHNMTMGRNCEQCKPF 359
Db 301 WRPAEGRNSNACKKCNNEHSISCHFDMAVYLATGNVSGGVCDCCQHNMTMGRNCEQCKPF 360
QY 360 YYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFSTGLIAGQCRCKLNVEGEHCDVC 419
Db 361 YYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFSTGLIAGQCRCKLNVEGEHCDVC 420
QY 420 KEGFYDLSSDDPFGCKSCACNPLGTIPGPNPCDSSTGHCHYCKRLVTGQHCDQCLPEHWGL 479
Db 421 KEGFYDLSSDDPFGCKS ----- 437
QY 480 SNLDGCRPCDCDLGGALNNSCFAESGQSCSRPHMIGRCNEVEPGYYFATLDHYLYAE 539
Db 438 ----- 437
QY 540 EANLGPVSIVERQYIQDIRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEQ 599
Db 438 ----- 437
QY 600 PDHWEKAVITVORPGRIPRTSSRCGNTIPDDDNQVVSLSPGSRVVLPRPVCPEKGTNYTV 659
Db 438 ----- 437
QY 660 RLELPQYTSSDSDVESPYTLIDSLVLMPCYCKSLDIFTVGGSGGVVTVNSAWETFORYRCL 719
Db 438 ----- 437
QY 720 ENSRSVVKTPMTDVCNRIIFSISALLHQTGLACECDPQGLSSVCDPENGQCQCRPNVVG 779
Db 438 ----- 437
QY 780 RTCNRCAPGTFFGPGSGCKPCECHLQGSVNAPCNVPTGQCHCFQGVYARQCDRCLPGHWG 839
Db 438 ----- 437
QY 840 FPSCQPCQCNHADDCCDPVTGECLNCQDYTMHNCERCLAGYYGDPFIIGSGDHCRPCPCP 899
Db 438 ----- 437
QY 900 DGPDGSRQFARSCYQDPVTLQACVCDPFGYIGSRCCDCASGYFGNPFSEVGGSCQPCQCHN 959
Db 438 ----- 437
QY 960 NIDTDPACDKETGRCLKCLYHTEGEHCQCFRFGYGDALRQDRCKVCNLYLTVOEHC 1019
Db 438 -----CVCNLYLTVOEHC 450
QY 1020 NGSDCQCDKATGQCLCLPNVIGQNCDCRCAPTWQLASGTGCDPCNCAHSGFSPSCNEFT 1079
Db 451 NGSDCQCDKATGQCLCLPNVIGQNCDCRCAPTWQLASGTGCDPCNCAHSGFSPSCNEFT 510
QY 1080 GQCCMPGFGGRTCSQCELFWGDVCEACDCDPRGIETPQCDQSTGQCVCEGVEGP 1139
Db 511 GQCCMPGFGGRTCSQCELFWGDVCEACDCDPRGIETPQCDQSTGQCVCEGVEGP 570
QY 1140 RDKCTRGSYGVFPDCTPCHQCFALWDVIAELTNRTHRFLEKAKALKISGVIGPYRET 1199
Db 571 RDKCTRGSYGVFPDCTPCHQCFALWDVIAELTNRTHRFLEKAKALKISGVIGPYRET 630
QY 1200 DSVERKVSEIKDILAQSPAAEPLKNIKNIFEEAEKLIKDVTEMAQVEVKLSDTTSQSN 1259
Db 631 DSVERKVSEIKDILAQSPAAEPLKNIKNIFEEAEKLIKDVTEMAQVEVKLSDTTSQSN 690
QY 1260 TAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNAST 1319
Db 691 TAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNAST 750

QY 1320 EPNSTVEQSALMRDRVEDVMVERESQFKEKEQEQARLLDELAKGLQSLDLSAAEMTCGT 1379
Dd
QY 751 EPNSTVEQSALMRDRVEDVMVERESQFKEKEQEQARLLDELAKGLQSLDLSAAEMTCGT 810
Dd
QY 1380 PPGASCSETECGGPNCRITDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLSSALAEVEQ 1439
Dd
QY 811 PPGASCSETECGGPNCRITDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLSSALAEVEQ 870
Dd
QY 1440 LSKMVSEAKLRADEAKQSAEDILLKTNAKEMDKSNEELRNLIKQIRNFLTQDSADLDS 1499
Dd
QY 871 LSKMVSEAKLRADEAKQSAEDILLKTNAKEMDKSNEELRNLIKQIRNFLTQDSADLDS 930
QY 1500 IEAVANEVLKMEMPSTPQOLQNLITEDIRERVESLSQVEVILQHSAAADIAEAEMLLEAKR 1559
Dd
QY 931 IEAVANEVLKMEMPSTPQOLQNLITEDIRERVESLSQVEVILQHSAAADIAEAEMLLEAKR 990
QY 1560 ASKSATDVKVTADMVKEALEEAEKAQVAEAKAIAKQADEDIQGTQNLITSIESETAASEET 1619
Dd
QY 991 ASKSATDVKVTADMVKEALEEAEKAQVAEAKAIAKQADEDIQGTQNLITSIESETAASEET 1050
QY 1620 LFNASQRISELERNVEELKRKAQNSGEAEYIEKVVTYVKQSAEDVKKTLDGELDEKYYK 1679
Dd
QY 1051 LFNASQRISELERNVEELKRKAQNSGEAEYIEKVVTYVKQSAEDVKKTLDGELDEKYYK 1110
QY 1680 VENLIAKTEESADARRKAEMLQNEAKTLLAQANSKLQLLKDLERKYEDNQRYLEDKAOE 1739
Dd
QY 1111 VENLIAKTEESADARRKAEMLQNEAKTLLAQANSKLQLLKDLERKYEDNQRYLEDKAOE 1170
QY 1740 LARLEGEVRSLLKDISQKVAVYSTCL 1765
Dd
QY 1171 LARLEGEVRSLLKDISQKVAVYSTCL 1196

RESULT 12

US-09-845-583A-6
; Sequence 6, Application US/09845583A
; Patent No. 6635616
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Brunken, William Joseph
; APPLICANT: Champliand, Marie-France
; APPLICANT: Hunter, Dale
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
; FILE REFERENCE: 10287-056001
; CURRENT APPLICATION NUMBER: US/09/845,583A
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/200,863
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1799
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-845-583A-6

Query Match 52.3%; Score 5046; DB 4; Length 1799;
Best Local Similarity 51.1%; Pred. No. 8.1e-285;
Matches 901; Conservative 304; Mismatches 544; Indels 14; Gaps 7;
QY 8 GCAEGSCYPATGDLIIIGRAQKLSVTSTGLHKPEPYCIIVSHLQEDKCKCFICNSQDPYHET 67
Dd 44 GCSRGSCYPATGDLIIIGRAQKLSVTSTGLHKPEPYCIIVSHLQEDKCKCFICNSQDPYHET 103
QY 68 LNPDSHLIENVVTFAPNRLKIWQSENGVENVTIQLDLEAEHFTHLIMTFTFRPAAM 127
Dd 104 DNPNSHRIQNVVTSFAPQRRTAWQSENGVENVTIQLDLEAEHFTHLIMTFTFRPAAM 163
QY 128 LIERSDFGKTGWYRYFAYDCEASFPGISTGPMKKVDDIICDSRYSDIEPSTEGEVIFR 187
Dd 164 LVERSADFGRTWHVYRYFSYDCGADFPGLAPRRWDDVVCESRYSEIEPSTEGEVIYR 223
QY 188 ALDPAFKIEDPYSPIQNLLKITNLRIFVKLHTLGDNLDSRMEIREKYYYAVYDMVVR 247

Dd 224 VLDPAIPDPYSSRIQNLKITNLRVNLTRLHTLGNLLDPRREIREKYYYALVELVIR 283
QY 248 GNCFCYGHASECAPVDGFNEEVGVMVGHCMCRHNTKINCELCMDYFHYDLWPWPABEGRN 307
Dd 284 GNCFCYGHASQCAPAPGAPAHABGVMVHGACICKHNTKINCELCEQCDYFQDLPWHPABEDGH 343
QY 308 SNACKKCNNEHSISCHFDMAVYLATGNVSGVCDCCOHNMTGRNCEQCKPFYQHPERD 367
Dd 344 THACKKCECNHGHSHCHFDMAVYLATGNVSGVCDCCOHNMTGRNCEQCKPFYQHPERD 403
QY 368 IRDPNFCERCTCDPAGSQNEGICDSTYDFTSTGLIAGQCRCKLNVEGEHCDVCKEGFYDLS 427
Dd 404 MRDPAVCPDCDDPMGSDQGGRCDDSHDDPVLGLVSGQCRCKEHHVVGTRCQCCRDGFFGLS 463
QY 428 SEDPFGCKSCACNPLGTIPGGNPCDSETGCHCYCKRLVTGHCQDQCLPEHWGLSNDLDGCR 487
Dd 464 ASDPRGQRCQCNRSRGTVPGSSPCDSSSGTCFCFKRLVTGHCDCRCLPGHWGLSHDLGCR 523
QY 488 PCDCDLGGALNNSCFAESGQSCSRPHMIGRQCNEVEPGYVFATLDHYLYEAEAEANLPGV 547
Dd 524 PCDCDVGALDPPQDEATGQCPCEQHMGRRCEQVQPGVFRPFDLHTLWEAAQAQ-GQVL 582
QY 548 SIVERQYIQDRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLPDHWEKAV 607
Dd 583 EVVERLVNRETPTSGPGFVRUREGQEVFLVTSLPAMDYDILLRWEPOVPEQWAELE 642
QY 608 ITVQRPGRIPTSRCNGTIPDDNQVVSLSPGSRVYVLPVPVCFEKGNTYVRLLELPQYT 667
Dd 643 LMVQRPQVSAHSPCGHVLPKDDRIQGMHPNTRVLVFPVPCLEPGISYKCLKLIG-T 701
QY 668 SSDSDVESPYT--LIDSLVLMPYCKSLDIFTVGGSGDGVVNTNSAWETFORYRCLENRSV 725
Dd 702 GGRAQPETSYSGLLIDSLVLQPHVLVLEMF----SGDAAALERRTTFFERYRCHEEGLMP 757
QY 726 VKTPMTDVCRNIIIFSISALLHQTGLACECDPQGSLSVCDPNNGQCCQCRPNVVGRTCNRC 785
Dd 758 SKAPLSETCAPLLISVSALIYNGALPCQCDPQGSLSSECSPHGGQCRCKPGVVGRRCDVC 817
QY 786 APGTFGFGPSGCKPCECHLQGSVNAFCNPVVTGQCHFCQGVYARQCDRCLPGHWGPPSCQP 845
Dd 818 ATGYGFGPAGQACQCSPDGALSALCEGTSGQCPRCRPGALRCDHCHQCRGQGWGFFNCRP 877
QY 846 CQCNHADDCCDPPVTGECLNCQDVTMGHNCERCLAGYGDPTIGSGDHCRPCPCPDGPDG 905
Dd 878 CVCNGRADECDDTHTGACLCGRDYGGEHCERCIAAGFHGDPRLPYGGQCRPCPCPEGPGSQ 937
QY 906 RQFARSCYQDPVTLQACVCDPGYIGSRCDCCASGYFGNPNSEVSGSCQPCQCHNNIDTTD 965
Dd 938 RHFATSHRDGYSQIVCHCRAGYTGRLRCEACAPGFGDPSPKPGRCQLCECSGNIDPMD 997
QY 966 PEACDKETGRCLKLYHTEGEHCQFCRFGYVGDALRQDCRCKVCNVLGTVQEHGNSD-C 1024
Dd 998 PDACDPHTGQCLRLHNTGEPHCGYCKPGFHHGQAARQSCHRCTCNLLGTPRRCPSTDLC 1057
QY 1025 QCDKATGQCLCLPNVIGQNCDCRCAPNWTQLASGTGCDPCNCAAHSGFSPSCNEFTGQCQC 1084
Dd 1058 HCDPSTGQCPCLPHVQGLNCDHCAPNFWNFTSGRGCPACACHPSRARGPTCNEFTGQCHC 1117
QY 1085 MPFGGRTCSQCQLFWGDDPVECRACDDPRGIETPQCDQSTGQCVCEGVEGPRCDKC 1144
Dd 1118 HAGFGGRTCSQCQLYWGDPGLQCRACDDPRGIDKPCQCHRSTGHCSCRPGVSGVRCDCQ 1177
QY 1145 TRGYSGVFPDCTPCHQCQFALWDVIAELTNRTHRFLEKAKALKISGIVGIPYRETVDVER 1204
Dd 1178 ARGFSGVFPACHPCHACFGDWDVVDLAARTRRLEQWAQELQOTGVLGAFESSFLNMQG 1237
QY 1205 KVSEIKDILAQSPAAEPLKNIGNLFEAEKL---IKDVTEMAQVEVKLSDDTTSQSNSTA 1261
Dd 1238 KLGVMQAIMSARNAS--AASTAKLVEATEGLRHEIGKTTTERLTQLAEALTAVQDENFNAN 1295
QY 1262 KELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSDITKYFQMSLEAEERVNASTTEP 1321

Db 1296 HALSGERDGFALNLTQLDQHLKHSNFLGAYDSIRHAHSQSTEARRANASTFAV 1355
QY 1322 NSTVEQSALMRDRVEDVMMERESQFKEQEQEARLLDELAKQLQSLDLSAAAEAMTCGTPP 1381
Db 1356 PSPVNSADTRRTTEVLMGAQKENFNROHLANQOALGRLSAHAHTLSLTGINELVCGAPG 1415
QY 1382 GASCSETECGGNCRITDEGRKCGGPGCGGLVTVAHNAWQKAMDLDODVLSALAEVEQLS 1441
Db 1416 DAPCATSPCGGAGCRDEDEGPRCGGLGCSGAAPADLALGRARHSQAEALQALVEGGIL 1475
QY 1442 KMVSEAKLRADEAKQSAEDILLKTNATKERMKSNEELRNLIKQIRNFLTQDSADLDSIE 1501
Db 1476 SRVSETRRQAEAAQRAQAALDKANASRGQVEQANQELRELIONVKDFLSQEGADPDSIE 1535
QY 1502 AVANEVLKMEMPSTPQQLONLTEDIRERVESLSQVEVILQHSAADIAEAEMLLLEAKRAS 1561
Db 1536 MVATRVLDISIPASPEQIQRLASEIAERVRSLADVDTILAHTMGDVRRAEQLQDAHRAR 1595
QY 1562 KSATDVKVITADMVKEALEEBAEKAQVAEAEKATKQADEDIQGTQNLTSIESETAASEETLF 1621
Db 1596 SRAEGERQKAETVQAALEBAQRAQGAQGAIRGAVVDTQNTQETLQRVQERMAGAELSIN 1655
QY 1622 NASQRISELERNVTELKRAAQAQNSGEAEYIEKVYTVKQSAEDVKKTLDDGELDEKYYKVE 1681
Db 1656 SAGERARQLDALLEALKKRAAGNSLAASABETAGSAQSRAREAEKQLREQVGDQYQTVR 1715
QY 1682 NLIAKKTEESADARRKAEMLQNEAKTLLAQANSKQLQLKLERKYEDNQRYLEDKAOELA 1741
Db 1716 ALAEKAEGLVLAQARAEQLRDEARDLLOAQDKLQRLQLEGTYEENERALEGKAAQLD 1775
QY 1742 RLEGEVRSLLKDOISQKVAVYSTC 1764
Db 1776 GLEARMRSVLQAINLQVQIYNTC 1798

RESULT 13

US-09-561-709B-11
; Sequence 11, Application US/09561709B
; Patent No. 6682911
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Champliand, Marie-France
; APPLICANT: Olson, Pamela
; APPLICANT: Koch, Manuel
; APPLICANT: Brunken, William
; TITLE OF INVENTION: LAMININS AND USES THEREOF
; FILE REFERENCE: 10287-060001
; CURRENT APPLICATION NUMBER: US/09/561,709B
; CURRENT FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 09/168,949
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: US 60/061,609
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1798
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-709B-11

Query Match 51.0%; Score 4923; DB 4; Length 1798;
Best Local Similarity 49.9%; Pred. No. 1.1e-277;
Matches 880; Conservative 307; Mismatches 564; Indels 12; Gaps 6;

QY 8 GCAEGSCYPATDILLIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICNSQDPYHET 67
Db 41 GCSRGSCYPATADLLVGRADRLTASSTCGLNGRQPYCIVSHLQDEKKCFCLDSRRPFSAR 100
QY 68 LNPDSHLIENVVTFAPNRLKIWQSENGVENVTIQLDLAEFFHFTHLIMTFTFRPAAM 127
Db 101 DNPHTHRIQNVVTSFAPQRRAAWQSQNGIPAVTIQLDLAEFFHFTHLIMTFTFRPAAM 160

QY 128 LIERSDFGKTGWVYRYFAYDCEASFPPISTGPMKKVDDIICDSRYSIDIEPSTEGEVIER 187
Db 161 LVERSADFGRTWHVYRYFSYDCGADFFGVPLAPPRHWDVVCESEYSEIEPSTEGEVYIR 220
QY 188 ALDPAFKIEDPSPRIQNLKLTINLRIFKFKLHTLGNLLDSRMEIREKYIYAVYDMVVR 247
Db 221 VLDPALPIPDYSSRIQNLKLTINLRVNLTRLHTLGNLLDPRREIREKYIYALVELVVR 280
QY 248 GNCFCYGHASECAPVDGFNEEVEGVMVGHCMCRHNTKGLNCELCMDYFHDLPWRPAEGRN 307
Db 281 GNCFCYGHASECAPAPGAPAHAEVMVHGACICKHNTGLNCEQCQDFYRDLWRPAEDGH 340
QY 308 SNACKKCNNEHSISCHFDMAVYLATGNVSGGVCDCCOHNMTGRNCEQCKPFYQHPERD 367
Db 341 SHACRKCDRHGHTHSCFDMAVYLGSGNVSGGVCDCCOHNMTAYRHCELCRFFFYRDTKD 400
QY 368 IRDPNFCERCTCDPAGSQNEGTCDSTYDFTSTGLIAGQCRCKLNVEGEHCDVCKEGFYDLS 427
Db 401 LRDPVAVCRSCDCDPMGSDGGRCDSDHDDPALGLVSGQCRCKEHVVGTTRCQCRDGFGLS 460
QY 428 SEDPFGCKSCACNPLGTIPGSGNPCDSETGHYCKYCKRLVTGQCDQCLPEHGLSNDLDGCR 487
Db 461 ISDPGSCRRCCQCNARGTVPSTPCDPSNGSCYCKRLVTGRCDRCLPGHWGLSLDLLGCR 520
QY 488 PCDCDLGALNNSCFABESGQSCSRPHMIGRCQNEVEPGYFATLDHLYVEAEANLPGV 547
Db 521 PCDCVGGALDPQCDEGTGQCHCRQHMVGRRCQEQVPGYFRPFLDHLIWEAENTR-GQVL 579
QY 548 SIVERQYIQDRIPSWTGAQFVRVPEGAYLEFFIDNIPYSMEYDILIRVEPQLPDHWEKAV 607
Db 580 DVVERLVTGETPSTGSGFVRVLEGQTLFVAVPNAMDYDILLRLEPQVPEQWAELE 639
QY 608 ITVORPGRIPSTSSRCNTIPDDDNQVVSLSPSGSYVVLPRPVCFEKGTNYTVRLELPQYT 667
Db 640 LIVORPGVPFAHSLCGHLVPRDDRIQGTLOPHARYLIFPNPVCLEPGISYKHLKLV-T 698
QY 668 SSDSDVESPYT---LIDSLVMPYCKSLDIFTVGGSGDGVVTNSAWETFORRCLENSR 723
Db 699 GGAQPEPTPYSGPGLLIDSLVLPVLEMF---SGDAAALERQATFERYQCHEEGL 754
QY 724 SVVKTMTDVCNRIIFSISALLHQTGLACECDPPQGSLSVCDPNNGGQCCRPNVVGRITCN 783
Db 755 VPSKTSPEACAPLLISLTIYNGALPCQCNPNQGSLSSECNPHGGQCLCKPGVWVRRCD 814
QY 784 RCAPGTFGFGPSGCKPOECHLQGSVNAFCNPVBTGQCHFCQGVYARQCDRCLPGHWGFPSC 843
Db 815 TCAPGYGFGPTGCAQCSRGALSSLCERTSGQCLRTGAFGLRCDACQRGWGFPPSC 874
QY 844 QPCQNGHADDCDPVTGECNCDYTMHNCERCLAGYVGDPIIGSGDHCRPCPCPDGP 903
Db 875 RPECVNGHADECNTHTGACLCGRDHTGHEHCERCIAGFHGDPRLPYGAQCRPCPCPEG 934
QY 904 SGRQFARSCYQDPVTLQACVCDPGYIGSRCDCCASGYFGNPNSEVGSQPCQCHNNIDT 963
Db 935 SQRHFATSCHQDEYSQIVCHCRAGYTLGRCEACAPGQFGDPSRPGRCQCECSGNIDP 994
QY 964 TDPEACDKETGRCLKLYHTEGEHCQFCRFGYVGDALRQDCRKCVCNLYLGTVOEHCNGSD 1023
Db 995 MDPDACDPHPGQCLRLHHTEGPHCAHSPGFHQAARQSCHRCTCNLLGTNPQQCPSPD 1054
QY 1024 -CQCDKATGQCLCLPNVIGQNCDCRCAPNNTWQLASGTGCDPCNCAAHSGPPSCNEFTGC 1082
Db 1055 QCHCDPSSGQCPCLPNVQALAVDRCAPNFNLTSGHGCPACLPSPGEGPTCNEFTGC 1114
QY 1083 QCMFGGGRTCSECELFWDGPDVECRACDCDPRGIETPQCDQSTGQCVCEGVEGPRCD 1142
Db 1115 HCLCGFGGRTCSECELFHWGDPGLQCHACDCDSRGIDTPQCHRTGHCTCRPGVSGVRC 1174
QY 1143 KCTRGYSGVFPDCTPCHQCFALWDVTIAELTNRTHRFLEKAKALKISGVIQYRETVDV 1202
Db 1175 QCARGFSIGIFPACHPCACFGDWDVVDLAARTQRLQRAQELQQTGLGAFESFWMH 1234
QY 1203 ERKVSEIKDIL-AQSPAAEPLKNIGNLFEEAEKLIKDVTEMMMAQVEVKLSDTTSQSNSTA 1261

Db 1235 QEKLGIQVIGARNTSAASTAQLVEATEELRREIGEATEHLTQLEADLTVDQENFNAN 1294
Qy 1262 KELDSIQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTTEP 1321
Db 1295 HALSGLERDRALNLTQLDQHLDLKHSNFLGAYDSIRHAHSQSAEAERRANTSALAV 1354
Qy 1322 NSTVEQSALMRDRVEDVMMERESQPEKEQEEQARLLDELAKQLQSLDLSAAEWTCGTPP 1381
Db 1355 PSPVNSASARHRTALMDAQEKEDFNSKHMANKORALGKLSAHTHTLSLTDLINELVCGAQG 1414
Qy 1382 GASCSFTECGGPNCRTEDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLSSALAEVQLS 1441
Db 1415 LHHDRTSPCGAGCRDEGQPRCGGLSCNGAAATADLALGRARHTQAELOALAEGBGSIL 1474
Qy 1442 KMVSEAKLRADAEAKQSAEDILLKTNATKEKMDKSNELRNLIKQIRNFLTQDSADLDSIE 1501
Db 1475 SRVAETRRQASEAQQAALDKANASRGQVEQANQELQELIQSVKDFLNQEGADPDSIE 1534
Qy 1502 AVANEVLKMEMPSTPQQLQNLTEJIRERVESLSQVEVILQHSAAADIARAEMLLLEEAKRAS 1561
Db 1535 MVATRVLELSIPASAEQIOHLGAIARVRSIADVDAILARTVGDVRRARQLLQDARRAR 1594
Qy 1562 KSATDVKTADVMVKEALEEAEKAQVAEAKAIKQADEDIQGTQNLTSIESETAASBETLF 1621
Db 1595 SWAEDEKQKAETVQAALAEQAQQAQGAIRGAVADTRDTEQTLYQVQERMAGAEERALS 1654
Qy 1622 NASQRISELRNVEELKRKAAQNSGEAEYIEKVVTYVKQSAEDVKKTLDGELDEKVKVE 1681
Db 1655 SAGERARQLDALLEALKLKRAGNSLAASTAEETAGSAQGRAGAEQQLRGLDQVQTVK 1714
Qy 1682 NLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLLKDLERKYEDNQRYLEDKAEOLA 1741
Db 1715 ALAEKAAQGVLAQAARAEQLPDEARDLLQAAQDKLQRLQLEEGTYEENERALESKAAQLD 1774
Qy 1742 RLEGEVRSLLKDISQKVAVYSTC 1764
Db 1775 GLEARMRSVLQAINLQVQIYNTC 1797

RESULT 14
US-09-845-583A-8
; Sequence 8, Application US/09845583A
; Patent No. 6635616
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Brunken, William Joseph
; APPLICANT: Champliand, Marie-France
; APPLICANT: Hunter, Dale
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
; FILE REFERENCE: 10287-056001
; CURRENT APPLICATION NUMBER: US/09/845,583A
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/200,863
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8:
; LENGTH: 1798
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-583A-8

Query Match 50.9%; Score 4918; DB 4; Length 1798;
Best Local Similarity 49.9%; Pred. No. 2.2e-277;
Matches 879; Conservative 307; Mismatches 565; Indels 12; Gaps 6;
Qy 8 GCAEGSCYPATGDLIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICNSQDPYHET 67
Db 41 GCSRGSCYPATADLLVGRADRLTASSTCGLNGRQPYCIVSHLQDEKKCFCLCDSSRRPFSAR 100
Qy 68 LNPDSHLIENVVTFAPNRLKIWQSENGVENVTIQLDLEAEHFTHLIMTFKTRPAAM 127

Db 101 DNPHTHRIQNVVTSFAPQRRAAWQSQNGIPAVTIQLDLEAEHFTHLIMTFKTRPAAM 160
Qy 128 LIERSDPFGKTGWVYRYFAYDCBASFPFGISTGPMKKVDDIICDSRYSYDIEPSTEGEVIER 187
Db 161 LVERSADFGRTWHVYRFSYHCGADFPVPLAPPRHWDDVVCESTRYSEIEPSTEGEVIYR 220
Qy 188 ALDPAFKIEDPYSPRIQNLKLTNLRKIFVKLHTLGDNLDSRMEIREKYYYAYVDMVVR 247
Db 221 VLDPAIPDPYSSRIQNLKLTNLRVNLTRLHTLGDNLDPREIREKYYYALYELVVR 280
Qy 248 GNCFCYGHASECAPVDGFNEEVEGMVHGHCRCRNTKGLNCLCMDYFHDLPWRPAEGRN 307
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Qy 368 IRDPNFCERCTCDPAGSQNEGICDSYTDFTSTGLIAGQCRCRKNVGEHCDVCKEGFYDLS 427
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Qy 428 SEDPFGCKSCACNPLGTIPGPNPCDSETGHYCKRLVTGQHCDCQLPEHGWGLSNDLDGCR 487
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Qy 488 PCDCDLGGALNNSCFAESGQSCSRPHMIGRCQNEVEPGYYFATLDHYLYEAEANLPGV 547
Db 521 PCDCDVGGALDPQCDDEGTGQCHCRQHMVGRRCQVQPGYFRPFLDHLIWEAENTR-GQVL 579
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Qy 608 ITVQRPGRIPTSRCGNTIPDDDNQVVSLSPGSRVYVLPVPCFEKGTNYTVRLELPQYT 667
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Job time : 24.3519 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:56:24 ; Search time 44.9032 Seconds
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Perfect score: 9654
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	9654	100.0	1765	14 US-10-037-182-8	Sequence 8, Appli
2	9654	100.0	1786	9 US-09-873-676-113	Sequence 113, App
3	9654	100.0	1786	9 US-09-938-275-6	Sequence 6, Appli
4	9654	100.0	1786	14 US-10-037-182-6	Sequence 6, Appli
5	9092	94.2	1786	9 US-09-938-275-7	Sequence 7, Appli
6	9092	94.2	1786	14 US-10-037-182-10	Sequence 10, Appl
7	8873	91.9	1725	14 US-10-037-182-12	Sequence 12, Appl
8	6044.5	62.6	1196	16 US-10-443-349-4	Sequence 4, Appli
9	5084	52.7	1801	9 US-09-938-275-8	Sequence 8, Appli
10	5048	52.3	1798	9 US-09-938-275-9	Sequence 9, Appli
11	5046	52.3	1799	9 US-09-845-583-6	Sequence 6, Appli
12	4918	50.9	1798	9 US-09-845-583-8	Sequence 8, Appli
13	3765	39.0	1808	15 US-10-369-493-5986	Sequence 5986, Ap
14	3076.5	31.9	1101	12 US-10-287-971-18	Sequence 18, Appl
15	2348	24.3	527	12 US-09-925-298-703	Sequence 703, App

16	2348	24.3	527	14	US-10-102-806-703	Sequence 703, App
17	1729.5	17.9	3672	15	US-10-369-493-6146	Sequence 6146, Ap
18	1696.5	17.6	1557	15	US-10-369-493-6816	Sequence 6816, Ap
19	1680.5	17.4	1609	14	US-10-037-182-14	Sequence 14, Appl
20	1680.5	17.4	1609	14	US-10-299-058-12	Sequence 12, Appl
21	1677	17.4	1572	14	US-10-037-182-20	Sequence 20, Appl
22	1677	17.4	1605	14	US-10-037-182-18	Sequence 18, Appl
23	1676.5	17.4	1609	9	US-09-938-275-11	Sequence 11, Appl
24	1676.5	17.4	1609	15	US-10-372-683-36	Sequence 36, Appl
25	1673	17.3	1576	14	US-10-037-182-16	Sequence 16, Appl
26	1653	17.1	1607	9	US-09-938-275-10	Sequence 10, Appl
27	1637	17.0	3712	12	US-10-037-417-48	Sequence 48, Appl
28	1637	17.0	3712	13	US-10-108-605-103	Sequence 103, App
29	1633	16.9	3712	12	US-10-037-417-51	Sequence 51, Appl
30	1605	16.6	3635	9	US-09-845-583-2	Sequence 2, Appli
31	1605	16.6	3635	12	US-10-037-417-47	Sequence 47, Appl
32	1605	16.6	3635	14	US-10-037-182-4	Sequence 4, Appli
33	1564.5	16.2	2743	14	US-10-037-182-36	Sequence 36, Appl
34	1564.5	16.2	3695	12	US-10-312-352-22	Sequence 22, Appl
35	1564.5	16.2	3695	14	US-10-037-182-2	Sequence 2, Appli
36	1560	16.2	3696	15	US-10-312-088-31	Sequence 31, Appl
37	1559.5	16.2	3070	10	US-09-961-403-7	Sequence 7, Appli
38	1559.5	16.2	3690	12	US-10-112-944-347	Sequence 347, App
39	1553.5	16.1	1172	9	US-09-919-172-16	Sequence 16, Appl
40	1553.5	16.1	1172	9	US-09-974-298-56	Sequence 56, Appl
41	1553.5	16.1	3705	15	US-10-312-088-30	Sequence 30, Appl
42	1552.5	16.1	1155	15	US-10-603-725-24	Sequence 24, Appl
43	1552.5	16.1	1167	15	US-10-603-725-20	Sequence 20, Appl
44	1552.5	16.1	1174	15	US-10-603-725-22	Sequence 22, Appl
45	1552.5	16.1	1186	15	US-10-603-725-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-10-037-182-8
; Sequence 8, Application US/10037182
; Publication No. US20030044899A1
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Doi, Masayuki
; APPLICANT: Thyboll, Jill
; TITLE OF INVENTION: Recombinant Laminin 10
; FILE REFERENCE: 99-274-F
; CURRENT APPLICATION NUMBER: US/10/037,182
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,449
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/279,282
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-037-182-8

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							Gaps
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RESULT 2

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; Sequence 113, Application US/09873676
; Patent No. US20020077289A1
; GENERAL INFORMATION:
; APPLICANT: MacDonald, Nicholas J.
; TITLE OF INVENTION: Angiostatin and Endostatin Binding Proteins and Methods of Use
; FILE REFERENCE: 05213-0378 (43170-259333)
; CURRENT APPLICATION NUMBER: US/09/873,676
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 60/209,065
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/289,387
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 113
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-873-676-113

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DB 262 VYDMVVRGNCFCYGHASECAPVDGNEEVEGMVHGCMCRHNTKGLNCELMDYFHDLPW 321
QY 301 RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGVGCDDCQHNTMGRNCEQCKPFY 360
DB 322 RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGVGCDDCQHNTMGRNCEQCKPFY 381
QY 361 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFSTGLIAGQCRCKLNVEGEHCDVCK 420
DB 382 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFSTGLIAGQCRCKLNVEGEHCDVCK 441
QY 421 EGFYDLSSDDPFGCKSCACNPLGTIPGGNPNCDSETGHYCKRLVTGQCHDQCLPEHWGLS 480
DB 442 EGFYDLSSDDPFGCKSCACNPLGTIPGGNPNCDSETGHYCKRLVTGQCHDQCLPEHWGLS 501
QY 481 NDLGCRPCDCDLGGALNNSCFAESGCSCSRPHMIGRQCNVEPEPGYYFATLDHYLYEAE 540
DB 502 NDLGCRPCDCDLGGALNNSCFAESGCSCSRPHMIGRQCNVEPEPGYYFATLDHYLYEAE 561
QY 541 ANLPGVSVIVERQYIQDRIPSWTGAFFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 600
DB 562 ANLPGVSVIVERQYIQDRIPSWTGAFFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 621
QY 601 DHWEKAVITVQRPGRIPRTSSRCGNTIPDDNQVVSLSPGSRVYVLPVPCFEKGTNYTVR 660
DB 622 DHWEKAVITVQRPGRIPRTSSRCGNTIPDDNQVVSLSPGSRVYVLPVPCFEKGTNYTVR 681
QY 661 LELPQYTSSDSDVESPYTLIDSLVLMPCYCKSLDIFTVGGSGDGVVNTNSAWETFORYRCLE 720
DB 682 LELPQYTSSDSDVESPYTLIDSLVLMPCYCKSLDIFTVGGSGDGVVNTNSAWETFORYRCLE 741
QY 721 NSRSVVKTPMTDVCVRNIIIFSISALLHQTGLACECDPQGLSSVCDPNPQGGCQCRPNVVR 780
DB 742 NSRSVVKTPMTDVCVRNIIIFSISALLHQTGLACECDPQGLSSVCDPNPQGGCQCRPNVVR 801
QY 781 TCNRCAPGTFGFGSPGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDRLPGHWGF 840
DB 802 TCNRCAPGTFGFGSPGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDRLPGHWGF 861
QY 841 PSCQPCQCNHADDCCDPVTGECNCDYTMGHNCRCLAGYGDPIIGSGHCRPCPCPD 900
DB 862 PSCQPCQCNHADDCCDPVTGECNCDYTMGHNCRCLAGYGDPIIGSGHCRPCPCPD 921
QY 901 GPDGRQFARSCYQDPVTLQACVCDPGYIGSRCCDCCASGYFNGNPNSEVGGSCQPCQCHNN 960
DB 922 GPDGRQFARSCYQDPVTLQACVCDPGYIGSRCCDCCASGYFNGNPNSEVGGSCQPCQCHNN 981
QY 961 IDTTDPEACDKETGRCLKLYHTEGEHCQFCRFGYYGDALRQDCRKCVCNVLGTVQEHCN 1020
DB 982 IDTTDPEACDKETGRCLKLYHTEGEHCQFCRFGYYGDALRQDCRKCVCNVLGTVQEHCN 1041
QY 1021 GSDCQCDKATGQCLCLPNVIGQNCDCRCPNTWQLASGTGCDPCNCAHSPGSPCNEFTG 1080
DB 1042 GSDCQCDKATGQCLCLPNVIGQNCDCRCPNTWQLASGTGCDPCNCAHSPGSPCNEFTG 1101
QY 1081 QCQCMFGGRTCECQELFWGDDVECRACDCDPRGIETPCDQSTGQCVCEGVEGPR 1140
DB 1102 QCQCMFGGRTCECQELFWGDDVECRACDCDPRGIETPCDQSTGQCVCEGVEGPR 1161
QY 1141 CDKCTRGSYGVFPDCTPCHQCFALWDVIIAELTNRTHRFLEKAKALKISGIGPYRETVD 1200
DB 1162 CDKCTRGSYGVFPDCTPCHQCFALWDVIIAELTNRTHRFLEKAKALKISGIGPYRETVD 1221
QY 1201 SVERKVSIEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDVTEMAQVEVKLSDTTSQSNST 1260

DB 1222 SVERKVSIEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDVTEMAQVEVKLSDTTSQSNST 1281
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DB 1282 AKELDSLQTEAESLQNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTTE 1341
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DB 1342 PNSTVEQSALMRDRVEDVMMERESQFKEQEEQARLLDELAKLQSLDLSAAAEVTCGTP 1401
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DB 1402 PGASCSETECGGPNCRCTDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLSEAEVEQL 1461
QY 1441 SKMVSEAKLRADAEKQSAEDILLKTATKATKMDKSNELNRLIKQIRNFLTQDSADLDSI 1500
DB 1462 SKMVSEAKLRADAEKQSAEDILLKTATKATKMDKSNELNRLIKQIRNFLTQDSADLDSI 1521
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DB 1522 EAVANEVLKMEMPSTPQQLQNLTEDIRERVESLSQVEVILQHSAAADIAEAEMLLEAKRA 1581
QY 1561 SKSATDVKVTADVMKEALEEAEKQAAQVAAEKAIKQADEDIQGTQNLTSIESETAASEETL 1620
DB 1582 SKSATDVKVTADVMKEALEEAEKQAAQVAAEKAIKQADEDIQGTQNLTSIESETAASEETL 1641
QY 1621 FNASQRISELERNVVELKRAAQNQSGEAEYIEKVYTVTKQSAEDVVKTLQDGLDEKYYKV 1680
DB 1642 FNASQRISELERNVVELKRAAQNQSGEAEYIEKVYTVTKQSAEDVVKTLQDGLDEKYYKV 1701
QY 1681 ENLIAKTTESADARRKAEMLQNEAKTLLAQANSKLQLLKDLERKVEDNQRYLEDKAQEL 1740
DB 1702 ENLIAKTTESADARRKAEMLQNEAKTLLAQANSKLQLLKDLERKVEDNQRYLEDKAQEL 1761
QY 1741 ARLEGEVRSLLKDISQKAVVYSTCL 1765
DB 1762 ARLEGEVRSLLKDISQKAVVYSTCL 1786

RESULT 3

US-09-938-275-6
; Sequence 6, Application US/09938275
; Patent No. US20020111309A1
; GENERAL INFORMATION:
; APPLICANT: Gerardo Castillo
; APPLICANT: Alan Snow
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications
; TITLE OF INVENTION: of Laminin and Laminin-Derived Protein Fragments
; FILE REFERENCE: PROTEO.P03
; CURRENT APPLICATION NUMBER: US/09/938,275
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Swissprot P07942
; DATABASE ENTRY DATE: 1988-08-01
US-09-938-275-6

Query Match 100.0%; Score 9654; DB 9; Length 1786;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QEPEFSYGCAGSCYPATGDLIGRAQKLSVTSTCGLHKPEPYCIVSHLOEDKKCFICNS 60
DB 22 QEPEFSYGCAGSCYPATGDLIGRAQKLSVTSTCGLHKPEPYCIVSHLOEDKKCFICNS 81
QY 61 QDPYHETLNPDSHLIENVVTTTFAPNRLKIWWQSENGVENVTIQDLEAEFFHTLIMTFK 120

Wed May 19 1994

Db 82 QDPYHETLNPDHSHLIENVVTTFAPNRLKIWQSENGVENVTIQLDLEAEFHTLIMTFK 141
QY 121 TFRPAAMLIERSSDFGKTGWVYRYPAYDCEASFPGISTGPMKKVDDIIICDSRYSDIEPST 180
Db 142 TFRPAAMLIERSSDFGKTGWVYRYPAYDCEASFPGISTGPMKKVDDIIICDSRYSDIEPST 201
QY 181 EGEVIFRALDPAFKIEDPSPRIQNLKLTNLRIFKVLHTLGDNLNLLDSRMEIREKYIYA 240
Db 202 EGEVIFRALDPAFKIEDPSPRIQNLKLTNLRIFKVLHTLGDNLNLLDSRMEIREKYIYA 261
QY 241 VYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHCHMCRRHNTKGLNCELAMDYFHDLPW 300
Db 262 VYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHCHMCRRHNTKGLNCELAMDYFHDLPW 321
QY 301 RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGGVCDCCQHNTMGRNCEQCKPFY 360
Db 322 RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGGVCDCCQHNTMGRNCEQCKPFY 381
QY 361 YQHPERDIRBNFCERCTCDPAGSQNEGICDSYTDFTSTGLIAGQCRCKLNVEGEHCDVCK 420
Db 382 YQHPERDIRBNFCERCTCDPAGSQNEGICDSYTDFTSTGLIAGQCRCKLNVEGEHCDVCK 441
QY 421 EGFYDLSSDPFGCKSCACNPLGTIPGGNPNCDSETHCYCKRLVTGQHCDQCLPEHWGLS 480
Db 442 EGFYDLSSDPFGCKSCACNPLGTIPGGNPNCDSETHCYCKRLVTGQHCDQCLPEHWGLS 501
QY 481 NDLGCRPCDCDLGGALNNSCFABSGQCSRPHMIGRQCNEVEPGYFATLDHYLYEAE 540
Db 502 NDLGCRPCDCDLGGALNNSCFABSGQCSRPHMIGRQCNEVEPGYFATLDHYLYEAE 561
QY 541 ANLGPVSIIVERQYIQDRIPSWTGAQFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 600
Db 562 ANLGPVSIIVERQYIQDRIPSWTGAQFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 621
QY 601 DHWEKAVITVQRPGRIPRTSSRCGNTIPDDNQVVSLSPGSRYVVLPRVPCFEKGTNYTVR 660
Db 622 DHWEKAVITVQRPGRIPRTSSRCGNTIPDDNQVVSLSPGSRYVVLPRVPCFEKGTNYTVR 681
QY 661 LELPQYTSDDSVESPYTLIDSLVLMPCYCKSLDIFTVGGSGDGVVNTNSAWETFORYRCLE 720
Db 682 LELPQYTSDDSVESPYTLIDSLVLMPCYCKSLDIFTVGGSGDGVVNTNSAWETFORYRCLE 741
QY 721 NSRSVVKTPMTDVCNRIIFSISALLHQTGLACECPQGSLSVCDPNQGGCQCRPNVVR 780
Db 742 NSRSVVKTPMTDVCNRIIFSISALLHQTGLACECPQGSLSVCDPNQGGCQCRPNVVR 801
QY 781 TCNRCAPGTGFGSPGCKPCCEHLQGSVNAFCNPVTGQCHCFQGVYARQCDRLCPGHWF 840
Db 802 TCNRCAPGTGFGSPGCKPCCEHLQGSVNAFCNPVTGQCHCFQGVYARQCDRLCPGHWF 861
QY 841 PSCQPCQCNHADDGDPVTGECNLCQDYTMGHNCERCLAGYGDPIIGSGDHCRPCPCPD 900
Db 862 PSCQPCQCNHADDGDPVTGECNLCQDYTMGHNCERCLAGYGDPIIGSGDHCRPCPCPD 921
QY 901 GPDGSRQFARSCYQDPVTLQACVCDPGYIGSRCDDCASGYFGNPSBEVGGSCQPCQCHNN 960
Db 922 GPDGSRQFARSCYQDPVTLQACVCDPGYIGSRCDDCASGYFGNPSBEVGGSCQPCQCHNN 981
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Db 1102 QCQCMFPGFGRCTSECELFWDGPDVECRACDPCRGITPQCDQSTGQCVCEVGEPR 1161
QY 1141 CDKCTRGSYGVFPDCTPCHQCFALWDVIIAELTNRTHRELEKAKALKISGVIGPYRETVD 1200
Db 1162 CDKCTRGSYGVFPDCTPCHQCFALWDVIIAELTNRTHRELEKAKALKISGVIGPYRETVD 1221

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Db 1222 SVERKVSBIKDILAQSPAAEPLKNIGNLFEEAEKLIKDVTEMMAQVEVKLSDTTQSQNST 1281
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Db 1282 AKELDSIQTEAESLQNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTTE 1341
QY 1321 PNSTVEQSALMRDRVEDVMMERESQFKEKQBEQARLLDELAKGLQSLDLSAAAEAMTCGTP 1380
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Db 1402 PGASCSETECGGPNCRITDEGERKCGGPGCGGLVTVVAHNAWQKAMDLDQDVLASAEVEQL 1461
QY 1441 SKMVSBAKLRADEAKQSAEDILLKTNATKEKMDKSNEELRNLIKQIRNFLTQDSADLDSI 1500
Db 1462 SKMVSBAKLRADEAKQSAEDILLKTNATKEKMDKSNEELRNLIKQIRNFLTQDSADLDSI 1521
QY 1501 EAVANEVLKMEPSTPQQLQNLTEDIRERVESLSQVEVILQHSAAADIARAEMLLEAAKRA 1560
Db 1522 EAVANEVLKMEPSTPQQLQNLTEDIRERVESLSQVEVILQHSAAADIARAEMLLEAAKRA 1581
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Db 1582 SKSATDVKVTADMVKEALEEAEAKAQVAAEKAQKQADEDIQGTQNLTSIESEETAASEETL 1641
QY 1621 FNASQRISELERNEVEELKRAAQNQSGEAEVIEKVYTVKQSAEDVKKTLDDGELDEKYYKV 1680
Db 1642 FNASQRISELERNEVEELKRAAQNQSGEAEVIEKVYTVKQSAEDVKKTLDDGELDEKYYKV 1701
QY 1681 ENLIJAKTEESADARRKAEMLQNEAKTLLAQANSKLOLLKDLERKVEDNORYLEDKQAEEL 1740
Db 1702 ENLIJAKTEESADARRKAEMLQNEAKTLLAQANSKLOLLKDLERKVEDNORYLEDKQAEEL 1761
QY 1741 ARLEGEVRSLLKDISQKVAVYSTCL 1765
Db 1762 ARLEGEVRSLLKDISQKVAVYSTCL 1786

RESULT 4

US-10-037-182-6
; Sequence 6, Application US/10037182
; Publication No. US20030044899A1
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Doi, Masayuki
; APPLICANT: Thyboll, Jill
; TITLE OF INVENTION: Recombinant Laminin 10
; FILE REFERENCE: 99-274-F
; CURRENT APPLICATION NUMBER: US/10/037,182
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,449
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/279,282
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-037-182-6

Query Match 100.0%; Score 9654; DB 14; Length 1786;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QEPFESYGAEGSCYPATGDLIIIGRAQKLSVTSTCGLHKEPYPYCVIVSHLQEDKQCFICNS 60
Db 22 QEPFESYGAEGSCYPATGDLIIIGRAQKLSVTSTCGLHKEPYPYCVIVSHLQEDKQCFICNS 81

QY 61 QDPYHETLNPDSHLIENVVTTTFAPNRLKIWWQSENGVENVTIQLDLEAEFHTLIMTFK 120
DB 82 QDPYHETLNPDSHLIENVVTTTFAPNRLKIWWQSENGVENVTIQLDLEAEFHTLIMTFK 141
QY 121 TFRPAAMLIERSSDFGKTGWVRYFAYDCEASFPGISGPMKKVDDIICDSRYSDIEPST 180
DB 142 TFRPAAMLIERSSDFGKTGWVRYFAYDCEASFPGISGPMKKVDDIICDSRYSDIEPST 201
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DB 202 EGEVIFRALDPAPFKIEDPYSPRIQNLKITNLRIKFVKLHTGLDNLLDSRMEIREKYYYA 261
QY 241 VYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHCHMCRHNTKGLNCELQWDFYHDLPW 300
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QY 361 YQHPERDIRDNFCERCTCDPAGSQNEGICDSYTFSTGLIAGQCRCRLNVEGEHCDVCK 420
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QY 421 EGFYDLSSDPFGCKSCACNPLGTIPGGNPCDSETGHYCKRLVGTGHCDCQLPEHWGLS 480
DB 442 EGFYDLSSDPFGCKSCACNPLGTIPGGNPCDSETGHYCKRLVGTGHCDCQLPEHWGLS 501
QY 481 NDLDGCRPCDCLGALNNSCFAESGQSCRPHEMIGRQNEVEPGYYFATLDHYLYEAE 540
DB 502 NDLDGCRPCDCLGALNNSCFAESGQSCRPHEMIGRQNEVEPGYYFATLDHYLYEAE 561
QY 541 ANLPGVSIIVERQYIQDRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 600
DB 562 ANLPGVSIIVERQYIQDRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 621
QY 601 DHWEKAVITVORPGRIPRTSSRCNGTIPDDDNQVVSLSPGSRYVWLPRPVCSEKGTNYTVR 660
DB 622 DHWEKAVITVORPGRIPRTSSRCNGTIPDDDNQVVSLSPGSRYVWLPRPVCSEKGTNYTVR 681
QY 661 LELPQYTSSDSVESPYTLIDSLVLMYPYCKSLDIFTVGGSGDGVVNTNSAWETFRYRCLE 720
DB 682 LELPQYTSSDSVESPYTLIDSLVLMYPYCKSLDIFTVGGSGDGVVNTNSAWETFRYRCLE 741
QY 721 NSRSVVKTPMTDVCRNIIIFSISALLHQTGLACECDPQGSLSVSCDPPNGGQCQCRPNVUGR 780
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DB 802 TCNRCAPGTFGFGSPGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCRCRLPGHWGF 861
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DB 862 PSCQPCQCNHADDGDPVTGECNLCQDYTMGHNCERCLAGYGDPIIGSGDHCRCPCPCPD 921
QY 901 GPDSGRQRFARSCYQDPVTLQACVCDPGYIGSRCDCCASGYFGNPSVGGSCQPCQCHNN 960
DB 922 GPDSGRQRFARSCYQDPVTLQACVCDPGYIGSRCDCCASGYFGNPSVGGSCQPCQCHNN 981
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DB 1162 CDKCTRGSYGVFPDCTPCHQCFAWDVIAELTNRTNTHRELEKAKALKISGVIGPYRETVD 1221
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DB 1222 SVERKVSEIKDILAQSPAAPAAEPLKNIGNLFEAEKLIKDVTEMMAQVEVKLSDTTSQSNST 1281
QY 1261 AKELDSLQTEAESLDNTVKELAEQLEFFIKNSDIRGALDSITKYFQMSLEAEERVNASTTE 1320
DB 1282 AKELDSLQTEAESLDNTVKELAEQLEFFIKNSDIRGALDSITKYFQMSLEAEERVNASTTE 1341
QY 1321 PNSTVEQSALMDRVEDVMMERESQFKEKQEEQARLLDELACKLQSLDLSAAAEWTCCTP 1380
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DB 1402 PGASCSETECGGPNCRCTDEGERKCGGPGCGGLVTVAHNAWKAMDLDQDVLASALAEVEQL 1461
QY 1441 SKMVSEAKLRADAEAKQSAEDILLKTNAKEMDKSNEELRNLIKQIRNFLTQDSADLDSI 1500
DB 1462 SKMVSEAKLRADAEAKQSAEDILLKTNAKEMDKSNEELRNLIKQIRNFLTQDSADLDSI 1521
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DB 1522 EAVANEVLKMEPSTPQOLQNLTERVESLSQVEVILQHSAAADIAEAEMLLEAKRA 1581
QY 1561 SKSATDVKVTADVMKEALEEAEKAAQVAAEKAIKQADEDIQGTQNLTSISETAASEETL 1620
DB 1582 SKSATDVKVTADVMKEALEEAEKAAQVAAEKAIKQADEDIQGTQNLTSISETAASEETL 1641
QY 1621 FNASQRISSELERNVVELKRAAQNQSGEAEYIEKVYTVKQSAEDVKTLDGELDEKVKV 1680
DB 1642 FNASQRISSELERNVVELKRAAQNQSGEAEYIEKVYTVKQSAEDVKTLDGELDEKVKV 1701
QY 1681 ENLIAKTEESADARRKAEMLQNEAKTLAQANSKLQLLKDLERKYEDNQRYLEDKQAE 1740
DB 1702 ENLIAKTEESADARRKAEMLQNEAKTLAQANSKLQLLKDLERKYEDNQRYLEDKQAE 1761
QY 1741 ARLEGEVRSLLKDISQKVAVYSTCL 1765
DB 1762 ARLEGEVRSLLKDISQKVAVYSTCL 1786

RESULT 5

US-09-938-275-7
; Sequence 7, Application US/09938275
; Patent No. US20020111309A1
; GENERAL INFORMATION:
; APPLICANT: Gerardo Castillo
; APPLICANT: Alan Snow
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications
; TITLE OF INVENTION: of Laminin and Laminin-Derived Protein Fragments
; FILE REFERENCE: PROTEO.P03
; CURRENT APPLICATION NUMBER: US/09/938,275
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Mus Musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Swissprot P02469
; DATABASE ENTRY DATE: 1989-07-01
US-09-938-275-7

Query Match 94.2%; Score 9092; DB 9; Length 1786;
Best Local Similarity 93.0%; Pred. No. 0;
Matches 1642; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

QY 1 QEPFESYGCABSCYPATGDLILIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKCKFCICNS 60

Db 22 QEPERSYGCAGSCYPATGDLIIAGRAQLSVTSCTGLHKPEPYCIVSHLQEDKCKFCIDS 81
QY 61 QDPYHETLNPDShLIENVVTTAPNRLKIWQSENGVENVTIQLDLEAEFFHFTHLIMTFK 120
Db 82 RDPYHETLNPDShLIENVVTTAPNRLKIWQSENGVENVTIQLDLEAEFFHFTHLIMTFK 141
QY 121 TFRPAAMLIERSSDFGKTGWYRYFAYDCEASPGISTGPMKKVDDIICDSRYSDIEPST 180
Db 142 TFRPAAMLIERSSDFGKTGWYRYFAYDCESSPGISTGPMKKVDDIICDSRYSDIEPST 201
QY 181 EGEVIFRALDPAFKIEDPYSPRIQNLLKITNLRIFKVLKHTLGLDNLDSRMEIREKYVYA 240
Db 202 EGEVIFRALDPAFKIEDPYSPRIQNLLKITNLRIFKVLKHTLGLDNLDSRMEIREKYVYA 261
QY 241 VYDMVVRGNCFCYGHASECAPVDGFGNEEVEGMVHGHCMCRHNTKGLNCELMDYFHDLPW 300
Db 262 VYDMVVRGNCFCYGHASECAPVDGFGNEEVEGMVHGHCMCRHNTKGLNCELMDYFHDLPW 321
QY 301 RPAEGRNSNACKKCNCHSISCHFDMAVYLATGNVSGVCDCCOHNMTGRNCEQCKPFY 360
Db 322 RPAEGRNSNACKKCNCHSISCHFDMAVYLATGNVSGVCDCCOHNMTGRNCEQCKPFY 381
QY 361 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYDFTSTGLIAGQCCKLNVGEHCDVCK 420
Db 382 FQHPERDIRDPNFCERCTCDPAGSENGGICDGYDFTSVGLIAGQCCKLNVGEHCDVCK 441
QY 421 EGFYDLSSEDPFGCKSCACNPLGTIPGPNPCDSETHCYCKRLVTGQCHDQCLPEHWGLS 480
Db 442 EGFYDLSSEDPFGCKSCACNPLGTIPGPNPCDSETHCYCKRLVTGQCHDQCLPEHWGLS 501
QY 481 NDLGCRPCDCLGALNNSCFAESGQSCRPHEMIGRQCNEVEPGYFATLDHYLYEABE 540
Db 502 NDLGCRPCDCLGALNNSCFAESGQSCRPHEMIGRQCNEVEPGYFATLDHYLYEABE 561
QY 541 ANLPGVSVIVERQYIQDRIPSWTGAFFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPOLP 600
Db 562 ANLPGVSVIVERQYIQDRIPSWTGAFFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPOLP 621
QY 601 DWHEKAVITVQRPGRIPTSRRCGNTIPDDNQVVSLSPGSRYVVLPRPVCFEKGTNTYVR 660
Db 622 DWHEKAVITVQRPGRIPTSRRCGNTIPDDNQVVSLSPGSRYVVLPRPVCFEKGTNTYVR 681
QY 661 LELPQYTSSDVSPEYTLIDSLVLMYPYCKSLDIFTVGGSGDGVVTNSAWETFORYRCLE 720
Db 682 LELPQYTSSDVSPEYTLIDSLVLMYPYCKSLDIFTVGGSGDGVVTNSAWETFORYRCLE 741
QY 721 NSRSVVKTPMTDVCNRIIPFISALLHOTGLACECDPQGLSSVCDPNGGQCQCRPNVYGR 780
Db 742 NSRSVVKTPMTDVCNRIIPFISALLHOTGLACECDPQGLSSVCDPNGGQCQCRPNVYGR 801
QY 781 TCRNRCAPGTGFGPSGCKPCCECHLQGSVNAFONPVVTGQCHFCQGVYARQCDRLPGHWGF 840
Db 802 TCRNRCAPGTGFGPSGCKPCCECHLQGSVNAFONPVVTGQCHFCQGVYARQCDRLPGHWGF 861
QY 841 PSCQPCQCNHADDCTPVTGECNLCQDYTMGHNCERCLAGYVYGDPIIGSGDHCRPCPCPD 900
Db 862 PSCQPCQCNHADDCTPVTGECNLCQDYTMGHNCERCLAGYVYGDPIIGSGDHCRPCPCPD 921
QY 901 GPDGRQFARSCYQDPVTLQACVCDPGLYIGSRCDCCASGYFGNPNSEVGGSCQPCQCHNN 960
Db 922 GPDGRQFARSCYQDPVTLQACVCDPGLYIGSRCDCCASGYFGNPNSEVGGSCQPCQCHNN 981
QY 961 IDTTDPEACDKETGRCLKCLYHTEGEHCQFGRFYGDALRQDCKKVCVNYLGTVOEHCN 1020
Db 982 IDTTDPEACDKETGRCLKCLYHTEGEHCQFGRFYGDALRQDCKKVCVNYLGTVOEHCN 1041
QY 1021 GSDCQCDKATGQCLCLPNVIGQNCRCAPNTWQLASGTGCDPCNCAAHSGFPGSCNEFTG 1080
Db 1042 GSDCQCDKATGQCLCLPNVIGQNCRCAPNTWQLASGTGCDPCNCAAHSGFPGSCNEFTG 1101
QY 1081 QCQCMFPGGRTCTSECQELFWGDPDVECRACDPRGIETPQCDQSTGQCVCVEGVEGPR 1140

Db 1102 QCQCMFPGGRTCTSECQELFWGDPDVECRACDPRGIETPQCDQSTGQCVCVEGVEGPR 1161
QY 1141 CDKCTRGYSGVFPDCTPCHQCFALMDVIIAELTNRTHRFLEKAKALKISGVIGPYRETVD 1200
Db 1162 CDKCTRGYSGVFPDCTPCHQCFALMDVIIAELTNRTHRFLEKAKALKISGVIGPYRETVD 1221
QY 1201 SVERKVSEIKDILAQSPAAPAEPLKIGNLFEEAEKLIKDVTEMMAQVEVKLSDTTSQSNST 1260
Db 1222 SVEKKVSEIKDILAQSPAAPAEPLKIGNLFEEAEKLIKDVTEMMAQVEVKLSDTTSQSNST 1281
QY 1261 AKELDSLQTEAESLSDNTVKELAEQLEFIFKNSDIRGALDSITKYPQMSLEAEERVNASTTE 1320
Db 1282 AGELGALQAEAESLSDNTVKELAEQLEFIFKNSDIRGALDSITKYPQMSLEAEERVNASTTE 1341
QY 1321 PNSTVEQSALMRDRVEDVMMERESQFKEQEQEQAARLLDELAKGLQSLDLSAAAEAMTCGTP 1380
Db 1342 PNSTVEQSALMRDRVEDVMMERESQFKEQEQEQAARLLDELAKGLQSLDLSAAAEAMTCGTP 1401
QY 1381 PGASCSETECGGPNCRCTDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLASAEVEQL 1440
Db 1402 PGASCSETECGGPNCRCTDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLASAEVEQL 1461
QY 1441 SKMVSEAKLRADAEAKQSAEDILLKTNATKEKMDKSNELRNLIKQIRNFLTQDSADLDSI 1500
Db 1462 SKMVSEAKLRADAEAKQSAEDILLKTNATKEKMDKSNELRNLIKQIRNFLTQDSADLDSI 1521
QY 1501 EAVANEVLKMEPSTPQOLNLTEDIRERVESLSQVEVILQHSAAADIARAEMLLLEEAKRA 1560
Db 1522 EAVANEVLKMEPSTPQOLNLTEDIRERVESLSQVEVILQHSAAADIARAEMLLLEEAKRA 1581
QY 1561 SKSATDVKVTADMVKEALEAEAKQAQAAEAKAIAKQADEDIQGTQNLTSIESETAASEETL 1620
Db 1582 SKSATDVKVTADMVKEALEAEAKQAQAAEAKAIAKQADEDIQGTQNLTSIESETAASEETL 1641
QY 1621 FNASQRISELERNEVEELKRAAQAQNSGEAEYIEKVYTVKQSAEDVKKTLGDELDEKYYKV 1680
Db 1642 FNASQRISELERNEVEELKRAAQAQNSGEAEYIEKVYTVKQSAEDVKKTLGDELDEKYYKV 1701
QY 1681 ENLIAKTEESADARRKAEMLQNEAKTLLAQANSKQLQKDLERKYEDNQRYLEDKAQEL 1740
Db 1702 ENLIAKTEESADARRKAEMLQNEAKTLLAQANSKQLQKDLERKYEDNQRYLEDKAQEL 1761
QY 1741 ARLEGEVRSLLKDISQKAVYVSTCL 1765
Db 1762 VRLEGEVRSLLKDISQKAVYVSTCL 1786

RESULT 6

US-10-037-182-10
; Sequence 10, Application US/10037182
; Publication No. US20030044899A1
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Doi, Masayuki
; APPLICANT: Thyboll, Jill
; TITLE OF INVENTION: Recombinant Laminin 10
; FILE REFERENCE: 99-274-F
; CURRENT APPLICATION NUMBER: US/10/037,182
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,449
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/279,282
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-037-182-10

Query Match 94.2%; Score 9092; DB 14; Length 1786;
Best Local Similarity 93.0%; Pred. No. 0;

Matches 1642; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

QY 1 QEPFSGYCAEGSCYPATGDLIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICNS 60
DB 22 QEPFSGYCAEGSCYPATGDLIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICDS 81
QY 61 QDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENVTIQLDLAEAFHFTHLIMTFK 120
DB 82 RDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENVTIQLDLAEAFHFTHLIMTFK 141
QY 121 TFRPAAMLIERSSDFGKTWGVYRYFAYDCEASFPGISGPMKKVDDIICDSRYSDIEPST 180
DB 142 TFRPAAMLIERSSDFGKTWGVYRYFAYDCEASFPGISGPMKKVDDIICDSRYSDIEPST 201
QY 181 EGEVIFRALDPAFKIEDPSPRIQNLKITNLRIKFVKLHTLGNLLDSRMEIREKYIYA 240
DB 202 EGEVIFRALDPAFKIEDPSPRIQNLKITNLRIKFVKLHTLGNLLDSRMEIREKYIYA 261
QY 241 VYDMVVRGNCFCYGHASECAPVDGFENEEVGMVGHGCMCRHNTKGLNCELMDFFYHDLDP 300
DB 262 VYDMVVRGNCFCYGHASECAPVDGFENEEVGMVGHGCMCRHNTKGLNCELMDFFYHDLDP 321
QY 301 RPAEGRNSNACKKCNNEHSSCHFDMAVYLATGNVSGGVCDCCQHNMTWGRNCEQCKPFY 360
DB 322 RPAEGRNSNACKKCNNEHSSCHFDMAVYLATGNVSGGVCDCCQHNMTWGRNCEQCKPFY 381
QY 361 YQHFERDIRDPNFCERCTCDPAGSQNEGICDSYDTPSTGLIAGQCRCKLNVEGEHCDVCK 420
DB 382 FQHPERDIRDPNFCERCTCDPAGSENGGICDGYTDFSVGLIAGQCRCKLHVEGERCDVCK 441
QY 421 EGFYDLSSDDPFGCKSCACNPLGTIPGGNCPDSETHCYCKRLVTGQHCDDQCLPEHWGLS 480
DB 442 EGFYDLSSDDPFGCKSCACNPLGTIPGGNCPDSETHCYCKRLVTGQHCDDQCLPEHWGLS 501
QY 481 NDLDGCRPCDCLGGALNNSCFAESGQCSCRPNMIGRQCNEVEPGYVPATLDHYLYEAE 540
DB 502 NDLDGCRPCDCLGGALNNSCFSESQSCSLPMIGRQCNEVESGYFTTLDHYLYEAE 561
QY 541 ANLPGVSVIVERQYIQRIPSWTGAFFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 600
DB 562 ANLPGVSVIVERQYIQRIPSWTGAFFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 621
QY 601 DHWEKAVITVQRPGRIPTRSSRCGNTIPDDDNQVVSLSPGSRVYVLPBPVCFEKGNTYTVR 660
DB 622 DHWEKAVITVQRPGRIPTRSSRCGNTIPDDDNQVVSLSPGSRVYVLPBPVCFEKGNTYTVR 681
QY 661 LELPQYTSDDSDVESPYTIDSLVLMPCYCKSLDIFTVGGSGDGVVTVNSAWETFORYRCLE 720
DB 682 LELPQYTSDDSDVESPYTIDSLVLMPCYCKSLDIFTVGGSGDGVVTVNSAWETFORYRCLE 741
QY 721 NSRSVVKTPTMTDVCNRIIFISALHQTGLACECDPQGSLSVCDPQSGGQCQCRPNVUGR 780
DB 742 NSRSVVKTPTMTDVCNRIIFISALHQTGLACECDPQGSLSVCDPQSGGQCQCRPNVUGR 801
QY 781 TCNRCAPGTGFGPGSGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDRLPGHWGF 840
DB 802 TCNRCAPGTGFGPGSGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDRLPGHWGF 861
QY 841 PSQPCQCNHADDGDPVTGECNLCQDYTMGNHCERCLAGYGDPIGSGDHCRCPCPCPD 900
DB 862 PSQPCQCNHADDGDPVTGECNLCQDYTMGNHCERCLAGYGDPIGSGDHCRCPCPCPD 921
QY 901 GPDGGRQFARSCYQDPVTIQLACVCDPQYIGSRCDCCASGYFGNPNSEVGGSCQPCQCHNN 960
DB 922 GPDGGRQFARSCYQDPVTIQLACVCDPQYIGSRCDCCASGYFGNPNSEVGGSCQPCQCHNN 981
QY 961 IDTTDPEACDKETGRCLKLYHTEGEHCQFCRFGYGDALRQDCRKCVCNLYLGTVOEHCN 1020
DB 982 IDTTDPEACDKETGRCLKLYHTEGEHCQFCRFGYGDALRQDCRKCVCNLYLGTVOEHCN 1041
QY 1021 GSDCQCDKATGQCLCPNVIGQNCDCRCPNTWQLASGTGCDPCNCAHSAHSPGSCNEFTG 1080
DB 1042 GSDCQCDKATGQCLCPNVIGQNCDCRCPNTWQLASGTGCDPCNCAHSAHSPGSCNEFTG 1101

QY 1081 QCQCMFGGRTCTSECQELFWGDPDVECRACDCDPRGIETPQCDQSTGQCVCVEGVEGPR 1140
DB 1102 QCQCMFGGRTCTSECQELFWGDPDVECRACDCDPRGIETPQCDQSTGQCVCVEGVEGPR 1161
QY 1141 CDKCTRGYGVFPDCTPCHQCPCFALWDVIIAELTNRTHRFLEKAKALKISGVIGPYRETVD 1200
DB 1162 CDKCTRGYGVFPDCTPCHQCPCFALWDVIIAELTNRTHRFLEKAKALKISGVIGPYRETVD 1221
QY 1201 SVERKVSSEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDVTEMMAQVEVKLSDTTSQSNST 1260
DB 1222 SVEKKVNEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDVTEMMAQVEVKLSDTTSQSNST 1281
QY 1261 AKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTTE 1320
DB 1282 AGELGALQAEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTTE 1341
QY 1321 PNSTVEQSALMRDRVEDVMERESQFKEQEEQARLLDELAKGLQSLDLSAAAEWTCGTP 1380
DB 1342 PNSTVEQSALMRDRVEDVMERESQFKEQEEQARLLDELAKGLQSLDLSAAAEWTCGTP 1401
QY 1381 PGASCSECEGPNCRTEDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLASAEVEQL 1440
DB 1402 PGASCSECEGPNCRTEDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLASAEVEQL 1461
QY 1441 SKMVSEAKLRADAEAKQSAEDIIKLTNATKERMKSNELNLIKQIRNFLTQDSADLDSI 1500
DB 1462 SKMVSEAKLRADAEAKQSAEDIIKLTNATKERMKSNELNLIKQIRNFLTQDSADLDSI 1521
QY 1501 EAVANEVLKMEMPTPQQLQNLTEDEIRERVESLSQVEVILQHSAAADIAEAEMLEAEAKRA 1560
DB 1522 EAVANEVLKMEMPTPQQLQNLTEDEIRERVESLSQVEVILQHSAAADIAEAEMLEAEAKRA 1581
QY 1561 SKSATDVKVTADVMKEALEEAEAKQAAEAKAIKQADEDIQGTQNLTSIESETAASEETL 1620
DB 1582 SKSATDVKVTADVMKEALEEAEAKQAAEAKAIKQADEDIQGTQNLTSIESETAASEETL 1641
QY 1621 FNASQRISBLERNVEELKRKAQNSGEAEYIEKVYVTVKQSAEDVKTLDGELDEKYKKV 1680
DB 1642 FNASQRISBLERNVEELKRKAQNSGEAEYIEKVYVTVKQSAEDVKTLDGELDEKYKKV 1701
QY 1681 ENLIAKTEESADARRKAELQNEAKTLLAQANSKQLLKLKDLERKYNQYLEDKAQEL 1740
DB 1702 ENLIAKTEESADARRKAELQNEAKTLLAQANSKQLLKLKDLERKYNQYLEDKAQEL 1761
QY 1741 ARLEGEVRSLLKDISQKAVVYSTCL 1765
DB 1762 VRLEGEVRSLLKDISQKAVVYSTCL 1786

RESULT 7
US-10-037-182-12
; Sequence 12, Application US/10037182
; Publication No. US20030044899A1
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Doi, Masayuki
; APPLICANT: Thyboll, Jill
; TITLE OF INVENTION: Recombinant Laminin 10
; FILE REFERENCE: 99-274-F
; CURRENT APPLICATION NUMBER: US/10/037,182
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,449
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/279,282
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1725
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-037-182-12

Query Match		91.9%;	Score 8873;	DB 14;	Length 1725;
Best Local Similarity		92.9%;	Pred. No. 0;		
Matches 1602;		Conservative 71;	Mismatches 52;	Indels 0;	Gaps 0;
QY	41	EPYCIIVSHLQEDKCKFCICNSQDPYHETLNPDSHLIENVTTFAPNRLKIWQSENGVENV	100		
Db	1	EPYCIIVSHLQEDKCKFCICNSQDPYHETLNPDSHLIENVTTFAPNRLKIWQSENGVENV	60		
QY	101	TIQLDLAEAFHFTHLIMTFKTRPAAMLIERSDFGKTWGVYRYFAYDCEASFPGISTGP	160		
Db	61	TIQLDLAEAFHFTHLIMTFKTRPAAMLIERSDFGKTWGVYRYFAYDCEASFPGISTGP	120		
QY	161	MKKVDDIICDSRYSIDIEPSTEGEVIIFRALDPAFKIEDPSPRIQNLKTNLRIKFKVLH	220		
Db	121	MKKVDDIICDSRYSIDIEPSTEGEVIIFRALDPAFKIEDPSPRIQNLKTNLRIKFKVLH	180		
QY	221	TLGDNLLDSRMEIREKYYAVVDMVVRGNCFCYGHASECAPVDGFNEVEGMVHGHCRCR	280		
Db	181	TLGDNLLDSRMEIREKYYAVVDMVVRGNCFCYGHASECAPVDGFNEVEGMVHGHCRCR	240		
QY	281	HNTKGLNCELMDFYHDLPRPAEGRNSNACKKCNNEHSISCHFDNAVYLATGNVSGGV	340		
Db	241	HNTKGLNCELMDFYHDLPRPAEGRNSNACKKCNNEHSISCHFDNAVYLATGNVSGGV	300		
QY	341	CDDCQHNWGRNCEQCKPFYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFDSIGL	400		
Db	301	CDNCQHNWGRNCEQCKPFYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFDSIGL	360		
QY	401	IAGQCRKLNVEGHECHDVCKEFPYDLSSDPFGCKSCACNPLGTIPGNCPCDSETGHCVY	460		
Db	361	IAGQCRKLNVEGHECHDVCKEFPYDLSSDPFGCKSCACNPLGTIPGNCPCDSETGHCVY	420		
QY	461	KRLVTGQHCHDOCLPEHMGLSNDLDGCRPCDCDLGALNNSCFAESGSCSRPHMIGRCN	520		
Db	421	KRLVTGQHCHDOCLPEHMGLSNDLDGCRPCDCDLGALNNSCFAESGSCSRPHMIGRCN	480		
QY	521	EVEPGYYFATLDHYLYEAEANLPGVSIIVERQYIQRIPSWTGAQFVRVPEGAYLEFFI	580		
Db	481	EVEPGYYFATLDHYLYEAEANLPGVSIIVERQYIQRIPSWTGAQFVRVPEGAYLEFFI	540		
QY	581	DNIPYSMEVDILIRYEPQLPDHWEKAVITVQRPGRIPTRSSRCGNTIPDDNQVVSLSPGS	640		
Db	541	DNIPYSMEVDILIRYEPQLPDHWEKAVITVQRPGRIPTRSSRCGNTIPDDNQVVSLSPGS	600		
QY	641	RYVVLPRPVCPEKGTNYTVRLPLQYTSDDSDVESPYTLIDSLVMPYCKSLDIFTVGGS	700		
Db	601	RYVVLPRPVCPEKGTNYTVRLPLQYTSDDSDVESPYTLIDSLVMPYCKSLDIFTVGGS	660		
QY	701	GDGVVNTSAWETFORYRCLENSRSVWKTMTDVCNRIIFSISALHGTGLACECDPQGS	760		
Db	661	GDGVVNTSAWETFORYRCLENSRSVWKTMTDVCNRIIFSISALHGTGLACECDPQGS	720		
QY	761	SSVCDPNGGQCRPNVVGRTNRCNRCAPGTFGFGPSGCKPCECHLQGSVNAFCNPVTGOCH	820		
Db	721	SSVCDPNGGQCRPNVVGRTNRCNRCAPGTFGFGPSGCKPCECHLQGSVNAFCNPVTGOCH	780		
QY	821	CFQGVYARQCDRCLPGHWGFPSCQPCQCNHADDPCDPTVTECLNCDYTMGHNCERCLAG	880		
Db	781	CFQGVYARQCDRCLPGHWGFPSCQPCQCNHADDPCDPTVTECLNCDYTMGHNCERCLAG	840		
QY	881	YGDPIIGSGDHCRPCPCPDGDSGRQFARSQYQDPVTLQLACVCDPGYIGSRCDDCAG	940		
Db	841	YGDPIIGSGDHCRPCPCPDGDSGRQFARSQYQDPVTLQLACVCDPGYIGSRCDDCAG	900		
QY	941	YFGNPSVGGSCQPCQCHNIDTDPACDKETGRCLKCLYHTEGHCQCFRFGYGGDAL	1000		
Db	901	YFGNPSVGGSCQPCQCHNIDTDPACDKETGRCLKCLYHTEGHCQCFRFGYGGDAL	960		
QY	1001	RQDCRKVCNVLGTQVQEHCHNGSDCQCDKATGQCLPLNVIGQNCRCAPNTWQLASGTC	1060		
Db	961	RQDCRKVCNVLGTQVQEHCHNGSDCQCDKATGQCLPLNVIGQNCRCAPNTWQLASGTC	1020		

QY	1061	DPCNCAHSGFSPSCNEFTGQCQCMPGFGGRTCSCEQELFWGDDPVECRACDCDPRGIET	1120
Db	1021	GPCNCAHSGFSPSCNEFTGQCQCMPGFGGRTCSCEQELFWGDDPVECRACDCDPRGIET	1080
QY	1121	PQCDQSTGQCVCEGVGPRCDKCTRGYSVGFPPDCTPCHQCQFALWDVIAELTNTRHFL	1180
Db	1081	PQCDQSTGQCVCEGVGPRCDKCTRGYSVGFPPDCTPCHQCQFALWDVIAELTNTRHFL	1140
QY	1181	EKAKALKISGVIGPYRETVDVSVERKVSEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDV	1240
Db	1141	EKAKALKISGVIGPYRETVDVSVERKVSEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDV	1200
QY	1241	EMMAQVEVKLSDTTSSQSNSTAKELDSLOTEAESLDNTVKELAEQLEFIKNSDIRGALDSI	1300
Db	1201	EMMAQVEVKLSDTTSSQSNSTAKELDSLOTEAESLDNTVKELAEQLEFIKNSDIRGALDSI	1260
QY	1301	TKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVMERESQFKEKQEEQARLLDEL	1360
Db	1261	TKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVMERESQFKEKQEEQARLLDEL	1320
QY	1361	AGKLQSLDLSAAAEVTCTGPPGASCSETECGGPNCRCTDEGERKCGGPGCGGLVTVAHNAW	1420
Db	1321	AGKLQSLDLSAAAEVTCTGPPGASCSETECGGPNCRCTDEGERKCGGPGCGGLVTVAHNAW	1380
QY	1421	QKAMDLDQDVLALAEVQLSKMVSEAKLRADAEAKQSAEDILLKTNATKEKMDKSNEDLR	1480
Db	1381	QKAMDLDQDVLALAEVQLSKMVSEAKLRADAEAKQSAEDILLKTNATKEKMDKSNEDLR	1440
QY	1481	NLIKQIRNFLTQDSADLDSIEAVANEVLKXMEMPTPQQLQNLTEDIRERVESLSQVEVIL	1540
Db	1441	NLIKQIRNFLTQDSADLDSIEAVANEVLKXMEMPTPQQLQNLTEDIRERVESLSQVEVIL	1500
QY	1541	QHSAAADIAEAEMLEAKRASKSATDVKTADVMVKEALEEAKQAAEKAIOADEDIQ	1600
Db	1501	QHSAAADIAEAEMLEAKRASKSATDVKTADVMVKEALEEAKQAAEKAIOADEDIQ	1560
QY	1601	GTQNLTSIESETAASEETLFNASQRISELERNEVELKRAQNSGEAEYIEKVYTVKQ	1660
Db	1561	GTQNLTSIESETAASEETLFNASQRISELERNEVELKRAQNSGEAEYIEKVYTVKQ	1620
QY	1661	SAEDVKKTLGDELDEKIKKVENLIAKTEESADARRKAEMLQNEAKTLAQANSKLQLLK	1720
Db	1621	SAEDVKKTLGDELDEKIKKVENLIAKTEESADARRKAEMLQNEAKTLAQANSKLQLLK	1680
QY	1721	DLERKYEDNQRYLEDKAEQELARLEGEVRSLLKDISQKAVYSTCL	1765
Db	1681	DLERKYEDNQRYLEDKAEQELARLEGEVRSLLKDISQKAVYSTCL	1725

RESULT 8
US-10-443-349-4
; Sequence 4, Application US/10443349
; Publication No. US20040023856A1
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert E.
; APPLICANT: Wagman, David W.
; TITLE OF INVENTION: BLK CHAIN OF LAMININ AND METHODS OF USE
; FILE REFERENCE: 10287/021003
; CURRENT APPLICATION NUMBER: US/10/443,349
; CURRENT FILING DATE: 2003-05-22
; PRIOR APPLICATION NUMBER: US/09/161,872
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: US 08/735,893
; PRIOR FILING DATE: 1996-10-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1196
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(250)

OTHER INFORMATION: Human B1 chain
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (251)... (437)
OTHER INFORMATION: Human B1 chain
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (438)... (807)
OTHER INFORMATION: Human B1 chain
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (808)... (840)
OTHER INFORMATION: Human B1 chain
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (841)... (1196)
OTHER INFORMATION: Human B1 chain
US-10-443-349-4

Query Match 62.6%; Score 6044.5; DB 16; Length 1196;
Best Local Similarity 67.6%; Pred. No. 0;
Matches 1194; Conservative 0; Mismatches 1; Indels 571; Gaps 2;
QY 1 QEPFSGCAEGSCYPATGDLIGRAQKLSVTS-TCGLHKPEPCIVSHLOEDKCKFCIN 59
Db 1 QEPFSGCAEGSCYPATGDLIGRAQKLSVTS-TCGLHKPEPCIVSHLOEDKCKFCIN 60
QY 60 SODPYHEINLPDASHLIENVTTFAPNRLKIWQSENGVENVTIQLDLAEFFHFLIMTF 119
Db 61 SODPYHEINLPDASHLIENVTTFAPNRLKIWQSENGVENVTIQLDLAEFFHFLIMTF 120
QY 120 KTFRPAAMLIERSDDFGKWTGVYRYFAYDCEASFPGISTGPMKKVDDIICDSRYSIEPS 179
Db 121 KTFRPAAMLIERSDDFGKWTGVYRYFAYDCEASFPGISTGPMKKVDDIICDSRYSIEPS 180
QY 180 TEGEVIFRALDPAFKIEDPYSRIQNLKLTNLRIFKVLHTLGLDNLDSRMEIREKYYY 239
Db 181 TEGEVIFRALDPAFKIEDPYSRIQNLKLTNLRIFKVLHTLGLDNLDSRMEIREKYYY 240
QY 240 AVYDMVVRGNCFCYGHASECAPVDGFEVEEVEGVMVHCHMCWRHNTKGLNCELMDFFYHDL 299
Db 241 AVYDMVVRGNCFCYGHASECAPVDGFEVEEVEGVMVHCHMCWRHNTKGLNCELMDFFYHDL 300
QY 300 WRPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGGVCDCCQHNMTGRNCEQCKPF 359
Db 301 WRPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGGVCDCCQHNMTGRNCEQCKPF 360
QY 360 YYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSTGLIAGQCRCKLNVEGEHCDVC 419
Db 361 YYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSTGLIAGQCRCKLNVEGEHCDVC 420
QY 420 KEGFYDLSSDDPFGCKSCACNPLGTIPGPNPCDSETHCYCKRLVTGQHCDDQLPEHWGL 479
Db 421 KEGFYDLSSDDPFGCKS----- 437
QY 480 SNDLDGCRPCDCDLGGALNNSCFAESGQSCSRPHMIGRQCNEVEPGYVPATLDHYLYEAE 539
Db 438 ----- 437
QY 540 EANTLPGVSIIVERQYIQDRIPSWTGAQFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQL 599
Db 438 ----- 437
QY 600 PDHWEKAVITVQRPRIPTSSRCNGTIPDDDNQVVSLSPGSRVYVLPVPCFEKGTNYTV 659
Db 438 ----- 437
QY 660 RLELPQVTSDDSDVESPYTLIDSLVLPYCKSLDIFTVGGSGDGVVINSAWETFORYRCL 719
Db 438 ----- 437
QY 720 ENSRSVVKTPMTDVCNRIIFSIALLHQTGLACECDPQGSLSVCDPENGQCQCRPNVVG 779

Db 438 ----- 437
QY 780 RTCNRCAPGTGFGPSGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDCRCLPGHWG 839
Db 438 ----- 437
QY 840 FPSQPCQCNGHADDCDPVTGECCLNCQDYTMGHNCRCLAGYGYGDPPIIGSGDHCRPCPCP 899
Db 438 ----- 437
QY 900 DGPDSGRQFARSCYQDPVTLQLACVCDPGYIGSRCDDCASGYFGNPSVGGSCQPCQCHN 959
Db 438 ----- 437
QY 960 NIDTTPACDKETGRCLKLYHTEGEHCQCFRFGYGDALRQDCRKCVCNYLGTVQEHHC 1019
Db 438 -----CVCNYLGTVQEHHC 450
QY 1020 NGSDCCQCDKATGQCLCLPNVIGONCDRCAPNTWQLASGTCCDPCNCAAHSGFSGSCNEFT 1079
Db 451 NGSDCCQCDKATGQCLCLPNVIGONCDRCAPNTWQLASGTCCDPCNCAAHSGFSGSCNEFT 510
QY 1080 GQCQCMPPGFGGRTCECQELFWGDPDVECRACDCDPRGIETPQCDQSTGQCVCVEGVEGP 1139
Db 511 GQCQCMPPGFGGRTCECQELFWGDPDVECRACDCDPRGIETPQCDQSTGQCVCVEGVEGP 570
QY 1140 RCDKCTRGYSVFPDCTPCHQCFALMDVIIAELTNTRHFRLEKAKALKISGVIGPYRETIV 1199
Db 571 RCDKCTRGYSVFPDCTPCHQCFALMDVIIAELTNTRHFRLEKAKALKISGVIGPYRETIV 630
QY 1200 DSVERKVSEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDVTEMAQVEVKLSDTTSQSNS 1259
Db 631 DSVERKVSEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDVTEMAQVEVKLSDTTSQSNS 690
QY 1260 TAKELDSLQTEAESLDNTVTKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTT 1319
Db 691 TAKELDSLQTEAESLDNTVTKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTT 750
QY 1320 EPNSTVEQSALMRDRVEDVMMERESQFKEQEEQARLLDELQAGLQSLDLSAAAEAMTCGT 1379
Db 751 EPNSTVEQSALMRDRVEDVMMERESQFKEQEEQARLLDELQAGLQSLDLSAAAEAMTCGT 810
QY 1380 PPGASCSETECGGPNCRDTDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLALAEVEQ 1439
Db 811 PPGASCSETECGGPNCRDTDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLALAEVEQ 870
QY 1440 LSKMVSEAKLRADAEAKQSAEDILLKTNATKEKMDKSNBEELRNLIKQIRNFLTQDSADLDS 1499
Db 871 LSKMVSEAKLRADAEAKQSAEDILLKTNATKEKMDKSNBEELRNLIKQIRNFLTQDSADLDS 930
QY 1500 IEAVANEVLKMEMPSTPQQLQNLTEDIRERVESLSQVEVILQHSAAADIARAEMLLEBAKR 1559
Db 931 IEAVANEVLKMEMPSTPQQLQNLTEDIRERVESLSQVEVILQHSAAADIARAEMLLEBAKR 990
QY 1560 ASKSATDVKVTADMVKEALEEAEKQAAEKAKIQADEDIQTQNLTSIESETAASEET 1619
Db 991 ASKSATDVKVTADMVKEALEEAEKQAAEKAKIQADEDIQTQNLTSIESETAASEET 1050
QY 1620 LFNASQRISELERNEVEELKRAQNSGEAEYIEKVYTVTKQSAEDVKKTLDEGELDEKYYK 1679
Db 1051 LFNASQRISELERNEVEELKRAQNSGEAEYIEKVYTVTKQSAEDVKKTLDEGELDEKYYK 1110
QY 1680 VENLIAKTEESADARRKAEMLQNEAKTLLAQANSKLLKDLERKYEDNQRYLEDKQAE 1739
Db 1111 VENLIAKTEESADARRKAEMLQNEAKTLLAQANSKLLKDLERKYEDNQRYLEDKQAE 1170
QY 1740 LARLEGEVRSLLKDISQKAVYSTCL 1765
Db 1171 LARLEGEVRSLLKDISQKAVYSTCL 1196

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:58 ; Search time 16.2434 Seconds
(without alignments)
10452.141 Million cell updates/sec

Title: US-10-037-182-8
Perfect score: 9654
Sequence: 1 QEPFESYGCAEGSCYPATG.....EVRSLKDISQKAVYSTCL 1765

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	9654	100.0	1786	1 MMHUB1	laminin beta-1 cha
2	9092	94.2	1786	1 MMMSB1	laminin beta-1 cha
3	5084	52.7	1801	1 MMRTS	laminin beta-2 cha
4	5050	52.3	1798	2 S53869	laminin beta-2 cha
5	4884.5	50.6	1797	2 A55677	laminin beta-2 cha
6	3844.5	39.8	1790	1 MMFFB1	laminin beta-1 cha
7	3765	39.0	1808	2 T15099	hypothetical prote
8	1755	18.2	1639	1 MMFFB2	laminin gamma-1 ch
9	1729.5	17.9	3672	2 T23433	hypothetical prote
10	1729.5	17.9	3704	2 T37316	probable laminin a
11	1696.5	17.6	1557	2 T28811	hypothetical prote
12	1676.5	17.4	1609	1 MMHUB2	laminin gamma-1 ch
13	1653	17.1	1607	1 MMMSB2	laminin gamma-1 ch
14	1637	17.0	3712	2 S18253	laminin alpha-1 ch
15	1605	16.6	3635	2 T10053	laminin alpha 5 ch
16	1583	16.4	303	2 B45067	laminin B1 chain -
17	1538.5	15.9	1170	2 A53612	laminin B1k chain
18	1535.5	15.9	3106	1 S53868	laminin alpha-1 ch
19	1525	15.8	3075	2 S14458	laminin alpha-1 ch
20	1507.5	15.6	3084	1 MMMSA	laminin alpha-1 ch
21	1485.5	15.4	1168	2 I56985	kalinin B1 - mouse
22	1307.5	13.5	2823	2 T23064	hypothetical prote
23	1307.5	13.5	2823	2 F87908	protein T22A3.8 li
24	1307.5	13.5	3102	2 T43291	laminin alpha chai
25	1001.5	10.4	616	2 I38231	S-laminin - human
26	871	9.0	1193	2 A44018	laminin B2t chain
27	862.5	8.9	1192	2 S69000	laminin gamma 2 ch
28	690.5	7.2	606	2 A54665	netrin-1 precursor
29	679	7.0	1620	2 T27283	hypothetical prote

30	669.5	6.9	1574	2 T13954	MEGF6 protein - ra
31	666	6.9	3707	2 S18252	heparan sulfate pr
32	663.5	6.9	1111	2 T26972	hypothetical prote
33	657	6.8	4391	2 A38096	perlecan precursor
34	600	6.2	581	2 B54665	netrin-2 precursor
35	580.5	6.0	1816	1 S68960	laminin alpha-4 ch
36	579	6.0	612	2 JH0799	laminin-related pr
37	577.5	6.0	1751	1 MMHUBH	laminin alpha-2 ch
38	568	5.9	400	2 T46383	hypothetical prote
39	527	5.5	2555	2 A40043	notch protein homo
40	526	5.4	2295	2 C88369	protein unc-52 [im
41	526	5.4	3375	2 T19821	hypothetical prote
42	523	5.4	1160	2 F88369	protein unc-52 [im
43	511	5.3	198	2 A45067	laminin B1 chain v
44	509	5.3	2524	2 A35844	Xotch protein - Af
45	506.5	5.2	2703	1 A24420	notch protein - fr

ALIGNMENTS

RESULT 1

MMHUB1

laminin beta-1 chain precursor - human

N;Alternate names: laminin chain B1

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text_change 19-Jan-2001

C;Accession: S13547; A28483; A26994; S23566

R;Vuolteenaho, R.; Chow, L.T.; Tryggvason, K.

J. Biol. Chem. 265, 15611-15616, 1990

A;Title: Structure of the human laminin B1 chain gene.

A;Reference number: S13547; MUID:90368768; PMID:1975589

A;Accession: S13547

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-1786 <VUO>

A;Cross-references: GB:M61951; GB:J02778; NID:G186911; PIDN:AAA59486.1; PID:G186913

A;Note: the nucleotide sequence was submitted to GenBank, February 1991

R;Pikkariainen, J.; Eddy, R.; Fukushima, Y.; Byers, M.; Shows, T.; Pihlajaniemi, T.; Sar

J. Biol. Chem. 262, 10454-10462, 1987

A;Title: Human laminin B1 chain. A multidomain protein with gene (LAMB1) locus in the q

A;Reference number: A28483; MUID:87280097; PMID:3611077

A;Accession: A28483

A;Molecule type: mRNA

A;Residues: 1-1786 <PIK>

A;Cross-references: GB:M61951; GB:J02778; NID:G186911; PIDN:AAA59486.1; PID:G186913

R;Jaya, M.; Modi, W.S.; Ricca, G.A.; Mudd, R.; Chiu, I.M.; O'Brien, S.J.; Drohan, W.N.

Am. J. Hum. Genet. 41, 605-615, 1987

A;Title: Isolation of a cDNA clone for the human laminin-B1 chain and its gene localizat

A;Reference number: A26994; MUID:88021029; PMID:3661559

A;Accession: A26994

A;Molecule type: mRNA

A;Residues: 1276-1469, 'V', 1471-1695, 'G', 1697-1709 <JAY>

A;Cross-references: EMBL:M20206; NID:G186914; PIDN:AAA59487.1; PID:G186915

R;Vuolteenaho, R.; Kallunki, T.; Chow, L.; Ikonen, J.; Pikkariainen, T.; Tryggvason, K.

In Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp. 175-193, Academic

A;Title: Genes for the human laminin B1 and B2 chains.

A;Reference number: S23566

A;Accession: S23566

A;Molecule type: DNA

A;Residues: 762-1786 <VU2>

A;Note: mRNA was also sequenced

C;Genetics:

A;Gene: GDB:LAMB1

A;Cross-references: GDB:119357; OMIM:150240

A;Map position: 7q31.1-7q31.3

A;Introns: 13/1; 71/3; 117/1; 141/3; 204/3; 226/1; 293/3; 334/1; 397/1; 457/1; 494/3; 52

64/3; 1513/1; 1582/2; 1629/3; 1688/3; 1742/1

C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin

C;Function:

A;Description: interact with cells and with other basement membrane proteins to promote

C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology

C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular

F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-1786/Product: laminin beta-1 chain #status predicted <MAT>
F:22-270/Domain: VI <DOM6>
F:271-548/Domain: V <DOM5>
F:271-332/Domain: laminin-type EGF-like homology <LE01>
F:335-395/Domain: laminin-type EGF-like homology <LE02>
F:398-455/Domain: laminin-type EGF-like homology <LE03>
F:458-507/Domain: laminin-type EGF-like homology <LE04>
F:463-468/Region: cell adhesion #status predicted
F:510-540/Domain: laminin-type EGF-like homology
F:549-774/Domain: IV <DOM4>
F:562-668/Region: cell adhesion #status predicted
F:773-818/Domain: laminin-type EGF-like homology <LE06>
F:775-1178/Domain: III <DOM3>
F:821-864/Domain: laminin-type EGF-like homology <LE07>
F:867-914/Domain: laminin-type EGF-like homology <LE08>
F:917-973/Domain: laminin-type EGF-like homology <LE09>
F:923-927/Region: cell adhesion #status predicted
F:950-954/Region: cell adhesion #status predicted
F:976-1025/Domain: laminin-type EGF-like homology <LE10>
F:1028-1081/Domain: laminin-type EGF-like homology <LE11>
F:1084-1129/Domain: laminin-type EGF-like homology <LE12>
F:1132-1176/Domain: laminin-type EGF-like homology <LE13>
F:1179-1397/Domain: II <DOM2>
F:1179-1397/Region: heptad repeats
F:1398-1430/Domain: alpha <ALP>
F:1431-1786/Domain: I <DOM1>
F:1431-1786/Region: heptad repeats
F:30-35/Disulfide bonds: #status predicted
F:120,356,519,677,965,1041,1195,1279,1336,1343,1487,1542,1643/Binding site: carbohydrate
F:1179,1182,1785/Disulfide bonds: interchain #status predicted

Query Match		100.0%;	Score 9654;	DB 1;	Length 1786;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 1765;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	QEPEFSYGCAEGSCYPATGDLIGRAQKLSVTSTGLHKPEPYCIVSHLQEDKKCFICNS	60		
Db	22	QEPEFSYGCAEGSCYPATGDLIGRAQKLSVTSTGLHKPEPYCIVSHLQEDKKCFICNS	81		
QY	61	QDPVHETLNPDSHLIENVVTFAPNRLKIWQSENGVENVTIQLDLEAEFFHFLIMTFK	120		
Db	82	QDPVHETLNPDSHLIENVVTFAPNRLKIWQSENGVENVTIQLDLEAEFFHFLIMTFK	141		
QY	121	TFRPAAMLIERSSDFGKTGWYRYFAYDCEASFPPISTGPMKKVDDIICDSRYSIDIEPST	180		
Db	142	TFRPAAMLIERSSDFGKTGWYRYFAYDCEASFPPISTGPMKKVDDIICDSRYSIDIEPST	201		
QY	181	EGEYIFRALDPFAFKIEDPSPRIQNLKIKFVKLHTLGNLDSRMEIREKYA	240		
Db	202	EGEYIFRALDPFAFKIEDPSPRIQNLKIKFVKLHTLGNLDSRMEIREKYA	261		
QY	241	VYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGCMCRHNTKGLNCELMDPFYHDLPW	300		
Db	262	VYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGCMCRHNTKGLNCELMDPFYHDLPW	321		
QY	301	RPABGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGVCDQCQHTMTGRNCEQCKPFY	360		
Db	322	RPABGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGVCDQCQHTMTGRNCEQCKPFY	381		
QY	361	YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSTGLIAGQCRKLNVEGEHCDVCK	420		
Db	382	YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSTGLIAGQCRKLNVEGEHCDVCK	441		
QY	421	EGFYDLSSDPFGCKSCACNPLGTIPGPNPCDSETGHYCYCKRLVTGQHCDCQCLPEHWGLS	480		
Db	442	EGFYDLSSDPFGCKSCACNPLGTIPGPNPCDSETGHYCYCKRLVTGQHCDCQCLPEHWGLS	501		
QY	481	NLDGCRPCDCDLGALNNSCFAESGQCSRPHMIGRQCNEVEPGYFATLDHYLYEAE	540		
Db	502	NLDGCRPCDCDLGALNNSCFAESGQCSRPHMIGRQCNEVEPGYFATLDHYLYEAE	561		
QY	541	ANLPGVSIYERQYIQDRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP	600		

Db	562	ANLPGVSIYERQYIQDRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP	621		
QY	601	DHWEKAVITVORPGRIPSSRCNGTIPDDDNQVVSLSFGSRYYVLPVPVCFEKGNTYTVR	660		
Db	622	DHWEKAVITVORPGRIPSSRCNGTIPDDDNQVVSLSFGSRYYVLPVPVCFEKGNTYTVR	681		
QY	661	LELPQYTSDDSDVESPYTLIDSLVLMPCYCKSLDIFTVGGSGDGVWVNSAWETFORYRCLE	720		
Db	682	LELPQYTSDDSDVESPYTLIDSLVLMPCYCKSLDIFTVGGSGDGVWVNSAWETFORYRCLE	741		
QY	721	NSRSVVKTPMTDVCNIIIFSISALLHQTGLACECDPQGSLSVSCDPNGGQCCQCRPNVVGR	780		
Db	742	NSRSVVKTPMTDVCNIIIFSISALLHQTGLACECDPQGSLSVSCDPNGGQCCQCRPNVVGR	801		
QY	781	TCNRCAPGTGFGPSGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDCRCLPGHWGF	840		
Db	802	TCNRCAPGTGFGPSGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDCRCLPGHWGF	861		
QY	841	PSCQPCQCNHADDGDPVTGECCLNCQDYTMGHNCERCLAGYVGDPIIGSGDHCRPCPCPD	900		
Db	862	PSCQPCQCNHADDGDPVTGECCLNCQDYTMGHNCERCLAGYVGDPIIGSGDHCRPCPCPD	921		
QY	901	GPDSGRQFARSCYQDPVTQLACVCDPGYIGSRCDDCASGYFGNPSVGGSCQPCQCHNN	960		
Db	922	GPDSGRQFARSCYQDPVTQLACVCDPGYIGSRCDDCASGYFGNPSVGGSCQPCQCHNN	981		
QY	961	IDTTPBACDKETGRCLKCLYHTEGHCQFCRFGYGDALRQDCRKCVCNLYLGTVQEHCN	1020		
Db	982	IDTTPBACDKETGRCLKCLYHTEGHCQFCRFGYGDALRQDCRKCVCNLYLGTVQEHCN	1041		
QY	1021	GSDCQCDKATGQCLCLPNVIGQNCDCRCPNTWQASGTGCDPCNCAHSGFSPSCNEFTG	1080		
Db	1042	GSDCQCDKATGQCLCLPNVIGQNCDCRCPNTWQASGTGCDPCNCAHSGFSPSCNEFTG	1101		
QY	1081	QCQMPGFGGRTCECQELFWGDDPVECRACDPRGIETPQCDQSTGQCVCEGVEGPR	1140		
Db	1102	QCQMPGFGGRTCECQELFWGDDPVECRACDPRGIETPQCDQSTGQCVCEGVEGPR	1161		
QY	1141	CDKTRGYSGVFPDCTPCHQCFALWDVIAELTNRTHRFLEKAKALKISGVIQPYRETVD	1200		
Db	1162	CDKTRGYSGVFPDCTPCHQCFALWDVIAELTNRTHRFLEKAKALKISGVIQPYRETVD	1221		
QY	1201	SVERKVSEIKDILAQSPAABPLKNIKNLFEAEKLIKDVTEMMAQVEVKLSDDTTSQSNST	1260		
Db	1222	SVERKVSEIKDILAQSPAABPLKNIKNLFEAEKLIKDVTEMMAQVEVKLSDDTTSQSNST	1281		
QY	1261	AKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSDITKYFQMSLEAEERVNASTTE	1320		
Db	1282	AKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSDITKYFQMSLEAEERVNASTTE	1341		
QY	1321	PNSTVEQSALMRDRVEDVMMERESQFKEKQEQEARLLDELQGLQSLDLSAAAEAMTCGTP	1380		
Db	1342	PNSTVEQSALMRDRVEDVMMERESQFKEKQEQEARLLDELQGLQSLDLSAAAEAMTCGTP	1401		
QY	1381	PGASCSETECGGPNCRTEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLALAEVEQL	1440		
Db	1402	PGASCSETECGGPNCRTEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLALAEVEQL	1461		
QY	1441	SKMVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNEELRNLIKQIRNFLTQDSADLDSI	1500		
Db	1462	SKMVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNEELRNLIKQIRNFLTQDSADLDSI	1521		
QY	1501	EAVANEVLKMEPSTPQQLONLTEDIRERVESLSQVEVILQHSADIAEAEMLLEEAKRA	1560		
Db	1522	EAVANEVLKMEPSTPQQLONLTEDIRERVESLSQVEVILQHSADIAEAEMLLEEAKRA	1581		
QY	1561	SKSATDVKVTADMVKEALEEAEKAQVAAEKAKQADEDIQGTQNLTSIESETAASEETL	1620		
Db	1582	SKSATDVKVTADMVKEALEEAEKAQVAAEKAKQADEDIQGTQNLTSIESETAASEETL	1641		
QY	1621	FNASQRISELERNVBELKRAAQNNGEAEYIEKVYTVKQSAEDVKTLDELDEKYYKV	1680		

Db 1642 FNASQRISSELRNVEELKRKAQNSGEAEYIEKVVTYVTKQSAEDVKKTLTGELDEKYYKV 1701

QY 1681 ENLIAKTTESADARRKAEMLQNEAKTLLAQANSKLQLLKDLERKYEDNQRYLEDKAQEL 1740
|||||

Db 1702 ENLIAKTTESADARRKAEMLQNEAKTLLAQANSKLQLLKDLERKYEDNQRYLEDKAQEL 1761
|||||

QY 1741 ARLEGEVRSLLKDISQKVAVYSTCL 1765
|||||

Db 1762 ARLEGEVRSLLKDISQKVAVYSTCL 1786
|||||

RESULT 2

MMMSB1

laminin beta-1 chain precursor - mouse

N;Alternate names: laminin chain B1

C;Species: Mus musculus (house mouse)

C;Date: 28-Feb-1986 #sequence revision 30-Jun-1991 #text change 10-Dec-1999

C;Accession: A26413; S02679; S05326; S14877; A02871; S02036; S13543

R;Sasaki, M.; Kato, S.; Kohno, K.; Martin, G.R.; Yamada, Y.

Proc. Natl. Acad. Sci. U.S.A. 84, 935-939, 1987

A;Title: Sequence of the cDNA encoding the laminin B1 chain reveals a multidomain protein

A;Reference number: A26413; MUID:87147212; PMID:3493487

A;Accession: A26413

A;Molecule type: mRNA

A;Residues: 1-1786 <SAS>

A;Cross-references: EMBL:M15525; NID:9198700

A;Note: translation in GenBank has additional 48 residues at the amino end

R;Fujiwara, S.; Shinkai, H.; Deutzmann, R.; Paulsson, M.; Timpl, R.

Biochem. J. 252, 453-461, 1988

A;Title: Structure and distribution of N-linked oligosaccharide chains on various domain

A;Reference number: S02678; MUID:88326259; PMID:2458101

A;Accession: S02679

A;Molecule type: protein

A;Residues: 28-42;932-946 <FUJ>

R;Hartl, L.; Oberbaeumer, I.; Deutzmann, R.

Eur. J. Biochem. 173, 629-635, 1988

A;Title: The N terminus of laminin A chain is homologous to the B chains.

A;Reference number: S00624; MUID:88225080; PMID:3267223

A;Accession: S05326

A;Molecule type: protein

A;Residues: 457-466;854-868;932-946 <HAR>

R;Mann, K.; Deutzmann, R.; Timpl, R.

Eur. J. Biochem. 178, 71-80, 1988

A;Title: Characterization of proteolytic fragments of the laminin-nidogen complex and th

A;Reference number: S08895; MUID:89078415; PMID:2462498

A;Accession: S14877

A;Molecule type: protein

A;Residues: 590-620 <MAN>

R;Barlow, D.P.; Green, N.M.; Kurkinen, M.; Hogan, B.L.M.

EMBO J. 3, 2355-2362, 1984

A;Title: Sequencing of laminin B chain cDNAs reveals C-terminal regions of coiled-coil a

A;Reference number: A02870; MUID:85051302; PMID:6209134

A;Accession: A02871

A;Molecule type: mRNA

A;Residues: 1292-1530, 'MEMP', 1535-1691, 'C', 1693-1748, 'N', 1750-1786 <BAR>

A;Cross-references: EMBL:X05212; NID:952861; PIDN:CAA28839.1; PID:9809042

R;Deutzmann, R.; Huber, J.; Schmetz, K.A.; Oberbaeumer, I.; Hartl, L.

Eur. J. Biochem. 177, 35-45, 1988

A;Title: Structural study of long arm fragments of laminin. Evidence for repetitive C-te

A;Reference number: S01790; MUID:89030693; PMID:3181157

A;Accession: S02036

A;Molecule type: protein

A;Residues: 1561-1587 <DEU>

R;Paulsson, M.; Deutzmann, R.; Timpl, R.; Dalzoppo, D.; Odermatt, E.; Engel, J.

EMBO J. 4, 309-316, 1985

A;Title: Evidence for coiled-coil alpha-helical regions in the long arm of laminin.

A;Reference number: S13543; MUID:85257455; PMID:3848400

A;Accession: S13543

A;Molecule type: protein

A;Residues: 1700-1748, 'N', 1750-1759 <PAU>

C;Genetics:

A;Gene: Lamb-1

A;Map position: 12

C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin

C;Function:

A;Description: interact with cells and with other basement membrane proteins to promote

C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology

C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-1786/Product: laminin beta-1 chain #status predicted <MAT>

F;22-270/Domain: VI <DOM6>

F;271-540/Domain: V <DOM5>

F;271-332/Domain: laminin-type EGF-like homology <LE01>

F;335-395/Domain: laminin-type EGF-like homology <LE02>

F;398-455/Domain: laminin-type EGF-like homology <LE03>

F;458-507/Domain: laminin-type EGF-like homology <LE04>

F;510-540/Domain: laminin-type EGF-like homology #status atypical <LE05>

F;541-772/Domain: IV <DOM4>

F;773-1182/Domain: III <DOM3>

F;773-818/Domain: laminin-type EGF-like homology <LE06>

F;821-864/Domain: laminin-type EGF-like homology <LE07>

F;867-914/Domain: laminin-type EGF-like homology <LE08>

F;917-973/Domain: laminin-type EGF-like homology <LE09>

F;976-1025/Domain: laminin-type EGF-like homology <LE10>

F;1028-1081/Domain: laminin-type EGF-like homology <LE11>

F;1084-1129/Domain: laminin-type EGF-like homology <LE12>

F;1132-1176/Domain: laminin-type EGF-like homology <LE13>

F;1183-1397/Domain: II <DOM2>

F;1183-1397/Region: heptad repeats

F;1398-1430/Domain: alpha <ALP>

F;1431-1786/Region: heptad repeats

F;1431-1786/Domain: I <DOM1>

F;22/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted

F;30-35/Disulfide bonds: #status predicted

F;120,356,519,677,1041,1195,1279,1336,1343,1487,1533,1542,1643/Binding site: carbohydra

F;1179,1182,1785/Disulfide bonds: interchain #status predicted

Query Match 94.2%; Score 9092; DB 1; Length 1786;
Best Local Similarity 93.0%; Pred. No. 0;
Matches 1642; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

QY 1 QEPFSGYSGAEGSCYPATGDLILIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICNS 60
|||

Db 22 QEPFSGYSGAEGSCYPATGDLILIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICDS 81
|||

QY 61 QDPYHETLNPDSHLIENVTTFAPNRLKIWQSENGVENVTIQLDLAEFFHFLIMTFK 120
:|

Db 82 RDPYHETLNPDSHLIENVTTFAPNRLKIWQSENGVENVTIQLDLAEFFHFLIMTFK 141
:|

QY 121 TFRPAAMLIERSSDPGKTGWYRYFAYDCEASFPGISTGPMKKVDDIICDSRYSDIEST 180
|||

Db 142 TFRPAAMLIERSSDPGKTGWYRYFAYDCEASFPGISTGPMKKVDDIICDSRYSDIEST 201
|||

QY 181 EGEVIFRALDPAPKIEDPYSPIQNLLKITNLRIFKVKLHITGDLNLLDSRMEIREKYVA 240
|||

Db 202 EGEVIFRALDPAPKIEDPYSPIQNLLKITNLRIFKVKLHITGDLNLLDSRMEIREKYVA 261
|||

QY 241 VYDMVVRGNCFCYGHASECAPVDGFNEEVEGVMVHGHCRCRHTKGLNCELMDFFYHDLPW 300
|||

Db 262 VYDMVVRGNCFCYGHASECAPVDGVNVEEVEGVMVHGHCRCRHTKGLNCELMDFFYHDLPW 321
|||

QY 301 RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGGVCDCCQHNMTGRNCEQCKPFY 360
|||

Db 322 RPAEGRNSNACKKNCNEHSISCHFDMAVFLATGNVSGGVCDNQHNTMGRNCEQCKPFY 381
|||

QY 361 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTGLIAGQCRCRKLNVEGEHCDCVK 420
:|

Db 382 FQHPERDIRDPNICEPCTCDPAGSENGGICDGYTDFSVGLIAGQCRCRKLHVEGERCDVK 441
:|

QY 421 EGFYDLSSDPFGCKSCACNPLGTIPGNGPCDSETGHGYCKRLVTGQHCDCQCLPEHWGLS 480
|||

Db 442 EGFYDLSEADPYGCKSCACNPLGTIPGNGPCDSETGYCYCKRLVTGQRCDCQCLPQHWGLS 501
|||

QY 481 NDLGCRPCDCDLGGALNNSCFAESGCSCRPHMIGRQCNEVEPGYYFATLDHYLYEAE 540
|||

Db 502 NDLGCRPCDCDLGGALNNSCSEDSGCSCLFHMIGRQCNEVESGYFTTLDHYLYEAE 561
|||

QY 541 ANLPGVSIYERQYIQRIPSWTGTAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 600
Db 562 ANLPGVVVVERQYIQRIPSWTGTGFRVPEGAYLEFFIDNIPYSMEYEILIRYEPQLP 621
QY 601 DHWEKAVITVORPGRIPSTSSRCNTIPDDNDQVVSLSLSPGSRVYVLPVPCFEKGTNYTVR 660
Db 622 DHWEKAVITVORPGRIPASSRCNTVPDDNDQVVSLSLSPGSRVYVLPVPCFEKGMNYYTVR 681
QY 661 LELPQYTSDDSDVESPYTLIDSLVLMPCYCKSLDIFTVGGSGDGVVNSAWETFORYRCLE 720
Db 682 LELPQYTAGSGDVESPYTFIDSLVLMPCYCKSLDIFTVGGSGDGVVNSAWETFORYRCLE 741
QY 721 NSRSVVKTPMTDVCNIIIFSISALLHQTGLACEDPQGLSSVCDPNGGQCQCRPNVVGR 780
Db 742 NSRSVVKTPMTDVCNIIIFSISALIHQTGLACEDPQGLSSVCDPNGGQCQCRPNVVGR 801
QY 781 TCNRCAPGTGFGPGCKPCECHLOGSVNAFCNPVTGQCHCFQGVYARQCDRLCPGHWF 840
Db 802 TCNRCAPGTGFGPGCKPCECHLOGSVNAFCNPVTGQCHCFQGVYARQCDRLCPGHWF 861
QY 841 PSCQPCQNGHADDCTPVTGECNLCQDVTGHCNRCERCLAGYGYGDBIIGSGDHCRCPCPD 900
Db 862 PSCQPCQNGHALDCTVTGECNLCQDVTGHCNRCERCLAGYGYGDBIIGSGDHCRCPCPD 921
QY 901 GPDGSGQFARSCYQDPVTLQACVCDPQYIGSRCDCCASGYEGNPEVGGSCQPCQCHNN 960
Db 922 GPDGSGQFARSCYQDPVTLQACVCDPQYIGSRCDCCASGYEGNPEVGGSCQPCQCHNN 981
QY 961 IDTTDEACDKETGRCLKCLYHTEGHCQFCRFGYVGDALRQDCKVCNLYLGTVEHCN 1020
Db 982 IDTTDEACDKETGRCLKCLYHTEGHCQFCRFGYVGDALRQDCKVCNLYLGTVEHCN 1041
QY 1021 GSDCQCDKATGQCLPLNVQNCDCRCPNTWQASGTGDCPCNNAHSGPSCNEFTG 1080
Db 1042 GSDCHCDKATGQCLPLNVQNCDCRCPNTWQASGTGDCPCNNAHSGPSCNEFTG 1101
QY 1081 QCQCMFGGGRCTSECQELFWGDDPVECRACDPRGIETPOCDSTGQCVCEVGEGR 1140
Db 1102 QCQCMFGGGRCTSECQELFWGDDPVECRACDPRGIETPOCDSTGQCVCEVGEGR 1161
QY 1141 CDKCTRGYSVGFDPCTPCHQCFALWDVIIAELTNRTHRFLEKAKALKISGVIGPYRETVD 1200
Db 1162 CDKCTRGYSVGFDPCTPCHQCFALWDIIIGELTNRTHRFLEKAKALKISGVIGPYRETVD 1221
QY 1201 SVERKVEIKDILAQSPAAPLKNIGNLFEBAEKLIKDVTEMAQVEVKLSDDTTSQNST 1260
Db 1222 SVEKVEIKDILAQSPAAPLKNIGNLFEBAEKLIKDVTEMAQVEVKLSDDTTSQNST 1281
QY 1261 AKELSLQTEAESLQNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTTE 1320
Db 1282 AGELGALQAEAESLQNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTTE 1341
QY 1321 PNSTVEQSALMRDRVEDVMMERESQFKEQBEQARLLDELAKLQSLDLSAAAEWTCGTP 1380
Db 1342 PNSTVEQSALMRDRVEDVMMERESQFKEQBEQARLLDELAKLQSLDLSAAAEWTCGTP 1401
QY 1381 PGASCSETECGGPNCRTEDEGERKCGGPGGGLVTVAHNAWOKAMDLDQDVLALAEVEQL 1440
Db 1402 PGASCSETECGGPNCRTEDEGERKCGGPGGGLVTVAHNAWOKAMDLDQDVLALAEVEQL 1461
QY 1441 SKMVSEAKLRADAEAKQSAEDILLKTNATKEMKDKSNEELRNLIKQIRNFLTQDSADLDSI 1500
Db 1462 SKMVSEAKLRADAEAKQSAEDILLKTNATKEMKDKSNEELRNLIKQIRNFLTQDSADLDSI 1521
QY 1501 EAVANEVLKMEMPSTPOOLQNLNTERIRVESLSQVEVILQSAADIAEAEMLEAEAKRA 1560
Db 1522 EAVANEVLKMEMPSTPOOLQNLNTERIRVESLSQVEVILQSAADIAEAEMLEAEAKRA 1581
QY 1561 SKSATDVKVTDVMVKEALEAEAKQVAAEAKIAKQADEIDQGTQNLNLTISIESETAASETL 1620
Db 1582 SKSATDVKVTDVMVKEALEAEAKQVAAEAKIAKQADEIDQGTQNLNLTISIESETAASETL 1641

QY 1621 FNASQRISELERNVVEELKRAAQAQNSGEAEYIEKVYVTVKQSAEDVKKTLTGELDEKYYKV 1680
Db 1642 TNASQRISELERNVVEELKRAAQAQNSGEAEYIEKVYVTVKQSAEDVKKTLTGELDEKYYKV 1701
QY 1681 ENLIACKTEESADARRKAEMLQNEAKTLLAQANSKLOLLKDLERKYEDNORYLEDKAOEL 1740
Db 1702 ESLLACKTEESADARRKAEMLQNEAKTLLAQANSKLOLLKDLERKYEDNORYLEDKAOEL 1761
QY 1741 ARLEGEVRSLLKDISOKVAVYSTCL 1765
Db 1762 VRLEGEVRSLLKDISOKVAVYSTCL 1786

RESULT 3
MMRTS
laminin beta-2 chain precursor - rat
N/Alternate names: laminin chain B3; S-laminin
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 10-Dec-1999
C/Accession: S03539
R/Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.
Nature 338, 229-234, 1989
A/Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the neur.
A/Reference number: S03539; MUID:89159410; PMID:2922051
A/Accession: S03539
A/Molecule type: mRNA
A/Residues: 1-1801 <HUN>
A/Cross-references: EMBL:X16563; NID:G57250; PIDN:CAA34561.1; PID:G57251
C/Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C/Function:
A/Description: interact with cells and with other basement membrane proteins to promote
C/Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C/Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular
F/1-35/Domain: signal sequence #status predicted <SIG>
F/36-1801/Product: laminin beta-2 chain #status predicted <MAT>
F/36-285/Domain: VI <DOM6>
F/286-555/Domain: V <DOM5>
F/286-347/Domain: laminin-type EGF-like homology <LE01>
F/350-410/Domain: laminin-type EGF-like homology <LE02>
F/413-470/Domain: laminin-type EGF-like homology <LE03>
F/473-522/Domain: laminin-type EGF-like homology <LE04>
F/525-555/Domain: laminin-type EGF-like homology #status atypical <LE05>
F/556-784/Domain: IV <DOM4>
F/786-831/Domain: laminin-type EGF-like homology <LE06>
F/788-1196/Domain: III <DOM3>
F/834-877/Domain: laminin-type EGF-like homology <LE07>
F/880-927/Domain: laminin-type EGF-like homology <LE08>
F/930-986/Domain: laminin-type EGF-like homology <LE09>
F/989-1038/Domain: laminin-type EGF-like homology <LE10>
F/1041-1095/Domain: laminin-type EGF-like homology <LE11>
F/1098-1143/Domain: laminin-type EGF-like homology <LE12>
F/1146-1190/Domain: laminin-type EGF-like homology <LE13>
F/1197-1412/Domain: II <DOM2>
F/1197-1412/Region: heptad repeats
F/1413-1445/Domain: alpha <ALP>
F/1446-1801/Region: heptad repeats
F/1446-1801/Domain: I <DOM1>
F/45-50/Disulfide bonds: #status predicted
F/251,371,1088,1252,1311,1351,1502/Binding site: carbohydrate (Asn) (covalent) #status I
F/1193,1196,1800/Disulfide bonds: interchain #status predicted

Query Match 52.7%; Score 5084; DB 1; Length 1801;
Best Local Similarity 51.5%; Pred. No. 7.6e-186;
Matches 910; Conservative 303; Mismatches 534; Indels 20; Gaps 8;
QY 8 GCAEGSCYPATGDLIGRAQKLSVTSTCGLHKHPYCIIVSHLQEDKKCFICNSQDPYHET 67
Db 44 GCSRGSCYPATGDLIGRAQKLSVTSTCGLHKHPYCIIVSHLQEDKKCFICNSQDPYHET 103
QY 68 LNPDSHLIENVVTVFAPNRLKIWQSENGVENVTIQDLAEAFHFTHLINTFKTFRPAA 127
Db 104 DNPNSHRIQNVTVTFAPNRLKIWQSENGVENVTIQDLAEAFHFTHLINTFKTFRPAA 163

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:28 ; Search time 98.6077 Seconds
(without alignments)
11631.021 Million cell updates/sec

Title: US-10-037-182-4
Perfect score: 19876
Sequence: 1 DLYCKLVGGPVAGDPNQTI.....QGKALTQRHAKPSVSPLLWH 3635

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	15839	79.7	3695	4 Q8TDF8	Q8tdf8 homo sapien
2	5012.5	25.2	3712	5 Q9VRW0	Q9vrw0 drosophila
3	4820.5	24.3	3704	5 P91904	P91904 caenorhabdi
4	4129	20.8	794	11 Q8R3Y7	Q8r3y7 mus musculu
5	3934.5	19.8	1486	4 O14637	O14637 homo sapien
6	2530	12.7	3102	5 O45614	O45614 caenorhabdi
7	2450	12.3	1806	4 Q96TG0	Q96tg0 homo sapien
8	2407.5	12.1	670	4 Q9BTT3	Q9btt3 homo sapien
9	2380	12.0	3375	5 Q8IP51	Q8ip51 drosophila
10	2359	11.9	3367	5 Q9XZC9	Q9xzc9 drosophila
11	2320	11.7	452	11 Q80VE8	Q8ove8 mus musculu
12	2154	10.8	1725	6 Q867A1	Q867a1 canis famil
13	2084.5	10.5	2731	5 Q9VJT5	Q9vjt5 drosophila
14	2067	10.4	1725	11 P70570	P70570 rattus norv
15	1683.5	8.5	1799	11 Q8R0Y0	Q8r0y0 mus musculu
16	1676	8.4	1792	13 O57484	O57484 gallus gall

17	1596	8.0	1785	13 Q8JHV7	Q8jhw7 brachydanio
18	1579.5	7.9	1761	4 Q86XN2	Q86xn2 homo sapien
19	1536	7.7	1827	13 Q8JHV6	Q8jhw6 brachydanio
20	1458	7.3	1631	4 Q9Y6U6	Q9y6u6 homo sapien
21	1405	7.1	1623	5 Q9U3U7	Q9u3u7 anopheles g
22	1361.5	6.8	1254	11 Q91VV0	Q91vv0 mus musculu
23	1266.5	6.4	1593	13 Q8JHV8	Q8jhw8 brachydanio
24	1212	6.1	254	11 P70636	P70636 rattus norv
25	1198	6.0	1007	13 Q90ZN3	Q90zn3 gallus gall
26	1144.5	5.8	1546	4 Q9NS27	Q9ns27 homo sapien
27	1143.5	5.8	695	11 Q8C9J2	Q8c9j2 mus musculu
28	1136.5	5.7	1546	4 O75445	O75445 homo sapien
29	1122	5.6	885	11 Q8BSJ0	Q8bsj0 mus musculu
30	1109.5	5.6	1461	11 Q9JLP3	Q9jlp3 mus musculu
31	1083	5.4	1067	5 O44565	O44565 caenorhabdi
32	1057	5.3	1512	11 Q8K3K1	Q8k3k1 rattus norv
33	1033	5.2	1574	11 O88281	O88281 rattus norv
34	984	5.0	4117	5 Q8IRV9	Q8irv9 drosophila
35	984	5.0	4179	5 Q9W4Y4	Q9w4y4 drosophila
36	979.5	4.9	4228	5 Q8IRV8	Q8irv8 drosophila
37	969	4.9	4223	5 Q8MPN3	Q8mpn3 drosophila
38	968	4.9	1664	5 Q9TVQ2	Q9tvq2 caenorhabdi
39	952	4.8	1086	4 Q8TAS6	Q8tas6 homo sapien
40	923.5	4.6	1196	6 Q867A2	Q867a2 canis famil
41	919.5	4.6	1190	6 Q8HZI9	Q8hzi9 equus cabal
42	916	4.6	1026	5 Q8SWY0	Q8swy0 drosophila
43	879.5	4.4	1168	5 Q967S8	Q967s8 schistocerc
44	872.5	4.4	3215	5 Q8IRV7	Q8irv7 drosophila
45	857.5	4.3	2447	5 Q9NEF9	Q9nef9 drosophila

ALIGNMENTS

RESULT 1

ID	Q8TDF8	PRELIMINARY;	PRT;	3695 AA.
AC	Q8TDF8;			
DT	01-JUN-2002 (TReMBLrel. 21, Created)			
DT	01-JUN-2002 (TReMBLrel. 21, Last sequence update)			
DT	01-OCT-2003 (TReMBLrel. 25, Last annotation update)			
DE	Laminin alpha5 chain precursor.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21935381; PubMed=11821406;			
RA	Doi M., Thyboll J., Kortessmaa J., Jansson K., Iivanainen A.,			
RA	Parvarden M., Timpl R., Hedin U., Swedenborg J., Tryggvason K.;			
RT	"Recombinant Human Laminin-10 (alphasbetaigammal). Production,			
RT	Purification, and Migration-Promoting Activity on Vascular Endothelial			
RT	Cells."			
RL	J. Biol. Chem. 277:12741-12748 (2002).			
DR	EMBL; AF443072; AAM12527.1; -			
DR	GO; GO:0005578; C:extracellular matrix; IEA.			
DR	GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.			
DR	GO; GO:0004872; F:receptor activity; IEA.			
DR	GO; GO:0005198; F:structural molecule activity; IEA.			
DR	GO; GO:0003743; F:translation initiation factor activity; IEA.			
DR	GO; GO:0005215; F:transporter activity; IEA.			
DR	GO; GO:0006413; P:translational initiation; IEA.			
DR	GO; GO:0006810; P:transport; IEA.			
DR	InterPro; IPR008985; ConA like lec_gl.			
DR	InterPro; IPR006209; EGF like.			
DR	InterPro; IPR000034; Laminin B.			
DR	InterPro; IPR002049; Laminin_EGF.			
DR	InterPro; IPR001791; Laminin_G.			
DR	InterPro; IPR008211; LamNT.			
DR	InterPro; IPR008212; Lam N2.			
DR	InterPro; IPR001638; SBP_bac_3.			
DR	InterPro; IPR001950; TIF_SUI1.			

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DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00052; laminin_B; 1.
DR Pfam; PF00053; laminin_EGF; 18.
DR Pfam; PF00054; laminin_G; 2.
DR Pfam; PF00055; laminin_Nterm; 1.
DR PRINTS; PR00011; EGF_LAMININ.
DR ProDom; PD003031; Laminin_B; 1.
DR ProDom; PD002082; Lam_N2; 1.
DR SMART; SM00180; EGF_Lam; 20.
DR SMART; SM00281; LamB; 1.
DR SMART; SM00282; LamG; 5.
DR SMART; SM00136; LamNT; 1.
DR PROSITE; PS00022; EGF_1; 19.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 19.
DR PROSITE; PS00025; LAM_G_DOMAIN; 5.
DR PROSITE; PS01039; SBP_BACTERIAL_3; 1.
DR PROSITE; PS01118; SUII_1; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
KW Laminin EGF-like domain; Signal.
FT SIGNAL 1 35 POTENTIAL.
FT CHAIN 36 3695 LAMININ ALPHAS CHAIN.
SQ SEQUENCE 3695 AA; 399642 MW; 69703B52536EFOA3 CRC64;

Query Match 79.7%; Score 15839; DB 4; Length 3695;
Best Local Similarity 79.4%; Pred. No. 0;
Matches 2874; Conservative 277; Mismatches 452; Indels 18; Gaps 8;

QY 1 DLYCKLVGGVAGGDPNQTIQGYCDICTAANSNKAHPVSNADTGTERWQSPPLSRGLE 60
DB 79 DLYCKLVGGVAGGDPNQTIQGYCDICTAANSNKAHPASNAIDGTERWQSPPLSRGLE 138

QY 61 YNEVNVTLDLGGVFHVAYVLIKEFANSRPDLWVLERSTDFGHTYQPWQFASSKRDCLER 120
DB 139 YNEVNVTLDLGGVFHVAYVLIKEFANSRPDLWVLERSMDFGRTYQPWQFASSKRDCLER 198

QY 121 FGPRTLETRITQDDVICTEYSRIVPLENGEIVVSLVNGRPGALNFYSPLLRDFTKATN 180
DB 199 FGPQTLERITRDAAICTEYSRIVPLENGEIVVSLVNGRPGAMNFYSPLLRFTKATN 258

QY 181 IRLRFLRINTLLGLHLMGKALRDPVTRRRYYYSIKDISIGRCVCHGHADVCDAKPLDPF 240
DB 259 VRLRFLRINTLLGLHLMGKALRDPVTRRRYYYSIKDISIGRCVCHGHADVCDAKPLDPF 318

QY 241 RLQACQHNTCGGSCDRCCPGFNQOPWKPAATDSANECQSCNCHGHAYDCYDPEVDRRN 300
DB 319 RLQCTCQHNTCGGTCDRCPCGFGNQOPWKPATANSANECQSCNCHGHATDCYDPEVDRRR 378

QY 301 ASQNQDNVYQGGVCLDCQHTTGINCERCLPGFFRAPDQPLDSPHVCPCDCESDFTDG 360
DB 379 ASQSLDGTYYQGGGVCIQCQHTAGVNCERCLPGFYRSPNHPDLSPHVCRCNCESDFTDG 438

QY 361 TCEDLTGRCYCRPNFTGELCAACAEGYTDFPHCYPLPSFPNNDTREQVLPAGQIVNCDN 420
DB 439 TCEDLTGRCYCRPNFSGERCDCVCAEGFTGFPSCYPTPS-SSNDTREQVLPAGQIVNCDN 497

QY 421 AAGTQGNACRKDPRLGRVCVKPNFRGAHCELCAPGFHGPSCHPCQCSPPGVANSLCDPES 480
DB 498 AAGTQGNACRKDPRLGRVRCCLCKPNFGQTHCELCAPGFYGPQCPCQCSPPGVADDRCDPDT 557

QY 481 GQCMRTQFEGDRCDHICALGVFHFPLCQLCGCSFAGTLPPEGCEAGRCQCRPGFDGPHCD 540
DB 558 GQCRCRVGFEGATCDRCAPGYFHFPLCQLCGCSFAGTLPPEGCEAGRCQCRPGFDGPHCD 617

QY 541 RCLPGYHGYPDCHACACDPRGALDQCGGVGLCHCRPGNTGATCQCSPPGYGFPSCIPC 600
DB 618 RCRPGYHGFPCQACTCDPRGALDQCGAGGLCRCPGYGTGTACQCSPPGFHGFPCVPC 677

QY 601 HCSADGSLHTTCDPTTGQCRORPRVTGLHCDMCPVGAYNFPYCEAGSCHPAGLAPANPAL 660
DB 678 HCSAEGSLHAACDPRSGQCSORPRVTGLRCDTCTVPGAYNFPYCEAGSCHPAGLAPVDPAL 737
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:25:32 ; Search time 48.4494 Seconds
(without alignments)
10415.614 Million cell updates/sec

Title: US-10-037-182-6
Perfect score: 9754
Sequence: 1 MGLQLLAFSLALCRARVR.....EVRSLKDISQKVAVYSTCL 1786

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9754	100.0	1786	2	AAW50893 Human lam
2	9754	100.0	1786	3	AAB16522 Human lam
3	9754	100.0	1786	3	AAB19797 Human lam
4	9754	100.0	1786	3	AAB48448 Human lam
5	9754	100.0	1786	4	AAB90788 Human she
6	9754	100.0	1786	5	ABB81590 Human lam
7	9738	99.8	1786	5	AAM48896 Laminin p
8	9718.5	99.6	1785	2	AAY15461 Human lam
9	9654	99.0	1765	3	AAB19798 Human lam
10	9654	99.0	1765	3	AAB48449 Human lam
11	9654	99.0	1765	5	ABB81591 Human lam
12	9144	93.7	1786	3	AAB19799 Mouse lam
13	9144	93.7	1786	3	AAB48450 Mouse lam
14	9144	93.7	1786	5	ABB81592 Mouse lam
15	9087	93.2	1776	2	AAW50894 Mouse lam
16	8967.5	91.9	1764	1	AAP91672 Primary a
17	8873	91.0	1725	3	AAB19800 Mouse lam
18	8873	91.0	1725	3	AAB48451 Mouse lam
19	8873	91.0	1725	5	ABB81593 Mouse lam
20	5088.5	52.2	1801	2	AAW50895 Rat lamin
21	5088.5	52.2	1801	7	ADE60383 Rat Prote
22	5052.5	51.8	1798	2	AAW50896 Human lam
23	5052.5	51.8	1798	7	ADE60385 Human pro
24	5051.5	51.8	1799	5	AAM50359 Mouse lam
25	4921.5	50.5	1798	5	AAU84346 Protein L

26	4921.5	50.5	1798	5	AAW50360 Human lam
27	3881	39.8	822	5	AAW48897 Laminin p
28	3852	39.5	1788	4	ABB62995 Drosophil
29	3832.5	39.3	1761	2	AAAY15457 Human lam
30	3625.5	37.2	1670	7	ADE07851 Novel pro
31	3076.5	31.5	1101	7	ADE28641 Human NOV
32	3044.5	31.2	1105	2	AAAY15459 SEQ ID 5
33	2776	28.5	466	2	AAAR07447 Human lam
34	2348	24.1	527	3	AAB58995 Breast an
35	2115	21.7	434	1	AAP60109 Human B1
36	1787	18.3	315	6	ABU70520 Human adi
37	1762.5	18.1	1639	4	ABB59807 Drosophil
38	1682	17.2	1605	3	AAB19805 Mouse lam
39	1682	17.2	1605	3	AAB48454 Mouse lam
40	1682	17.2	1605	5	ABB81596 Mouse lam
41	1680.5	17.2	1609	3	AAB19801 Human lam
42	1680.5	17.2	1609	3	AAB48452 Human lam
43	1680.5	17.2	1609	5	ABB81594 Human lam
44	1680.5	17.2	1609	7	ADC01887 Human lam
45	1680.5	17.2	1617	3	AAB19803 Human lam

ALIGNMENTS

RESULT 1
AAW50893
ID AAW50893 standard; protein; 1786 AA.
XX
AC AAW50893;
XX
DT 07-DEC-1998 (first entry)
XX
DE Human laminin B1 chain.
XX
KW Laminin; human; beta-amyloid; amyloidosis; Alzheimer's disease;
KW Down's syndrome; hereditary cerebral haemorrhage; inflammation;
KW malignancy; Familial Mediterranean Fever; multiple myeloma;
KW type II diabetes; prion disease; Creutzfeldt-Jacob disease; CJD;
KW Gerstmann-Strausler syndrome; kuru; scrapie; haemodialysis;
KW carpal tunnel syndrome; senile cardiac amyloid polyneuropathy;
KW Familial Amyloidotic Polyneuropathy; thyroid carcinoma; diagnosis;
KW therapy.
XX
OS Homo sapiens.
XX
PN WO9815179-A1.
XX
PD 16-APR-1998.
XX
PF 08-OCT-1997; 97WO-US018145.
XX
PR 08-OCT-1996; 96US-0027981P;
XX (UNIW) UNIV WASHINGTON.
XX
PI Castillo G, Snow AD;
XX
DR WPI; 1998-240534/21.
XX
PT Use of laminin and fragments - for developing products for use in the
diagnosis and treatment of amyloid disease, e.g. Alzheimer's disease or
CJD.
XX
PS Claim 15; Page 86-89; 132pp; English.
XX
CC This is the amino acid sequence of the human laminin B1 chain. The
primary object of the invention is to use laminin, laminin-derived
protein fragments and/or laminin-derived polypeptides as potent
inhibitors of amyloid formation, deposition, accumulation and/or
persistence in Alzheimer's disease and other amyloidoses. The laminin
products (see AAW50888-98) may include mouse or human laminin A or A1
chain, laminin B1 or B2 chain, laminin A2 chain (merosin), laminin G1

CC chain, the globular repeats of the laminin A1 chain and the beta-amyloid
CC binding domain of the laminin A chain. A claimed method for treating an
CC amyloid disease comprises administering a polypeptide having a
CC conformational similarity to a fragment of a laminin protein. A method
CC for diagnosing an amyloid disease involves determining levels of laminin
CC in a sample. Production of laminin or its fourth globular repeat in vivo
CC provides a method for in vivo inhibition of beta-amyloid amyloidosis. The
CC products and methods can be used for the diagnosis, prognosis, monitoring
CC and treatment of amyloidosis such as Alzheimer's disease, Down's syndrome
CC and hereditary cerebral haemorrhage with amyloidosis of the Dutch type
CC (where the specific amyloid is the beta-amyloid protein), the amyloidosis
CC associated with chronic inflammation, various forms of malignancy and
CC Familial Mediterranean Fever (AA amyloid or inflammation-association
CC amyloidosis), the amyloidosis associated with multiple myeloma and other
CC B-cell abnormalities (AL amyloid), the amyloidosis associated with type
CC II diabetes (amylin or islet amyloid), the amyloidosis associated with
CC prion diseases including Creutzfeldt-Jacob disease, Gertsmann-Straussler
CC syndrome, kuru and animal scrapie (Prp amyloid), the amyloidosis
CC associated with long-term haemodialysis and carpal tunnel syndrome (beta
CC 2-microglobulin amyloid), the amyloidosis associated with senile cardiac
CC amyloid and Familial Amyloidotic Polyneuropathy (prealbumin or
CC transthyretin amyloid), and the amyloidosis associated with endocrine
CC tumours such as medullary carcinoma of the thyroid (variant of
CC procalcitonin)
xx
SQ Sequence 1786 AA;

Query Match 100.0%; Score 9754; DB 2; Length 1786;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLLQLLAFSFLALCRARVRAQEPFSGAEGSCYPATGDLILGKRAQLSVTSTCGLHK 60
DB 1 MGLLQLLAFSFLALCRARVRAQEPFSGAEGSCYPATGDLILGKRAQLSVTSTCGLHK 60
QY 61 PEPYCIVSHLQEDKKCFICNSQDPYHETLNPDLSHLEIENVVTFAPNRLKIWQSENGVEN 120
DB 61 PEPYCIVSHLQEDKKCFICNSQDPYHETLNPDLSHLEIENVVTFAPNRLKIWQSENGVEN 120
QY 121 VTQLDLAEAFHFTHLIMTFTFRPAAMLIERSDFGKTGWVYRYPAYDCEASFPGISTG 180
DB 121 VTQLDLAEAFHFTHLIMTFTFRPAAMLIERSDFGKTGWVYRYPAYDCEASFPGISTG 180
QY 181 PMKKVDDIICDSRYSDIEPSTEGEVIIFRALDPAFKIEDPYSPIQNLLKITNLRIFVKVL 240
DB 181 PMKKVDDIICDSRYSDIEPSTEGEVIIFRALDPAFKIEDPYSPIQNLLKITNLRIFVKVL 240
QY 241 HTLGDNLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGENEEVEGMVHGCMC 300
DB 241 HTLGDNLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGENEEVEGMVHGCMC 300
QY 301 RHNTKGLNCELMDFYHDLFWRPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGG 360
DB 301 RHNTKGLNCELMDFYHDLFWRPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGG 360
QY 361 VCDDCQHNTMGRNCEQCKPFYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSG 420
DB 361 VCDDCQHNTMGRNCEQCKPFYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSG 420
QY 421 LIAGQCRCKLNVEGEHCDVCKEGFYDLSSDPFGCKSCACNPLGTIPGNGPCDSETGHCY 480
DB 421 LIAGQCRCKLNVEGEHCDVCKEGFYDLSSDPFGCKSCACNPLGTIPGNGPCDSETGHCY 480
QY 481 CKRLVTGQHCDCQLPEHWGLSNDLDGCRPCDCDLGGALNNSCFAESGQSCRPHMIGRQC 540
DB 481 CKRLVTGQHCDCQLPEHWGLSNDLDGCRPCDCDLGGALNNSCFAESGQSCRPHMIGRQC 540
QY 541 NEVEPGYYFATLDHLYLAEAEANLPGVSIIVERQYIQDRIPSWTGAGFVRVPEGAYLEFF 600
DB 541 NEVEPGYYFATLDHLYLAEAEANLPGVSIIVERQYIQDRIPSWTGAGFVRVPEGAYLEFF 600
QY 601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPTSRRCGNTIPDDNQVWSLSPG 660
DB 601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPTSRRCGNTIPDDNQVWSLSPG 660

DB 601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPTSRRCGNTIPDDNQVWSLSPG 660
QY 661 SRYVVLPRPVCFEKGNTYVRLELPQYTSDDSDVESPYTLIDSLVMPYCKSLDIFTVGG 720
DB 661 SRYVVLPRPVCFEKGNTYVRLELPQYTSDDSDVESPYTLIDSLVMPYCKSLDIFTVGG 720
QY 721 SGDGVTNSAWETFORYRCLENSRSVVKTPMTDVCRNIIIFSALLHQTGLACECDPQGS 780
DB 721 SGDGVTNSAWETFORYRCLENSRSVVKTPMTDVCRNIIIFSALLHQTGLACECDPQGS 780
QY 781 LSSVCDPNGGQCQCRPNVVGRTNRCNRCAPGTFFGFGSPGCKPCECHLQGSVNAFCNPVTGQC 840
DB 781 LSSVCDPNGGQCQCRPNVVGRTNRCNRCAPGTFFGFGSPGCKPCECHLQGSVNAFCNPVTGQC 840
QY 841 HCFQGVYARQCDRCLPGHWGFPSCQPCQCNHGADDCDPVTGECNLQCDYTMGHNCERCLA 900
DB 841 HCFQGVYARQCDRCLPGHWGFPSCQPCQCNHGADDCDPVTGECNLQCDYTMGHNCERCLA 900
QY 901 GYGGDPIIGSGDHCRPCPCPDGPDGSRQFARSCYQDPVTLQACVCDPGYIGSRCDDCAS 960
DB 901 GYGGDPIIGSGDHCRPCPCPDGPDGSRQFARSCYQDPVTLQACVCDPGYIGSRCDDCAS 960
QY 961 GYFGNPSEVGGSCQPCQCHNNIDTTDPEACDKETGRCLKCLYHTEGHCQFCRFGYGGDA 1020
DB 961 GYFGNPSEVGGSCQPCQCHNNIDTTDPEACDKETGRCLKCLYHTEGHCQFCRFGYGGDA 1020
QY 1021 LRQDCRKVCNYLGTVOEHCHGSDCCQCDKATGQCCLCLPNVIGQNCRCAPNTWQLASGTG 1080
DB 1021 LRQDCRKVCNYLGTVOEHCHGSDCCQCDKATGQCCLCLPNVIGQNCRCAPNTWQLASGTG 1080
QY 1081 CDPNCNAAHSFGPSCNEFTGQCQCMPGFGGRTCECOELFWGDDPVECRACDCDPRGIE 1140
DB 1081 CDPNCNAAHSFGPSCNEFTGQCQCMPGFGGRTCECOELFWGDDPVECRACDCDPRGIE 1140
QY 1141 TPQCDQSTGQCVCEGVEGPRCDKCTRGYSVGFDPCTPCHQCQFALWDVIIAELTNRTHRF 1200
DB 1141 TPQCDQSTGQCVCEGVEGPRCDKCTRGYSVGFDPCTPCHQCQFALWDVIIAELTNRTHRF 1200
QY 1201 LEKAKALKISGVIGPYRETVDVSVERKVSEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDV 1260
DB 1201 LEKAKALKISGVIGPYRETVDVSVERKVSEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDV 1260
QY 1261 TEMMAQVEVKLSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDS 1320
DB 1261 TEMMAQVEVKLSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDS 1320
QY 1321 ITKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVMMERESQFKEKEQEEQARLLDE 1380
DB 1321 ITKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVMMERESQFKEKEQEEQARLLDE 1380
QY 1381 LAGKLQSLDLSAAAEWTCGTPPGASCSETECGGNCRCTDEGERKCGGPGCGGLVTVAHNA 1440
DB 1381 LAGKLQSLDLSAAAEWTCGTPPGASCSETECGGNCRCTDEGERKCGGPGCGGLVTVAHNA 1440
QY 1441 WQKAMDLDQDVLALAEVEQLSKMVSEAKLRADAEAKQSAEDILLKTNATKEKMDKSNEEL 1500
DB 1441 WQKAMDLDQDVLALAEVEQLSKMVSEAKLRADAEAKQSAEDILLKTNATKEKMDKSNEEL 1500
QY 1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKMEMPSTPQQLQNLTEDIRERVESLSQVEVI 1560
DB 1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKMEMPSTPQQLQNLTEDIRERVESLSQVEVI 1560
QY 1561 LQHSAAADIAEAEMLEAEAKRASKSATDVKTADVMVKEALEEAEAKQVAAEAKIKQADEDI 1620
DB 1561 LQHSAAADIAEAEMLEAEAKRASKSATDVKTADVMVKEALEEAEAKQVAAEAKIKQADEDI 1620
QY 1621 QGTQNLITSIESETAASEETLFNASQRISELERNVEELKRKAQNSGEAEYIEKVVTYVK 1680
DB 1621 QGTQNLITSIESETAASEETLFNASQRISELERNVEELKRKAQNSGEAEYIEKVVTYVK 1680
QY 1681 QSAEDVKKTLTGELDEKYYKVENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLL 1740
DB 1681 QSAEDVKKTLTGELDEKYYKVENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLL 1740

QY 1741 KDLERKYEDNORYLEDKAQELARLEGEVRSLLKDISQKVAVYSTCL 1786
DB 1741 KDLERKYEDNORYLEDKAQELARLEGEVRSLLKDISQKVAVYSTCL 1786

RESULT 2
AAB16522
ID AAB16522 standard; protein; 1786 AA.

XX AAB16522;
XX 27-OCT-2000 (first entry)

DE Human laminin protein sequence.

XX Angiogenesis-inhibiting protein receptor; angiogenesis; angiostatin;
KW endostatin; plasminogen; laminin; treatment; wound healing; solid tumour;
KW psoriasis; scleroderma; myocardial angiogenesis; Crohn's disease;
KW cerebral collateral; arteriovenous malformation; rubeosis; cancer;
KW diabetic retinopathy; arthritis; wound healing; peptic ulcer;
KW Helicobacter related disease; fracture; cat scratch fever.

XX Homo sapiens.

XX WO200032631-A2.

PN 08-JUN-2000.

PF 06-DEC-1999; 99WO-US028897.

PR 04-DEC-1998; 98US-00206059.

XX (ENTR-) ENTREMED INC.

PA Macdonald NJ, Sim KL;

PI WPI; 2000-412290/35.

XX New angiogenesis-inhibiting protein receptors, useful in methods for
PT treating diseases and processes that are mediated by angiogenesis, such
PT as solid tumors, psoriasis, scleroderma and myocardial angiogenesis.

PS Claim 1; Fig 6A; 100pp; English.

XX This invention relates to angiogenesis-inhibiting protein receptors, and
CC the DNA sequences encoding them. Angiogenesis is the generation of new
CC blood vessels into a tissue, and normally occurs in wound healing, foetal
CC and embryonal development and the formation of the corpus luteum,
CC endometrium and placenta. Angiostatin is a protein (see AAB16450 and
CC AAA68202) involved in angiogenesis, and has an amino acid sequence
CC similar to that of a plasminogen fragment (see murine plasminogen
CC AAB16490). Angiostatin has the ability to inhibit angiogenesis.

CC Endostatin is also an angiogenesis inhibiting protein (see AAB16451 and
CC AAA68203). Sequences AAA68242 and AAB16522 represent coding and protein
CC sequences of human laminin. Laminin is an angiostatin binding protein,
CC and some of the peptides of the invention share homology with regions of
CC laminin. Peptides AAB16452-B16521 (excluding AAB16490) are the
CC angiogenesis-inhibiting protein receptor fragments of the invention. The
CC peptides bind either angiostatin or endostatin and can be used in methods
CC for treating diseases and processes that are mediated by angiogenesis,
CC such as solid tumors, psoriasis, scleroderma, myocardial angiogenesis,
CC Crohn's disease, cerebral collaterals, arteriovenous malformations,
CC rubeosis, diabetic retinopathy, arthritis, wound healing, peptic ulcers,
CC Helicobacter related diseases, fractures, placenta and cat scratch
CC fever. They are useful for the detection and prognosis of cancer. DNA
CC sequences A628204-A628241 encode the peptides of the invention

XX Sequence 1786 AA;

Query Match 100.0%; Score 9754; DB 3; Length 1786;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLLQLLAFSLALCRARVRAQEPFESYGAEGSCYPATGDLILLIGRAQKLSVTSTCGLHK 60
DB 1 MGLLQLLAFSLALCRARVRAQEPFESYGAEGSCYPATGDLILLIGRAQKLSVTSTCGLHK 60
QY 61 PEPYCIIVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVVTTFAPNRLKIWWQSENGVEN 120
DB 61 PEPYCIIVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVVTTFAPNRLKIWWQSENGVEN 120
QY 121 VTQLDLEABFHTLIMTFKTFRPAAMLIERSSDFGKTGWGVYRYFAYDCEASFPFISTG 180
DB 121 VTQLDLEABFHTLIMTFKTFRPAAMLIERSSDFGKTGWGVYRYFAYDCEASFPFISTG 180
QY 181 PMKKVDDIICDSRYSYDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLKLTNLRKIFVKL 240
DB 181 PMKKVDDIICDSRYSYDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLKLTNLRKIFVKL 240
QY 241 HTLGDNLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGHCMC 300
DB 241 HTLGDNLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGHCMC 300
QY 301 RHNTKGLNCELMDFYHDLMPRAEGRNSNACKKCNNEHSISCHFDMAVYLATGNVSGG 360
DB 301 RHNTKGLNCELMDFYHDLMPRAEGRNSNACKKCNNEHSISCHFDMAVYLATGNVSGG 360
QY 361 VDDCCQHNMTGRNCEQCKPFYQHPERDIRDPNFCERCTCDPAGSQNEGICDSTDFSTG 420
DB 361 VDDCCQHNMTGRNCEQCKPFYQHPERDIRDPNFCERCTCDPAGSQNEGICDSTDFSTG 420
QY 421 LIAGQCRCKLNVEGEHCDVCKEGFYDLSSDPFGCKSCACNPLGTIPGGNPCDSETGHY 480
DB 421 LIAGQCRCKLNVEGEHCDVCKEGFYDLSSDPFGCKSCACNPLGTIPGGNPCDSETGHY 480
QY 481 CKRLVTGQHCDQCLPEHMGLSNDLDGCRPCDCLGGALNNSCFAESGGQSCRPHMIGRQC 540
DB 481 CKRLVTGQHCDQCLPEHMGLSNDLDGCRPCDCLGGALNNSCFAESGGQSCRPHMIGRQC 540
QY 541 NEVEPGYFATLDHYLYEAEANLPGVSIIVERQYIQDRIPSWTGAQFVRVPEGAYLEFF 600
DB 541 NEVEPGYFATLDHYLYEAEANLPGVSIIVERQYIQDRIPSWTGAQFVRVPEGAYLEFF 600
QY 601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPTSRRCNGTIPDDNQVLSLSPG 660
DB 601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPTSRRCNGTIPDDNQVLSLSPG 660
QY 661 SRYVVLPRPVCFEKGTNYTVRLLELPQYTSDDSVESPYTLIDSLVLMPCYKSLDIFTVGG 720
DB 661 SRYVVLPRPVCFEKGTNYTVRLLELPQYTSDDSVESPYTLIDSLVLMPCYKSLDIFTVGG 720
QY 721 SGDVVTNSAWETFORYRCLNSRSVVKTPMTDVCNRIIFSISALLHQTGLACECDPQGS 780
DB 721 SGDVVTNSAWETFORYRCLNSRSVVKTPMTDVCNRIIFSISALLHQTGLACECDPQGS 780
QY 781 LSSVCDPNGGQCCQCRPNVVGRTCNRCAPGTFFGPGSGCKPCECHLQGSVNAFCNPVTGQC 840
DB 781 LSSVCDPNGGQCCQCRPNVVGRTCNRCAPGTFFGPGSGCKPCECHLQGSVNAFCNPVTGQC 840
QY 841 HCFQGVYARQCDRCLPGHWGFPSCQPCQCNHADDCCDPVTGECLNCQDVTMGHNCERCLA 900
DB 841 HCFQGVYARQCDRCLPGHWGFPSCQPCQCNHADDCCDPVTGECLNCQDVTMGHNCERCLA 900
QY 901 GYGDPIIGSDHCRPCPDGPDGSGRQFARSCYQDPVTLQLACVCDPFGYIGSRCDDCAS 960
DB 901 GYGDPIIGSDHCRPCPDGPDGSGRQFARSCYQDPVTLQLACVCDPFGYIGSRCDDCAS 960
QY 961 GYFNPSFVGGSCQPCQCHNNIDTTDPEACDKETGRCLKCLYHTEGHCQFCRFGYYGDA 1020
DB 961 GYFNPSFVGGSCQPCQCHNNIDTTDPEACDKETGRCLKCLYHTEGHCQFCRFGYYGDA 1020
QY 1021 LRQDCKKVCNVLGTVEHCHNGSDCCQDKATGQCLCLPNVIGQNCRCAPNTWQLASGTG 1080
DB 1021 LRQDCKKVCNVLGTVEHCHNGSDCCQDKATGQCLCLPNVIGQNCRCAPNTWQLASGTG 1080

QY 1081 CDPCNCAAHSGPSCNEFTGQCQCMGPGGRTCEQELFWGDDPDVECRACDCDPRGIE 1140
DB 1081 CDPCNCAAHSGPSCNEFTGQCQCMGPGGRTCEQELFWGDDPDVECRACDCDPRGIE 1140
QY 1141 TPQCDOSTGQCVCEGVEGPRCDKCTRGYSGVFPDCTPCHQCFALWDVIIAELTNTRHF 1200
DB 1141 TPQCDOSTGQCVCEGVEGPRCDKCTRGYSGVFPDCTPCHQCFALWDVIIAELTNTRHF 1200
QY 1201 LEKAKALKISGIVGIPYRETVDVSVERKVSEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDV 1260
DB 1201 LEKAKALKISGIVGIPYRETVDVSVERKVSEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDV 1260
QY 1261 TEMMAQVEVKLSDDTTSQSNSTAKELDSLQTEAESILDNTVKELAEQLEFIKNSDIRGALDS 1320
DB 1261 TEMMAQVEVKLSDDTTSQSNSTAKELDSLQTEAESILDNTVKELAEQLEFIKNSDIRGALDS 1320
QY 1321 ITKYFQMSLEAEERVNASTTEPNSTVEQSALMRDVEDVMMERESQFKEQEQARLLDE 1380
DB 1321 ITKYFQMSLEAEERVNASTTEPNSTVEQSALMRDVEDVMMERESQFKEQEQARLLDE 1380
QY 1381 LAGKLSQSLDSAAAEAMTCGPPGASCSETECGGNCRTDEGERKCGPGCGGLVTVAHNA 1440
DB 1381 LAGKLSQSLDSAAAEAMTCGPPGASCSETECGGNCRTDEGERKCGPGCGGLVTVAHNA 1440
QY 1441 WQKAMDLDQDVLASAEVQLSKWSEAKLRADKQSAEDILLKTNATKEKMDKSNEEL 1500
DB 1441 WQKAMDLDQDVLASAEVQLSKWSEAKLRADKQSAEDILLKTNATKEKMDKSNEEL 1500
QY 1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKMEPSTPQQLNLTEDIRERVESLSQVEVI 1560
DB 1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKMEPSTPQQLNLTEDIRERVESLSQVEVI 1560
QY 1561 LQHSAAADIAEAEMLLLEAKRASKSATDVKVTADMVKEALEEAEKQAAQVAEAKAIKQADEDI 1620
DB 1561 LQHSAAADIAEAEMLLLEAKRASKSATDVKVTADMVKEALEEAEKQAAQVAEAKAIKQADEDI 1620
QY 1621 QGTQNLTSIESETAASEETLFNASQRISELERNVVEELKRAAQNSGEAEYIEKVVTVK 1680
DB 1621 QGTQNLTSIESETAASEETLFNASQRISELERNVVEELKRAAQNSGEAEYIEKVVTVK 1680
QY 1681 QSAEDVKKTLTGELDEKVKVENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLL 1740
DB 1681 QSAEDVKKTLTGELDEKVKVENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLL 1740
QY 1741 KDLERKVEDNQRYLEDKQELARLEGEVRSLLKDISQKAVYSTCL 1786
DB 1741 KDLERKVEDNQRYLEDKQELARLEGEVRSLLKDISQKAVYSTCL 1786

RESULT 3
AAB19797
ID AAB19797 standard; protein; 1786 AA.
XX
AC AAB19797;
XX
DT 05-MAR-2001 (first entry)
XX
DE Human laminin 2 beta-1 chain.
XX
KW Laminin 2; human; nerve regeneration; angiogenic; cell adhesion;
KW degenerative muscle disorder; muscular dystrophy; cell therapy.
XX
OS Homo sapiens.
XX
FH Key
FT Peptide
FT /label= Signal_peptide
FT protein
FT /label= Mature_protein
XX
PN WO200066730-A2.
XX
PD 09-NOV-2000.

XX 28-APR-2000; 2000WO-US011378.
XX 30-APR-1999; 99US-01311720P.
PR 15-JUN-1999; 99US-0139198P.
PR 12-JUL-1999; 99US-0143289P.
PR 24-SEP-1999; 99US-0155945P.
XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
PA Yurchenco P;
XX WPI; 2000-687537/67.
DR N-PSDB; AAA88897.
XX Purified laminin 2 protein, useful for research and therapeutic purposes
PT including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.
XX Claim 5; Page 186-191; 305pp; English.
PS The present sequence is that of the beta-1 chain of human laminin 2.
XX Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1
CC (100 kDa) chains. It is thought to be specifically required for
CC stabilizing myotubes during skeletal muscle development, and for
CC preventing apoptosis. Genetic defects in its structure or expression are
CC associated with a major type of congenital muscular dystrophy. Laminin 2
CC is also thought to be important in Schwann cell/basal lamina
CC interactions. The invention provides laminin 2 alpha-2, beta-1 and gamma-
CC 1 chain polypeptides (see AAB19791-806) and the polynucleotides encoding
CC them (see AAA8891-906), methods for making recombinant laminin 2, cells
CC that express recombinant laminin 2, and methods for using purified
CC laminin 2 for research and therapeutic purposes including peripheral
CC nerve regeneration, treatment of degenerative muscle disorders,
CC angiogenesis regulation, promoting cell attachment and migration, ex vivo
CC cell therapy, improving the take of grafts, improving the
CC biocompatibility of medical devices and preparing improved culture
CC devices and media
XX SQ Sequence 1786 AA;

Query Match 100.0%; Score 9754; DB 3; Length 1786;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLQLLAFSLALCRARVRAQEPFESYGAEAGSCYPATGDLIGRAQKLSVTSTCGLHK 60
DB 1 MGLQLLAFSLALCRARVRAQEPFESYGAEAGSCYPATGDLIGRAQKLSVTSTCGLHK 60
QY 61 PEYICIVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVVTFAPNRLKIWWQSENGVEN 120
DB 61 PEYICIVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVVTFAPNRLKIWWQSENGVEN 120
QY 121 VTIQLDLEAEFHFTHLIMTFKTRPAAMLIERSSDFGKTGWVYRYPAYDCEASPPGISTG 180
DB 121 VTIQLDLEAEFHFTHLIMTFKTRPAAMLIERSSDFGKTGWVYRYPAYDCEASPPGISTG 180
QY 181 PMKKVDDIIICDSRYSIDIEPSTEGEVIIFRALDPAPKIEDPSPRIQNLKITNLRIFVKL 240
DB 181 PMKKVDDIIICDSRYSIDIEPSTEGEVIIFRALDPAPKIEDPSPRIQNLKITNLRIFVKL 240
QY 241 HTLGDNLLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGCHMC 300
DB 241 HTLGDNLLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGCHMC 300
QY 301 RHNTKGLNCELMDFYHDLPRPAPAGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGG 360
DB 301 RHNTKGLNCELMDFYHDLPRPAPAGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGG 360
QY 361 VCDDCQHNTMGRNCEQCKPFYQHPERDIRDPNFCERCTCDPAGSQNEGICDSTYDFSTG 420
DB 361 VCDDCQHNTMGRNCEQCKPFYQHPERDIRDPNFCERCTCDPAGSQNEGICDSTYDFSTG 420

QY 421 LTAGQCRCKLNVEGEHCDVCKEGFYDLSSDPFGCKSCACNPLGTIPGGNPCDSETHCY 480
Dd 421 LTAGQCRCKLNVEGEHCDVCKEGFYDLSSDPFGCKSCACNPLGTIPGGNPCDSETHCY 480
QY 481 CKRLVTGQHCDQCLPEHWGLSNDLDGCRPCDCLGGALNNSCFAESGCSCRPHMIGRQC 540
Dd 481 CKRLVTGQHCDQCLPEHWGLSNDLDGCRPCDCLGGALNNSCFAESGCSCRPHMIGRQC 540
QY 541 NEVEPGYFATLDHYLYEAEANLPGVSIIVERQYIQDRIPSWTGAGFVRVPEGAYLEFF 600
Dd 541 NEVEPGYFATLDHYLYEAEANLPGVSIIVERQYIQDRIPSWTGAGFVRVPEGAYLEFF 600
QY 601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPTSRCNGTIPDDDNQVVSLSPG 660
Dd 601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPTSRCNGTIPDDDNQVVSLSPG 660
QY 661 SRYVVLPRPVCFEKGTNYTVRLELPQYTSDDSDVESPYTLIDSLVLMPCYSKSLDIFTVGG 720
Dd 661 SRYVVLPRPVCFEKGTNYTVRLELPQYTSDDSDVESPYTLIDSLVLMPCYSKSLDIFTVGG 720
QY 721 SGDGVTNSAWETFORYRCLENSRSVVKTPMTDVCRNIIIFSALLHQTGLACECDPQGS 780
Dd 721 SGDGVTNSAWETFORYRCLENSRSVVKTPMTDVCRNIIIFSALLHQTGLACECDPQGS 780
QY 781 LSSVCDPNNGGQCQCRPNVVGRTCNRCAPGTFGFGPSGCKPCECHLQGSVNAFCNPVTQC 840
Dd 781 LSSVCDPNNGGQCQCRPNVVGRTCNRCAPGTFGFGPSGCKPCECHLQGSVNAFCNPVTQC 840
QY 841 HCFQGVYARQCRCCLPGHWGFPSPCQPCQNGHADDCTPVTGECLNCQDVTMGNRCERCLA 900
Dd 841 HCFQGVYARQCRCCLPGHWGFPSPCQPCQNGHADDCTPVTGECLNCQDVTMGNRCERCLA 900
QY 901 GYGDPIIGSGDHCRPCPCPDGPDGSGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCAS 960
Dd 901 GYGDPIIGSGDHCRPCPCPDGPDGSGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCAS 960
QY 961 GYFGNPSEVGSCQPCQCHNNIDTTPDACDKETGRCLKCLYHTEGEHCQFCRFGYYGDA 1020
Dd 961 GYFGNPSEVGSCQPCQCHNNIDTTPDACDKETGRCLKCLYHTEGEHCQFCRFGYYGDA 1020
QY 1021 LRQDCRKVCNYLGTVQEHGNGSDCQCKATGQCLCLPNVIGQNCRCAPNTWQLASGTG 1080
Dd 1021 LRQDCRKVCNYLGTVQEHGNGSDCQCKATGQCLCLPNVIGQNCRCAPNTWQLASGTG 1080
QY 1081 CDPNCNAAHSFGPSCNEFTGQCQCMFGFGRTCECQELFWGDPDVECRACDCDPRGIE 1140
Dd 1081 CDPNCNAAHSFGPSCNEFTGQCQCMFGFGRTCECQELFWGDPDVECRACDCDPRGIE 1140
QY 1141 TPQCDQSTGQCVCEGVEGPRCDKCTRYSYGVFPDCTPCHQCFALWDVIIAELTNRTHRF 1200
Dd 1141 TPQCDQSTGQCVCEGVEGPRCDKCTRYSYGVFPDCTPCHQCFALWDVIIAELTNRTHRF 1200
QY 1201 LEKAKALKISGVIQPYRETVDVSVERKVSEIKDILAQSPAEPKLNIGNLFEEAEKLIKDV 1260
Dd 1201 LEKAKALKISGVIQPYRETVDVSVERKVSEIKDILAQSPAEPKLNIGNLFEEAEKLIKDV 1260
QY 1261 TEMMAQVEVKLSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDS 1320
Dd 1261 TEMMAQVEVKLSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDS 1320
QY 1321 ITKYFQMSLEAEERVNASITTEPNSTVEQSALMRDRVEDVMMERESQFKEQEQAARLLDE 1380
Dd 1321 ITKYFQMSLEAEERVNASITTEPNSTVEQSALMRDRVEDVMMERESQFKEQEQAARLLDE 1380
QY 1381 LAGKIQSLDLSAAAEAMTCGPPGASCSETECGGPNCRTEGERKCGGPGCGGLVTVAHNA 1440
Dd 1381 LAGKIQSLDLSAAAEAMTCGPPGASCSETECGGPNCRTEGERKCGGPGCGGLVTVAHNA 1440
QY 1441 WQKAMDLDQDVLALAEVEQLSKMVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNEEL 1500
Dd 1441 WQKAMDLDQDVLALAEVEQLSKMVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNEEL 1500
QY 1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKMEMPSTPQQLQNLTEDIRERVESLSQVEVI 1560

Dd 1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKMEMPSTPQQLQNLTEDIRERVESLSQVEVI 1560
QY 1561 LQHSAAADIARAEMLLLEEAKRASKSATDVKVTADMVKEALEEAEKAQVAAEKAIKQADEDI 1620
Dd 1561 LQHSAAADIARAEMLLLEEAKRASKSATDVKVTADMVKEALEEAEKAQVAAEKAIKQADEDI 1620
QY 1621 QGTQNLTSIESETAASEETLFNASQRISELERNVVELKRAAQNSGEAEYIEKVVTYTVK 1680
Dd 1621 QGTQNLTSIESETAASEETLFNASQRISELERNVVELKRAAQNSGEAEYIEKVVTYTVK 1680
QY 1681 QSAEDVKKTLDGELDEKYYKKVENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLL 1740
Dd 1681 QSAEDVKKTLDGELDEKYYKKVENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLL 1740
QY 1741 KDLEKRYEDNQRYLEDKAQELARLEGEVRSLLKDISQKAVYSTCL 1786
Dd 1741 KDLEKRYEDNQRYLEDKAQELARLEGEVRSLLKDISQKAVYSTCL 1786

RESULT 4
AAB48448

ID AAB48448 standard; protein; 1786 AA.

AC AAB48448;

XX 02-MAR-2001 (first entry)

DT Human laminin 8 polypeptide, SEQ ID NO: 14.

XX Human; laminin 8; neuroprotective; angiogenic; osteopathic;
KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;
KW vascular tissue injury; neural injury; angiogenesis regulation.

OS Homo sapiens.

XX WO200066732-A2.

PN 09-NOV-2000.

XX 28-APR-2000; 2000WO-US011543.

XX 30-APR-1999; 99US-0131720P.

PR 21-AUG-1999; 99US-0149738P.

PR 24-SEP-1999; 99US-0155945P.

PR 11-FEB-2000; 2000US-0182012P.

XX (BIOS-) BIOSTRATUM INC.

PA Kortessmaa J, Tryggvason K;

XX WPI; 2000-687539/67.

XX N-PSDB; AAC83709.

PT Purified laminin 8 protein, useful for research and therapeutic purposes
PT including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.

PS Claim 5; Page 150-155; 245pp; English.

XX The present sequence is a laminin 8 polypeptide chain. Laminins are a
CC family of heterotrimeric glycoproteins that function via binding
CC interactions with neighbouring cell receptors and by forming laminin
CC networks. They are signalling molecules which influence cellular
CC function. Laminin 8 is useful for treating injuries to tissue of
CC mesenchymal origin, such as bone, cartilage, tendon, and ligament.
CC treating injuries to vascular tissue, promoting cell attachment and
CC migration, ex vivo cell therapy, improving the biocompatibility of
CC medical devices, and preparing improved cell culture devices and media.
CC Laminin 8 is also useful for promoting re-endothelialisation at the site
CC of vascular injuries, improving the take of grafts, improving the
CC biocompatibility of medical devices, treating neural injuries (neural
CC regeneration), regulating angiogenesis, and promoting cell attachment and


```
XX 02-OCT-2000; 2000WO-JP006840.
PF
XX
XX 01-OCT-1999; 99JP-00280976.
PR
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
PA
XX (NOJI/) NOJIMA H.
XX
PI Nojima H, Yoshisue H, Obayashi M, Ota T, Kawabata A, Sakurada K;
PI Kuga T, Sekine S, Nakamura Y, Sugano S;
XX
XX WPI; 2001-266308/27.
DR
DR N-PSDB; AAH02911.
XX
XX DNA sequences, proteins encoded by them and antibodies against them
PT useful in diagnosis and treatment of vascular disease caused by
PT arteriosclerosis.
XX
XX Claim 60; Page 440-449; 678pp; Japanese.
PS
XX
XX The present invention provides the protein and coding sequences of a
CC number of human shear stress response proteins. These are useful in the
CC diagnosis, treatment and screening of vascular diseases caused by
CC arteriosclerosis, including heart failure, post-PTCA restenosis and
CC hypertension
XX
XX Sequence 1786 AA;
SQ
Query Match 100.0%; Score 9754; DB 4; Length 1786;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLQLLAFSLALCRARVRAQBEFESYGAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60
Db
QY 61 PEPYCIVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVEN 120
Db
QY 121 VTIQDLAEAFHFTHLIMTFTFRPAAMLIERSDFGKTGWGVYRYFAYDCEASFPGISTG 180
Db
QY 181 PMKKVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLLKITNLRKIFVKL 240
Db
QY 241 HTLGDNLDSRMEIREKYYYAVYDMVVRGNCFCYGHASECAPVDGFEVEGVHGHCMC 300
Db
QY 301 RHNTKGLNCEL CMDFYHDL PWRPABGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGG 360
Db
QY 361 VCDDCQHNTMGRNCEQCKPFYVYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSTG 420
Db
QY 421 LIAGQCRCKLNVEGEHCDVCKEGFYDLSSDPFGCKSCACNPLGTIPGPNPCDSETHCY 480
Db
QY 481 CKRLVTGHCDQCLPEHWGLSNDLDGCRPCDCDLGGALNNSCFAESGQCSRPHMIGRQC 540
Db
QY 541 NEVEPGYFATLDHYLYEAEANLPGVSI VERQYIQDRIPSWTGA GVRVPEGAYLEFF 600
Db
QY 541 NEVEPGYFATLDHYLYEAEANLPGVSI VERQYIQDRIPSWTGA GVRVPEGAYLEFF 600
QY 601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIFTSSRCGNTIPDDDNQVVSLSPG 660
```

```
Db
601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIFTSSRCGNTIPDDDNQVVSLSPG 660
QY
661 SRYVVLPRPVCFEKGTNYTVRIELPQYTSSSDVESPYTLIDSLVLMYPYCKSLDIFTVGG 720
Db
661 SRYVVLPRPVCFEKGTNYTVRIELPQYTSSSDVESPYTLIDSLVLMYPYCKSLDIFTVGG 720
QY
721 SGDGVVNTSAWETFQYRCLENSRSVVKTPMTDVCNRNIIFSISALLHQTGLACECDPQGS 780
Db
721 SGDGVVNTSAWETFQYRCLENSRSVVKTPMTDVCNRNIIFSISALLHQTGLACECDPQGS 780
QY
781 LSSVCDPNGGQCQCRPNVVGRTCNRCAPGTFGFGPSGCKPECHLQGSVNAFCNPVTGQC 840
Db
781 LSSVCDPNGGQCQCRPNVVGRTCNRCAPGTFGFGPSGCKPECHLQGSVNAFCNPVTGQC 840
QY
841 HCFQGVYARQCDRCLPGHWGFPSCQPCQCNGHADDCCDPVTGECNLCODYTMGHNCERCLA 900
Db
841 HCFQGVYARQCDRCLPGHWGFPSCQPCQCNGHADDCCDPVTGECNLCODYTMGHNCERCLA 900
QY
901 GYGDPIIGSGDHCRCPCPCPDGSDGRQFARSCYQDPVTIQLACVCDPGYIGSRCDDCAS 960
Db
901 GYGDPIIGSGDHCRCPCPCPDGSDGRQFARSCYQDPVTIQLACVCDPGYIGSRCDDCAS 960
QY
961 GYFGNPFSEVGGSCQPCQCHNNIDTDDPEACDKETGRCLKCLYHTEGEHCQFCRFGYVGDA 1020
Db
961 GYFGNPFSEVGGSCQPCQCHNNIDTDDPEACDKETGRCLKCLYHTEGEHCQFCRFGYVGDA 1020
QY
1021 LRQDCRKVCVNYLGTVQEHGNSGDCQCDKATGQCCLPNVIGQNCDRCAPNTWQLASGTG 1080
Db
1021 LRQDCRKVCVNYLGTVQEHGNSGDCQCDKATGQCCLPNVIGQNCDRCAPNTWQLASGTG 1080
QY
1081 CDPNCNAAHSFGPSCNEFTGQCQCMFPGFGRRTCEQELFWGDDPVECRACDCDPRGIE 1140
Db
1081 CDPNCNAAHSFGPSCNEFTGQCQCMFPGFGRRTCEQELFWGDDPVECRACDCDPRGIE 1140
QY
1141 TPQCDSQTCQVCVEGVEGPRCDKCTRGYSVFPDCTPCHQCFCFALWDVIIAELTNRTHRF 1200
Db
1141 TPQCDSQTCQVCVEGVEGPRCDKCTRGYSVFPDCTPCHQCFCFALWDVIIAELTNRTHRF 1200
QY
1201 LEKAKALKISGVIGPYRETVDSEVERKVSEIKDILAQSPAAPLKNIGNLFEEAEKLIKDV 1260
Db
1201 LEKAKALKISGVIGPYRETVDSEVERKVSEIKDILAQSPAAPLKNIGNLFEEAEKLIKDV 1260
QY
1261 TEMMAQVEVKLSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDS 1320
Db
1261 TEMMAQVEVKLSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDS 1320
QY
1321 ITKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVVMERESQFKEKQEQEARLLDE 1380
Db
1321 ITKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVVMERESQFKEKQEQEARLLDE 1380
QY
1381 LAGKLSLDLSAAAEAMTCGTPPGASCSETECGGPNCRTDEGERKCGGPGCGGLVTVAHNA 1440
Db
1381 LAGKLSLDLSAAAEAMTCGTPPGASCSETECGGPNCRTDEGERKCGGPGCGGLVTVAHNA 1440
QY
1441 WQKAMDLDQDVL SALAEVEQLSKMVSEAKLRADAEAKQSAEDILLKTNA TKEMDKSNEEL 1500
Db
1441 WQKAMDLDQDVL SALAEVEQLSKMVSEAKLRADAEAKQSAEDILLKTNA TKEMDKSNEEL 1500
QY
1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKMEMPSTPQQLQNLTEDIRERVESLSQVEVI 1560
Db
1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKMEMPSTPQQLQNLTEDIRERVESLSQVEVI 1560
QY
1561 LQHSAAADIARAEMLLEAKRASKSATDVKTADVMVKEALBEAEKAQVAEKAIKQADEDI 1620
Db
1561 LQHSAAADIARAEMLLEAKRASKSATDVKTADVMVKEALBEAEKAQVAEKAIKQADEDI 1620
QY
1621 QGTQNLTSIESETAASEETLFNASQRISELERNVEELKRKAQNSGEAEYIEKVVTYVK 1680
Db
1621 QGTQNLTSIESETAASEETLFNASQRISELERNVEELKRKAQNSGEAEYIEKVVTYVK 1680
QY
1681 QSAEDVKKTLDGELDEKYYKKVENLIIAKKTEESADARRKAEMLQNEAKTLLAQANSKLQLL 1740
```

Db 1681 QSAEDVKKTLGELDEKYKKVENLIAKTEESADARRKAEMLQNEAKTLAQANSKLQLL 1740

QY 1741 KDLERKYEDNQRYLEDKAQELARLEGEVRSLLKDISQKVAVYSTCL 1786

Db 1741 KDLERKYEDNQRYLEDKAQELARLEGEVRSLLKDISQKVAVYSTCL 1786

RESULT 6

ID ABB81590

XX ABB81590 standard; protein; 1786 AA.

AC ABB81590;

XX

DT 19-SEP-2002 (first entry)

XX

DE Human laminin 10 second chain protein sequence SEQ ID NO:6.

XX

KW Laminin alpha 5; laminin 10; vulnerary; cell growth; differentiation; tissue repair development; laminin; healing; vascular tissue; re-endothelialisation; vascular injury; cell attachment; cell stasis; proliferation; migration.

KW

KW

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1. .21

FT /label= signal

FT Protein 22. .1786

FT /label= laminin_10_second_chain

XX

PN WO200250111-A2.

XX

PD 27-JUN-2002.

XX

PF 21-DEC-2001; 2001WO-US051035.

XX

PR 21-DEC-2000; 2000US-0257449P.

PR 28-MAR-2001; 2001US-0279282P.

PR 13-NOV-2001; 2001US-00279282.

XX

PA (BIOS-) BIOSTRATUM INC.

XX

PI Tryggvason K, Doi M, Thyboll J;

XX

DR WPI; 2002-557650/59.

DR N-PSDB; ABQ72908.

XX

PT New human laminin-10 proteins, useful for accelerating the healing of vascular tissue, improving the biocompatibility of grafts, or for promoting re-endothelialization at the site of vascular injuries.

PT

XX

PS Claim 9; Page 113-119; 231pp; English.

XX

CC The present invention describes human laminin alpha 5. Also described is an isolated laminin 10. Laminin 10 has vulnerary activity. Laminins are useful in maintaining cell/tissue phenotype as well as promoting cell growth and differentiation in tissue repair development. Specifically, laminin 10 can be used for accelerating the healing injuries of vascular tissue, improving the biocompatibility of grafts useful for treating such injuries, for promoting re-endothelialisation at the site of vascular injuries, and promote cell attachment and subsequent cell stasis, proliferation, differentiation, and/or migration. The present sequence represents a second chain protein of laminin 10, from the present invention

CC

XX

SQ Sequence 1786 AA;

Query Match 100.0%; Score 9754; DB 5; Length 1786;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLLQLLAFSLALCRARVRAQEPFSGCAEGSCYPATGDLILLIGRAQKLSVTSTCGLHK 60

Db 1 MGLLQLLAFSLALCRARVRAQEPFSGCAEGSCYPATGDLILLIGRAQKLSVTSTCGLHK 60

QY 61 PEPYCIIVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVVTTFAPNRLKIWWQSENGVEN 120

Db 61 PEPYCIIVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVVTTFAPNRLKIWWQSENGVEN 120

QY 121 VTIQLDLAEAFHFTHLIMTKTFRPAAMLIERSSDFGKTGWVYRYFAYDCEASFPFGISTG 180

Db 121 VTIQLDLAEAFHFTHLIMTKTFRPAAMLIERSSDFGKTGWVYRYFAYDCEASFPFGISTG 180

QY 181 PMKKVDDIIICDSRYSDIEPSTEGEVIFRALDPAPKIEDPSPRIQNLLKITNLRIKFKVL 240

Db 181 PMKKVDDIIICDSRYSDIEPSTEGEVIFRALDPAPKIEDPSPRIQNLLKITNLRIKFKVL 240

QY 241 HTLGDNLLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGHCMC 300

Db 241 HTLGDNLLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGHCMC 300

QY 301 RHNTKGLNCELMDFYHDLPWPAEGRNSNACKKCNNEHSISCHFDMAVYLATGNVSGG 360

Db 301 RHNTKGLNCELMDFYHDLPWPAEGRNSNACKKCNNEHSISCHFDMAVYLATGNVSGG 360

QY 361 VDDCQHNTMGRNCEQCKPFYYQHPERDIRDNFCERCTCDPAGSQNEGICDSYTDFTSTG 420

Db 361 VDDCQHNTMGRNCEQCKPFYYQHPERDIRDNFCERCTCDPAGSQNEGICDSYTDFTSTG 420

QY 421 LIAGQCRCKLNVEGEHCDVCKEGFYDLSSDPFGCKSCACNPLGTIPGGNPNCDSETGHCHY 480

Db 421 LIAGQCRCKLNVEGEHCDVCKEGFYDLSSDPFGCKSCACNPLGTIPGGNPNCDSETGHCHY 480

QY 481 CKRLVTGQHCDQCLPEHWGLSNDLDGCRPCDCLGGALNNSCFAESGQCSRPHMIGRQC 540

Db 481 CKRLVTGQHCDQCLPEHWGLSNDLDGCRPCDCLGGALNNSCFAESGQCSRPHMIGRQC 540

QY 541 NEVEPGYYFATLDHYLYEAEEANLPGVSIIVERQYIQDRIPSWTGAGFVRVPEGAYLEFF 600

Db 541 NEVEPGYYFATLDHYLYEAEEANLPGVSIIVERQYIQDRIPSWTGAGFVRVPEGAYLEFF 600

QY 601 IDNIPYSMEYDILIRYEPOLPDHWEKAVITVORPGRIPRTSSRCGNTIPDDNQVWSLSPG 660

Db 601 IDNIPYSMEYDILIRYEPOLPDHWEKAVITVORPGRIPRTSSRCGNTIPDDNQVWSLSPG 660

QY 661 SRYVVLPRPVCFEKGTNYTVRLELPQYTSDDSDVSPYTLIDSLVLMPYCKSLDIFTVGG 720

Db 661 SRYVVLPRPVCFEKGTNYTVRLELPQYTSDDSDVSPYTLIDSLVLMPYCKSLDIFTVGG 720

QY 721 SGDGVTNSAWETFORVRCLENSRSVVKTPMTDVCORNIIFSISALLHQTLGACEDPQGS 780

Db 721 SGDGVTNSAWETFORVRCLENSRSVVKTPMTDVCORNIIFSISALLHQTLGACEDPQGS 780

QY 781 LSSVCDPNGGQCCQCRPNVVGRTCNRCAPGTFEGFSGCKPCECHLQGSVNAFCNPVTGQC 840

Db 781 LSSVCDPNGGQCCQCRPNVVGRTCNRCAPGTFEGFSGCKPCECHLQGSVNAFCNPVTGQC 840

QY 841 HCFQGVYARQCDRCLPGHWGFPSCQPCQCNGHADDCCDPTVTECLNCQDVTMGNHCERCLA 900

Db 841 HCFQGVYARQCDRCLPGHWGFPSCQPCQCNGHADDCCDPTVTECLNCQDVTMGNHCERCLA 900

QY 901 GYIGDPIIGSGDHCRPCPCPDGSDSGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCAS 960

Db 901 GYIGDPIIGSGDHCRPCPCPDGSDSGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCAS 960

QY 961 GYFGNPSEVGGSCQPCQCHNNIDTTDPEACDKETGRCLKCLYHTEGEHCQFCRFGYVYGD 1020

Db 961 GYFGNPSEVGGSCQPCQCHNNIDTTDPEACDKETGRCLKCLYHTEGEHCQFCRFGYVYGD 1020

QY 1021 LRQDCRKVCVNYLGTVQEHNGSDCCQDKATGQCLCLPNVIGQNCDCRCAPNTWQLASGTG 1080

Db 1021 LRQDCRKVCVNYLGTVQEHNGSDCCQDKATGQCLCLPNVIGQNCDCRCAPNTWQLASGTG 1080

QY 1081 CDPNCNAAHSFGPSCNEFTQCQCMPFGGRTCSCEQLFWGDPDVECRACDCDPRGIE 1140

Db 1081 CDPNCNAAHSFGPSCNEFTQCQCMPFGGRTCSCEQLFWGDPDVECRACDCDPRGIE 1140

QY 1141 TPQCDQSTGQVCVGEVGPGRCDKCTRGYSGVFPDCTPCHQCFALWDVIIAELTNRTRHF 1200
DB 1141 TPQCDQSTGQVCVGEVGPGRCDKCTRGYSGVFPDCTPCHQCFALWDVIIAELTNRTRHF 1200
QY 1201 LEKAKALKISGVIGPYRETVDVSVERKVSEIKDILAQSPAAPLKNIGNLFEEAEKLIKDV 1260
DB 1201 LEKAKALKISGVIGPYRETVDVSVERKVSEIKDILAQSPAAPLKNIGNLFEEAEKLIKDV 1260
QY 1261 TEMMAQVEVKLSDDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDS 1320
DB 1261 TEMMAQVEVKLSDDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDS 1320
QY 1321 ITKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVNMERESQFKEKEEQARLLDE 1380
DB 1321 ITKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVNMERESQFKEKEEQARLLDE 1380
QY 1381 LAGKLSLDSAAAEMTCGTPPGASCSETECGGPNCRNCRTEDEGERKCGGPGCGGLVTVAHNA 1440
DB 1381 LAGKLSLDSAAAEMTCGTPPGASCSETECGGPNCRNCRTEDEGERKCGGPGCGGLVTVAHNA 1440
QY 1441 WQKAMDLDDQVLSALAEVEQLSKMVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNEEL 1500
DB 1441 WQKAMDLDDQVLSALAEVEQLSKMVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNEEL 1500
QY 1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKMEMPSTPQQLNLTEDIRERVESLSQVEVI 1560
DB 1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKMEMPSTPQQLNLTEDIRERVESLSQVEVI 1560
QY 1561 LQHSAAADIAEAEMWLEEAKRASKSATDVKTADVMVKEALEEAQAQVAEKAQKQADEDI 1620
DB 1561 LQHSAAADIAEAEMWLEEAKRASKSATDVKTADVMVKEALEEAQAQVAEKAQKQADEDI 1620
QY 1621 QGTQNLTSIESETAASEETLFNASQRISELERNVVEELKRKAQNSGEAEYIEKVYTVK 1680
DB 1621 QGTQNLTSIESETAASEETLFNASQRISELERNVVEELKRKAQNSGEAEYIEKVYTVK 1680
QY 1681 QSAEDVVKTLDDGELDEKYYKVENLIQKTEESADARRKAEMLQNEAKTLLAQANSKLQLL 1740
DB 1681 QSAEDVVKTLDDGELDEKYYKVENLIQKTEESADARRKAEMLQNEAKTLLAQANSKLQLL 1740
QY 1741 KDLERKYEDNQRYLEDKAQELARLEGEVRSLLKDISQKVAVYSTCL 1786
DB 1741 KDLERKYEDNQRYLEDKAQELARLEGEVRSLLKDISQKVAVYSTCL 1786

RESULT 7
AAM48896
ID AAM48896 standard; protein; 1786 AA.
XX
AC AAM48896;
XX
DT 04-APR-2002 (first entry)
XX
DE Laminin protein.
XX
KW Human; angiostatin; endostatin; angiogenesis; cancer; metastasis;
KW psoriasis; scleroderma; Crohn's disease; corneal disease; retinopathy;
KW arthritis; wound healing; Helicobacter pylori; peptic ulcer;
KW gene therapy; angiostatin antagonist; endostatin antagonist;
KW antiangiogenic; cytostatic; antiarthritic; antiinflammatory;
KW cerebroprotective; antidiabetic; virucide; antipyretic; vulnerary;
KW gynaecological; cat scratch fever.
XX
OS Unidentified.
XX
PN WO200193897-A2.
XX
PD 13-DEC-2001.
XX
PF 04-JUN-2001; 2001WO-US017947.
XX
PR 02-JUN-2000; 2000US-0209065P.

PR 08-MAY-2001; 2001US-0289387P.
XX (ENTR-) ENTREMED INC.
XX
PI Sim KL, Macdonald NJ;
XX
DR WPI; 2002-130569/17.
DR N-PSDB; ABA97525.
XX
PT Regulating angiogenesis and treatment of angiogenesis-mediated diseases,
PT e.g. hemangioma, tumors or cancer, by administering a tropomyosin binding
PT compound or actin disrupting compound.
XX
PS Example 11; Fig 6A; 95pp; English.
XX
CC The present invention relates to methods of regulating angiogenesis in an
CC individual by administering an angiogenesis regulating composition
CC comprising a tropomyosin binding compound or an actin disrupting
CC compound. The compositions are useful for treating diseases and processes
CC mediated by angiogenesis including haemangioma, solid tumours, blood
CC bourne tumours, leukaemia, metastasis, Crohn's disease, coronary or
CC cerebral collaterals, arthritis, diabetic neovascularisation, macular
CC degeneration, wound healing, Helicobacter related diseases, ovulation,
CC menstruation, and cat scratch fever. The present sequence is a protein
CC described in the exemplification of the invention
XX
SQ Sequence 1786 AA;
Query Match 99.8%; Score 9738; DB 5; Length 1786;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1784; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MGLLQLLAFSLALCRARVRAQEPESYGAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60
DB 1 MGLLQLLAFSLALCRARVRAQEPESYGAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60
QY 61 PEPYCIIVSHLQEDKKCFICNSQDPYHETLNPDLSHLIENVVTFAPNRLKIWQSENGVEN 120
DB 61 PEPYCIIVSHLQEDKKCFICNSQDPYHETLNPDLSHLIENVVTFAPNRLKIWQSENGVEN 120
QY 121 VTQLDLEAEFHTLIMTFTFRPAAMLIERSDDFGKTGWYRYFAYDCEASFPGISTG 180
DB 121 VTQLDLEAEFHTLIMTFTFRPAAMLIERSDDFGKTGWYRYFAYDCEASFPGISTG 180
QY 181 PMKKVDDIIICDSRYSIEPSTEGEVIFRALDPAFKIEDPYSPIQNLLKITNLRIFVKL 240
DB 181 PMKKVDDIIICDSRYSIEPSTEGEVIFRALDPAFKIEDPYSPIQNLLKITNLRIFVKL 240
QY 241 HTLGDNLDSRMEIREKYYYAVYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGHC 300
DB 241 HTLGDNLDSRMEIREKYYYAVYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGHC 300
QY 301 RHNTKGLNCELMDFYHDLWPRAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGG 360
DB 301 RHNTKGLNCELMDFYHDLWPRAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGG 360
QY 361 VCDDCOHNTMGRNCEQCKPFYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSG 420
DB 361 VCDDCOHNTMGRNCEQCKPFYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSG 420
QY 421 LIAGQCRCKLNVEGEHCDVCKEGFYDLSSDDPFCKKSCACNPLGTIPGPNPCDSETGH 480
DB 421 LIAGQCRCKLNVEGEHCDVCKEGFYDLSSDDPFCKKSCACNPLGTIPGPNPCDSETGH 480
QY 481 CKRLVTGQHCHDQCLPEHWGLSNDLDCRPPCDLGGALNNSCFAESGCSCRPHMIGRQC 540
DB 481 CKRLVTGQHCHDQCLPEHWGLSNDLDCRPPCDLGGALNNSCFAESGCSCRPHMIGRQC 540
QY 541 NEVEPGYYFATLDHYLYEAEBANLGPVSIIVERQYIQDRIPSWTGAQFVRVPEGAYLEFF 600
DB 541 NEVEPGYYFATLDHYLYEAEBANLGPVSIIVERQYIQDRIPSWTGAQFVRVPEGAYLEFF 600
QY 601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPRTSSRCNTIPDDDDNQVVSLS 660

Db 601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPRTSSRCGNTIXDDNDQNVVSLSPG 660
QY 661 SRYVVLPRPVCEKGTNYTVRLELPQYTSSDSDESPTLIDSLVLMYPYCKSLDIFTVGG 720
Db 661 SRYVVLPRPVCEKGTNYTVRLELPQYTSSDSDESPTLIDSLVLMYPYCKSLDIFTVGG 720
QY 721 SGDGVTNSAWETFORYRCLENSRSVVKTPMTDVCRNIIIFSISALLHQTGLACECDPOGS 780
Db 721 SGDGVTNSAWETFORYRCLENSRSVVKTPMTDVCRNIIIFSISALLHQTGLACECDPOGS 780
QY 781 LSSVCDPNGGQCQCPNPNVGRTCNRCAPGTGFGPSGCKPCECHLQGSVNAFCNPVTGQC 840
Db 781 LSSVCDPNGGQCQCPNPNVGRTCNRCAPGTGFGPSGCKPCECHLQGSVNAFCNPVTGQC 840
QY 841 HCFQGVYARQCRCPLPGHWGFPSCQPCQCNHGADDCDPTVTECLNCQDYTMGHNCERCLA 900
Db 841 HCFQGVYARQCRCPLPGHWGFPSCQPCQCNHGADDCDPTVTECLNCQDYTMGHNCERCLA 900
QY 901 GYGDPIIGSDHCRPCPCPDGPDGSGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCAS 960
Db 901 GYGDPIIGSDHCRPCPCPDGPDGSGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCAS 960
QY 961 GYFGNPSEVGGSCQPCQCHNNIDTTDPEACDKETGRCLKCLYHTEGEHCQFCRFGYYGDA 1020
Db 961 GYFGNPSEVGGSCQPCQCHNNIDTTDPEACDKETGRCLKCLYHTEGEHCQFCRFGYYGDA 1020
QY 1021 LRQDCRKVCNYLGTVQEHCHGSDCQCKATGQCCLCPNVIGQNCDCRCAPNTWQLASGTG 1080
Db 1021 LRQDCRKVCNYLGTVQEHCHGSDCQCKATGQCCLCPNVIGQNCDCRCAPNTWQLASGTG 1080
QY 1081 CDPNCNAAHSFGPSCNEFTGQCQCMGPFGRGTCSECQELFWGDPDVECRACDCDPRGIE 1140
Db 1081 CDPNCNAAHSFGPSCNEFTGQCQCMGPFGRGTCSECQELFWGDPDVECRACDCDPRGIE 1140
QY 1141 TPQCDQSTGQCVCEGVGPRCDKCTRIGYSGVFPDCTPCHQCPCALWDVIAELTNRTHRF 1200
Db 1141 TPQCDQSTGQCVCEGVGPRCDKCTRIGYSGVFPDCTPCHQCPCALWDVIAELTNRTHRF 1200
QY 1201 LEKAKALKISGVIGPYRETVDSEVERKVSEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDV 1260
Db 1201 LEKAKALKISGVIGPYRETVDSEVERKVSEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDV 1260
QY 1261 TEMMAQVEVKLSDDTSQSNSTAKELDSLQIEAESLDNTVKELAEQLEFIKNSDIRGALDS 1320
Db 1261 TEMMAQVEVKLSDDTSQSNSTAKELDSLQIEAESLDNTVKELAEQLEFIKNSDIRGALDS 1320
QY 1321 ITKYFQMSLEAEERVNASTTEPNSTVEQSAIMRDRVEDVMMERESQFKEKQEEQARLLDE 1380
Db 1321 ITKYFQMSLEAEERVNASTTEPNSTVEQSAIMRDRVEDVMMERESQFKEKQEEQARLLDE 1380
QY 1381 LAGKLQSLDLSAAAEEMTCGTPPGASCSETTECGGPNCRDTEGERKCGPGCGGLVTVAHNA 1440
Db 1381 LAGKLQSLDLSAAAEEMTCGTPPGASCSETTECGGPNCRDTEGERKCGPGCGGLVTVAHNA 1440
QY 1441 WQKAMDLDQDVLALAEVEQLSKMVSEAKLRADAEAKQSAEDILLKTATKEMDKSNEEL 1500
Db 1441 WQKAMDLDQDVLALAEVEQLSKMVSEAKLRADAEAKQSAEDILLKTATKEMDKSNEEL 1500
QY 1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKMEPSTPQQLNLTEDIRERVESLSQVEVI 1560
Db 1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKMEPSTPQQLNLTEDIRERVESLSQVEVI 1560
QY 1561 LQHSAAADIARAEMLLEEAKRASKSATDVKVTADMVKEALEEAEAKQVAAEKAQKQADEDI 1620
Db 1561 LQHSAAADIARAEMLLEEAKRASKSATDVKVTADMVKEALEEAEAKQVAAEKAQKQADEDI 1620
QY 1621 QGTQNLLTSIESETAASEETLFNASQRISELERNVVEELKRKAQNSGEAEYIEKVYTVK 1680
Db 1621 QGTQNLLTSIESETAASEETLFNASQRISELERNVVEELKRKAQNSGEAEYIEKVYTVK 1680
QY 1681 QSAEDVKKTLDGELDEKYKKVENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLL 1740

Db 1681 QSAEDVKKTLDGELDEKYKKVENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLL 1740
QY 1741 KDLEKRYEDNQRYLEDKAQELARLEGEVRSLLKDISQKVAVYSTCL 1786
Db 1741 KDLEKRYEDNQRYLEDKAQELARLEGEVRSLLKDISQKVAVYSTCL 1786
RESULT 8
AA15461
ID AA15461 standard; protein; 1785 AA.
XX
AC AA15461;
DT 26-JUL-1999 (first entry)
XX
DE Human laminin beta 1 subunit.
XX
DE Laminin 12; alpha 2; beta 1; gamma 3; subunit; nerve regeneration;
KW connective tissue adhesion; tissue repair; wound; nerve growth;
KW laminin beta 1 subunit.
XX
OS Homo sapiens.
XX
XX WO9919348-A1.
XX
PD 22-APR-1999.
XX
PF 08-OCT-1998; 98WO-US021391.
XX
PR 10-OCT-1997; 97US-0061609P.
XX
PA (GEO) GEN HOSPITAL CORP.
XX
XX Burgeson RE, Champliand M, Olson P, Koch M, Brunken W;
PI
XX
DR WPI; 1999-326542/27.
DR N-PSDB; AAX59769.
XX
PT Purified laminin 12 useful for promoting tissue repair and promoting
PT nerve growth.
XX
PS Disclosure; Fig 4; 86pp; English.
XX
CC The specification describes laminin 12 which includes an alpha 2, beta 1
CC and gamma 3 subunit. Laminin is a connective tissue adhesion molecule.
CC Laminin is useful for promoting tissue repair due to wounds and to
CC promote nerve growth or regeneration. The present sequence represents
CC human laminin beta 1 subunit
XX
SQ Sequence 1785 AA;
Query Match 99.6%; Score 9718.5; DB 2; Length 1785;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1783; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 MGLLQLLAESFLALCRARVRAQEPFESYGCAGSCYPATGDLIGRAQKLSVTSTCGLHK 60
Db 1 MGLLQLLAESFLALCRARVRAQEPFESYGCAGSCYPATGDLIGRAQKLSVTSTCGLHK 60
QY 61 PEPYCIVSHLQEDKKQFICNSQDPYHETLNPDSHLIENVTTFAPNRLKIWWQSENGVEN 120
Db 61 PEPYCIVSHLQEDKKQFICNSQDPYHETLNPDSHLIENVTTFAPNRLKIWWQSENGVEN 120
QY 121 VTIQDLLEAEFFHFTLIMTFKTRPAAMLIERSDDFGKTGWVRYFAYDCEASFPFGISTG 180
Db 121 VTIQDLLEAEFFHFTLIMTFKTRPAAMLIERSDDFGKTGWVRYFAYDCEASFPFGISTG 180
QY 181 PMKVDDIIICDSRYSIDIEPSTEGEVIFRALDPAFKIEDPYSPIQNLLKITNLRKFKVKL 240
Db 181 PMKVDDIIICDSRYSIDIEPSTEGEVIFRALDPAFKIEDPYSPIQNLLKITNLRKFKVKL 240
QY 241 HTIGDNLDDSRMEIREKYYIYAVYDMVVRGNCFCYGHASECAPVDGFENEEVGMVHGCMC 300

Db 241. HTLGDNLLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGCMC 300
QY 301 RHNTKGLNCEL CMDFYHDL PWRPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGG 360
Db 301 RHNTKGLNCEL CMDFYHDL PWRPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGG 360
QY 361 VCDDCQHNTMGRNCEQCKPFYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSG 420
Db 361 VCDDCQHNTMGRNCEQCKPFYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSG 420
QY 421 LIAGQCRCKLNVEGEHCDVCKEGFYDLSSDPFGCKSCACNPLGTIPGPNPCDSETGHY 480
Db 421 LIAGQCRCKLNVEGEHCDVCKEGFYDLSSDPFGCKSCACNPLGTIPGPNPCDSETGHY 480
QY 481 CKRLVTGQHCDQCLPEHWGLSNDLDGCRPCDCLGGALNNSCFAESGQSCSRPHMIGRQC 540
Db 481 CKRLVTGQHCDQCLPEHWGLSNDLDGCRPCDCLGGALNNSCFAESGQSCSRPHMIGRQC 540
QY 541 NEVEPGYYFATLDHYLYEAEANLPGVSI VERQYIQDRIPSWTGAGFVRVPEGAYLEFF 600
Db 541 NEVEPGYYFATLDHYLYEAEANLPGVSI VERQYIQDRIPSWTGAGFVRVPEGAYLEFF 600
QY 601 IDNIPYSMEYDILIRYEPQLPDHWKAVITVORPGRIP TSSRCNGTIPDDNQWVSLSPG 660
Db 601 IDNIPYSMEYDILIRYEPQLPDHWKAVITVORPGRIP TSSRCNGTIPDDNQWVSLSPG 660
QY 661 SRYVVLPRPVCFEKGTNYTVRLPQYTSDDSVESPYTLIDSLVLMPIKSLDIFTVGG 720
Db 661 SRYVVLPRPVCFEKGTNYTVRLPQYTSDDSVESPYTLIDSLVLMPIKSLDIFTVGG 720
QY 721 SGDGWVTNSAWETFQRYRCLENSRSVVKTPMTDVCRNIIFSI SALLHQTGLACECDPQGS 780
Db 721 SGDGWVTNSAWETFQRYRCLENSRSVVKTPMTDVCRNIIFSI SALLHQTGLACECDPQGS 780
QY 781 LSSVCDPNGGQCQCRPNVVGRTCNRCAPGTFGFGSGCKPCECHLQGSVNAPCNVPTGQC 840
Db 781 LSSVCDPNGGQCQCRPNVVGRTCNRCAPGTFGFGSGCKPCECHLQGSVNAPCNVPTGQC 840
QY 841 HCFQGVYARQCDCRLPGHWGFPSPQCQCNGHADCDPVTGECLNCQDVTMGNHCERCLA 900
Db 841 HCFQGVYARQCDCRLPGHWGFPSPQCQCNGHADCDPVTGECLNCQDVTMGNHCERCLA 900
QY 901 GYGDPIIGSGDHCRPCPCPDGPDGSGRQFARSCYQDPVTLQLACVCDPGYIGSRCDDCAS 960
Db 901 GYGDPIIGSGDHCRPCPCPDGPDGSGRQFARSCYQDPVTLQLACVCDPGYIGSRCDDCAS 960
QY 961 GYFGNPSEVGGSCQPCQCHNNIDTTDPEACDKETGRCLKCLYHTEGEHCQCFRFGYYGDA 1020
Db 961 GYFGNPSEVGGSCQPCQCHNNIDTTDPEACDKETGRCLKCLYHTEGEHCQCFRFGYYGDA 1020
QY 1021 LRQDCRKVCVNYLGTVQEHNGSDCQCCKATGQCCLCLPNVIGQNCDCRCA PNTWQLASGTG 1080
Db 1021 LRQDCRKVCVNYLGTVQEHNGSDCQCCKATGQCCLCLPNVIGQNCDCRCA PNTWQLASGTG 1080
QY 1081 CDPNCNAAHSFGPSCNEFTGQCQCMPGFGGRTCSQCQLFWGDPDVECRACDCDPRGIE 1140
Db 1081 CDPNCNAAHSFGPSCNEFTGQCQCMPGFGGRTCSQCQLFWGDPDVECRACDCDPRGIE 1140
QY 1141 TPQCDQSTGQCVCEGVGPRCDKCTRGYSGVFPDCTPCHQCFCALWDV IIAELTNRTHRF 1200
Db 1141 TPQCDQSTGQCVCEGVGPRCDKCTRGYSGVFPDCTPCHQCFCALWDV IIAELTNRTHRF 1200
QY 1201 LEKAKALKISGVIGPYRETVDVSVERKVSEIKDILAQSPAAEPLKNIGNLFEEAEKLIKOV 1260
Db 1201 LEKAKALKISGVIGPYRETVDVSVERKVSEIKDILAQSPAAEPLKNIGNLFEEAEKLIKOV 1260
QY 1261 TEMMAQVEVKLSDDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQL EFTIKNSDIRGALDS 1320
Db 1261 TEMMAQVEVKLSDDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQL EFTIKNSDIRGALDS 1320
QY 1321 ITKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVMMERE -SQFKEQEEQARLLD 1379
Db 1321 ITKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVMMERE -SQFKEQEEQARLLD 1380

QY 1380 ELACKLQSLDLSAAAE MTCGTPPGASCSETECGGPNCR TDEGERKCGGPGCGGLVTVAHN 1439
Db 1381 ELACKLQSLDLSAAAE MTCGTPPGASCSETECGGPNCR TDEGERKCGGPGCGGLVTVAHN 1440
QY 1440 AWQKAMDLDQDVL SALAEVEQLSKMVSEAKLRAD EAKQSAEDILLKT NATKEKMDKSNEE 1499
Db 1441 AWQKAMDLDQDVL SALAEVEQLSKMVSEAKLRAD EAKQSAEDILLKT NATKEKMDKSNEE 1500
QY 1500 LRNLKIQIRNFLTQDSADLDSIEAVANEVLKME MPSTPQQLQNLTEDIRERVESLSQVEV 1559
Db 1501 LRNLKIQIRNFLTQDSADLDSIEAVANEVLKME MPSTPQQLQNLTEDIRERVESLSQVEV 1560
QY 1560 ILQHSAAADIARAEMLLEEAKRASKSATDVKVTAD MVKEALEEAEAKQAQVAAEKA I KQADED 1619
Db 1561 ILQHSAAADIARAEMLLEEAKRASKSATDVKVTAD MVKEALEEAEAKQAQVAAEKA I KQADED 1620
QY 1620 IQGTQNL LTSIESETAASEETL FNASQRISELER NVVEELKRKAAQNSGEAEYIEKVYTV 1679
Db 1621 IQGTQNL LTSIESETAASEETL FNASQRISELER NVVEELKRKAAQNSGEAEYIEKVYTV 1680
QY 1680 KQSAEDVKKTL DGELDEK YKKVENLIAKKT EESADARRKA EMLQNEAKTLLAQANSKLQL 1739
Db 1681 KQSAEDVKKTL DGELDEK YKKVENLIAKKT EESADARRKA EMLQNEAKTLLAQANSKLQL 1740
QY 1740 LKDLERKYEDNQRYLEDKAOELARLEGEVRSLLKDI SOKVAVYST 1784
Db 1741 LKDLERKYEDNQRYLEDKAOELARLEGEVRSLLKDI SOKVAVYST 1785

RESULT 9

AAB19798

ID AAB19798 standard; protein; 1765 AA.

AC AAB19798;

DT 05-MAR-2001 (first entry)

XX Human laminin 2 mature beta-1 chain.

DE Laminin 2; human; nerve regeneration; angiogenic; cell adhesion; degenerative muscle disorder; muscular dystrophy; cell therapy.

XX Homo sapiens.

OS WO200066730-A2.

XX 09-NOV-2000.

XX 28-APR-2000; 2000WO-US011378.

XX 30-APR-1999; 99US-0131720P.

PR 15-JUN-1999; 99US-0139198P.

PR 12-JUL-1999; 99US-0143289P.

PR 24-SEP-1999; 99US-0155945P.

XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.

PI Yurchenco P;

XX WPI; 2000-687537/67.

DR N-PSDB; AAA88898.

XX Purified laminin 2 protein, useful for research and therapeutic purposes including peripheral nerve regeneration, treatment of degenerative muscle disorders, angiogenesis regulation, and ex vivo cell therapy.

PS Claim 5; Page 199-204; 305pp; English.

XX The present sequence is that of the human laminin 2 beta-1 chain mature protein. Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1 (100 kDa) chains. It is thought to be specifically required for stabilizing myotubes during skeletal muscle development, and for

CC preventing apoptosis. Genetic defects in its structure or expression are
CC associated with a major type of congenital muscular dystrophy. Laminin 2
CC is also thought to be important in Schwann cell/basal lamina
CC interactions. The invention provides laminin 2 alpha-2, beta-1 and gamma-
CC 1 chain polypeptides (see AAB19791-806) and the polynucleotides encoding
CC them (see AAB8891-906), methods for making recombinant laminin 2, cells
CC that express recombinant laminin 2, and methods for using purified
CC laminin 2 for research and therapeutic purposes including peripheral
CC nerve regeneration, treatment of degenerative muscle disorders,
CC angiogenesis regulation, promoting cell attachment and migration, ex vivo
CC cell therapy, improving the take of grafts, improving the
CC biocompatibility of medical devices and preparing improved culture
CC devices and media
XX
SQ Sequence 1765 AA;

Query Match 99.0%; Score 9654; DB 3; Length 1765;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 QEPEFSYGCAGSCYPATGDLIIAGRAQKLSVTSTCGLHKPEPYCIIVSHLQEDKKCFICNS 81
DB 1 QEPEFSYGCAGSCYPATGDLIIAGRAQKLSVTSTCGLHKPEPYCIIVSHLQEDKKCFICNS 60
QY 82 QDPYHETLNPDLSHLIENVVTFAPNRLKIWQSENGVENVTIQLDLAEAFHFTLIMTFK 141
DB 61 QDPYHETLNPDLSHLIENVVTFAPNRLKIWQSENGVENVTIQLDLAEAFHFTLIMTFK 120
QY 142 TFRPAAMLIERSDFGKTGWYRYFAYDCEASPGISTGPMKKVDDIICDSRYSIDIEPST 201
DB 121 TFRPAAMLIERSDFGKTGWYRYFAYDCEASPGISTGPMKKVDDIICDSRYSIDIEPST 180
QY 202 EGEVIFRALDPAFKIEDPSPRIQNLKLTNLRIFKVLHTLGNLLDSRMEIREKYIYA 261
DB 181 EGEVIFRALDPAFKIEDPSPRIQNLKLTNLRIFKVLHTLGNLLDSRMEIREKYIYA 240
QY 262 VYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGCHCMRHTKGLNCELMDFFYHDLPLW 321
DB 241 VYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGCHCMRHTKGLNCELMDFFYHDLPLW 300
QY 322 RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGVCCDDCQHTMTGRNCEQCKPYP 381
DB 301 RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGVCCDDCQHTMTGRNCEQCKPYP 360
QY 382 YQHPERDIRDPNFCERCCTCDPAGSQNEGICDSYTDFTSTGLIAGQCRCKLNVEGEHCDVCK 441
DB 361 YQHPERDIRDPNFCERCCTCDPAGSQNEGICDSYTDFTSTGLIAGQCRCKLNVEGEHCDVCK 420
QY 442 EGFYDLSSDPFGCKSCACNPLGTIPGGNCPDSETHCYCKRLVTGQHCDCQCLPEHWGLS 501
DB 421 EGFYDLSSDPFGCKSCACNPLGTIPGGNCPDSETHCYCKRLVTGQHCDCQCLPEHWGLS 480
QY 502 NDLDGCRPCDCDLGGALNNSCFAESGGQSCSRPHMIGRQCNEVEPGYFFATLDHYLYEAE 561
DB 481 NDLDGCRPCDCDLGGALNNSCFAESGGQSCSRPHMIGRQCNEVEPGYFFATLDHYLYEAE 540
QY 562 ANLGPVSVIVERQYIQDRIPSWTGAQFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 621
DB 541 ANLGPVSVIVERQYIQDRIPSWTGAQFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 600
QY 622 DHWEKAVITVQRPGRIPTRSSRCGNTIPDDNQVVSLSPGSRVYVLPVPVCFEKGNTYTVR 681
DB 601 DHWEKAVITVQRPGRIPTRSSRCGNTIPDDNQVVSLSPGSRVYVLPVPVCFEKGNTYTVR 660
QY 682 LELPQYTSSDSDVESPYTLIDSLVLMPCYKSLDIFTVGGSGDGVVNTNSAWETFORICLSE 741
DB 661 LELPQYTSSDSDVESPYTLIDSLVLMPCYKSLDIFTVGGSGDGVVNTNSAWETFORICLSE 720
QY 742 NSRSVVKTPMTDVCNRIIFISALLHQTGLACECDPQGSLSVCDPNGGQCQCRPNVYVGR 801
DB 721 NSRSVVKTPMTDVCNRIIFISALLHQTGLACECDPQGSLSVCDPNGGQCQCRPNVYVGR 780
QY 802 TCNRCAPGTFGPGSGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDRCCLPGHWGF 861

DB 781 TCNRCAPGTFGPGSGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDRCCLPGHWGF 840
QY 862 PSCQPCQCNHADDCCDPVTGECNQCQDYTMGHNCERCCLAGYVGDPIIGSGDHCRPCPCPD 921
DB 841 PSCQPCQCNHADDCCDPVTGECNQCQDYTMGHNCERCCLAGYVGDPIIGSGDHCRPCPCPD 900
QY 922 GPDSGRQFARSCYQDPVTIQLACVCDPVGIGRCDCCASGYFGNPNSEVGGSCQPCQCHNN 981
DB 901 GPDSGRQFARSCYQDPVTIQLACVCDPVGIGRCDCCASGYFGNPNSEVGGSCQPCQCHNN 960
QY 982 IDTTDPEACDKETGRCLKCLVHTEGEHCQFCRFYGYGDALRQDCRKCVCNLYLGTVEHCN 1041
DB 961 IDTTDPEACDKETGRCLKCLVHTEGEHCQFCRFYGYGDALRQDCRKCVCNLYLGTVEHCN 1020
QY 1042 GSDCQCDKATGQCLCLPNVIGQNCDCRCAPTWQLASGTGCDPCNCAHAFSGPSCNEFTG 1101
DB 1021 GSDCQCDKATGQCLCLPNVIGQNCDCRCAPTWQLASGTGCDPCNCAHAFSGPSCNEFTG 1080
QY 1102 QCQCMPPGFGRTCTSECQELFWGDPDVECRACDCDPRGTETPQCDQSTGQCVCEGVEGPR 1161
DB 1081 QCQCMPPGFGRTCTSECQELFWGDPDVECRACDCDPRGTETPQCDQSTGQCVCEGVEGPR 1140
QY 1162 CDKCTRGYSGVFPDCTPCHQCFALMDVIIAELTNRTHRFLEKAKALKISGVIGYRETVD 1221
DB 1141 CDKCTRGYSGVFPDCTPCHQCFALMDVIIAELTNRTHRFLEKAKALKISGVIGYRETVD 1200
QY 1222 SVERKVSIEKIDILAQSPAAPLKNIGNLFEEAEKLIKDVTEMMAQVEVKLSDTTSQSNST 1281
DB 1201 SVERKVSIEKIDILAQSPAAPLKNIGNLFEEAEKLIKDVTEMMAQVEVKLSDTTSQSNST 1260
QY 1282 AKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTTE 1341
DB 1261 AKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTTE 1320
QY 1342 PNSTVEQSALMRDRVEDVMMERESQFKEQEEQARLLDELAKGLQSLDLSAAEMTCGTP 1401
DB 1321 PNSTVEQSALMRDRVEDVMMERESQFKEQEEQARLLDELAKGLQSLDLSAAEMTCGTP 1380
QY 1402 PGASCSETECGGPNCRITDEGRKCGGPGCGGLVTVAHNAWQKAMDLDQVLSALAEVEQL 1461
DB 1381 PGASCSETECGGPNCRITDEGRKCGGPGCGGLVTVAHNAWQKAMDLDQVLSALAEVEQL 1440
QY 1462 SKMVSEAKLRADAEAKQSAEDILLKTNATKEMDKSNEELRNLIKQIRNFLTQDSADLDSI 1521
DB 1441 SKMVSEAKLRADAEAKQSAEDILLKTNATKEMDKSNEELRNLIKQIRNFLTQDSADLDSI 1500
QY 1522 EAVANEVLKMEPSTPQQLNLTEDIRERVESLSQVEVILQHSAAIDIAEAEMLLEAKRA 1581
DB 1501 EAVANEVLKMEPSTPQQLNLTEDIRERVESLSQVEVILQHSAAIDIAEAEMLLEAKRA 1560
QY 1582 SKSATDVKVTADVMKEALBEAEAKQAQAAEKAIAKQADEDIQGTQNLNLTSESSEETL 1641
DB 1561 SKSATDVKVTADVMKEALBEAEAKQAQAAEKAIAKQADEDIQGTQNLNLTSESSEETL 1620
QY 1642 FNASQRISELERNVSELKRAAQNQSGEAEYIEKVYTVKQSAEDVKKTLDGELDEKYKV 1701
DB 1621 FNASQRISELERNVSELKRAAQNQSGEAEYIEKVYTVKQSAEDVKKTLDGELDEKYKV 1680
QY 1702 ENLIAKKTESADARRKAEMLQNEAKTLQAQNSKLQALLKOLERYEDNQRYLEDKAQEL 1761
DB 1681 ENLIAKKTESADARRKAEMLQNEAKTLQAQNSKLQALLKOLERYEDNQRYLEDKAQEL 1740
QY 1762 ARLEGEVRSLLKDISQKVAVYSTCL 1786
DB 1741 ARLEGEVRSLLKDISQKVAVYSTCL 1765

RESULT 10
AAB48449
ID AAB48449 standard; protein; 1765 AA.
XX
AC AAB48449;

XX 02-MAR-2001 (first entry)
DT Human laminin 8 polypeptide, SEQ ID NO: 16.
XX
DE Human; laminin 8; neuroprotective; angiogenic; osteopathic;
KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;
KW vascular tissue injury; neural injury; angiogenesis regulation.
XX
OS Homo sapiens.
XX
PN WO200066732-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US011543.
XX
PR 30-APR-1999; 99US-0131720P.
PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.
PR 11-FEB-2000; 2000US-0182012P.
XX
PA (BIOS-) BIOSTRATUM INC.
XX
PA Kortessmaa J, Tryggvason K;
PI WPI; 2000-687539/67.
XX N-PSDB; AAC83710.
DR
DR Purified laminin 8 protein, useful for research and therapeutic purposes
PT including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.
XX
PS Claim 5; Page 163-168; 245pp; English.
XX
CC The present sequence is a laminin 8 polypeptide chain. Laminins are a
CC family of heterotrimeric glycoproteins that function via binding
CC interactions with neighbouring cell receptors and by forming laminin
CC networks. They are signalling molecules which influence cellular
CC function. Laminin 8 is useful for treating injuries to tissue of
CC mesenchymal origin, such as bone, cartilage, tendon, and ligament,
CC treating injuries to vascular tissue, promoting cell attachment and
CC migration, ex vivo cell therapy, improving the biocompatibility of
CC medical devices, and preparing improved cell culture devices and media.
CC Laminin 8 is also useful for promoting re-endothelialisation at the site
CC of vascular injuries, improving the take of grafts, improving the
CC biocompatibility of medical devices, treating neural injuries (neural
CC regeneration), regulating angiogenesis, and promoting cell attachment and
CC migration
XX
SQ Sequence 1765 AA;
Query Match 99.0%; Score 9654; DB 3; Length 1765;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps - 0;
QY 22 QEBEFSYGCAEGSCYPATGDLIIIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICNS 81
Db 1 QEBEFSYGCAEGSCYPATGDLIIIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICNS 60
QY 82 QDPYHETLNPDSHLIENVVTTFAPNRLKIWWQSENGVENVTIQLDLAEAFHFTHLIMTFK 141
Db 61 QDPYHETLNPDSHLIENVVTTFAPNRLKIWWQSENGVENVTIQLDLAEAFHFTHLIMTFK 120
QY 142 TFRPAAMLIERSDFGKTGWVYRYFAYDCEASFPFGISTGPMKKVDDIIICDSRYSDIEPST 201
Db 121 TFRPAAMLIERSDFGKTGWVYRYFAYDCEASFPFGISTGPMKKVDDIIICDSRYSDIEPST 180
QY 202 EGEVIFRALDPAFKIEDPSPRIQNLKLTNLRKFVKLHTLGDNLDSRMEIREKYIYA 261
Db 181 EGEVIFRALDPAFKIEDPSPRIQNLKLTNLRKFVKLHTLGDNLDSRMEIREKYIYA 240
QY 262 VYDMVVRGNCFCYGHASECAPVDGFNEVEGMVHGHCMCRHNTKGLNCELMDYFHDLPW 321

Db 241 VYDMVVRGNCFCYGHASECAPVDGFNEVEGMVHGHCMCRHNTKGLNCELMDYFHDLPW 300
QY 322 RPAEGRNSACKKNCNEHSISCHFDMAVYLATGNVSGVCDCCQHNMTGRNCEQCKPFY 381
Db 301 RPAEGRNSACKKNCNEHSISCHFDMAVYLATGNVSGVCDCCQHNMTGRNCEQCKPFY 360
QY 382 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFSTGLIAGQCRCKLNVEGEHCDVCK 441
Db 361 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFSTGLIAGQCRCKLNVEGEHCDVCK 420
QY 442 EGFYDLSSDPFGCKSCACNPLGTIPGGNPNCDSETGHYCKRLVTGQHCDCQCLPEHWGLS 501
Db 421 EGFYDLSSDPFGCKSCACNPLGTIPGGNPNCDSETGHYCKRLVTGQHCDCQCLPEHWGLS 480
QY 502 NDLDGCRPCDCDLGGALNNSCFAESGQCSRPHMIGRCQNEVEPGYYFATLDHYLYEABE 561
Db 481 NDLDGCRPCDCDLGGALNNSCFAESGQCSRPHMIGRCQNEVEPGYYFATLDHYLYEABE 540
QY 562 ANLPGVSIVERQYIQDRIPSWTGAQFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 621
Db 541 ANLPGVSIVERQYIQDRIPSWTGAQFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 600
QY 622 DHWEKAVITVORPGRIPRTSSRCNTIPDDDNQVVSLSFGSRVYVLPVPCFEKGTNYTVR 681
Db 601 DHWEKAVITVORPGRIPRTSSRCNTIPDDDNQVVSLSFGSRVYVLPVPCFEKGTNYTVR 660
QY 682 LELPQYTSDDSDVESPYTLIDSLVMPYCKSLDIFTVGSGDGVVNTNSAWETQRYRCLE 741
Db 661 LELPQYTSDDSDVESPYTLIDSLVMPYCKSLDIFTVGSGDGVVNTNSAWETQRYRCLE 720
QY 742 NSRSVVKTPMTDVCNIIIFSISALLHOTGLACECDPQSLSSVCDPNGGQCCQCRPNVGR 801
Db 721 NSRSVVKTPMTDVCNIIIFSISALLHOTGLACECDPQSLSSVCDPNGGQCCQCRPNVGR 780
QY 802 TCNRCAPGTFGFGPSGCKPCCEHLQGSVNAFCNPVTGQCHCFQGVYARQCDECLPGHWGF 861
Db 781 TCNRCAPGTFGFGPSGCKPCCEHLQGSVNAFCNPVTGQCHCFQGVYARQCDECLPGHWGF 840
QY 862 PSCQPCQCNHADDGDPVTGELNCDQYTMGNHCERCLAGYGDPIIGSGDHCRPCPCPD 921
Db 841 PSCQPCQCNHADDGDPVTGELNCDQYTMGNHCERCLAGYGDPIIGSGDHCRPCPCPD 900
QY 922 GPDSGRQFARSCYQDPVTIQLACVCDPQYIGSRCDCCASGYFGNPNSEVSGSCQPCQCHN 981
Db 901 GPDSGRQFARSCYQDPVTIQLACVCDPQYIGSRCDCCASGYFGNPNSEVSGSCQPCQCHN 960
QY 982 IDTTDPEACDKETGRCLKLYHTEGEHCQFCRFGYGDALRQDCRCKVCNVLGTVOEHCN 1041
Db 961 IDTTDPEACDKETGRCLKLYHTEGEHCQFCRFGYGDALRQDCRCKVCNVLGTVOEHCN 1020
QY 1042 GSDCCQDKATGQCLCLPNVIGQNCDCRCAPNTWOLASGTGCDPCNCAHSGPSCNEFTG 1101
Db 1021 GSDCCQDKATGQCLCLPNVIGQNCDCRCAPNTWOLASGTGCDPCNCAHSGPSCNEFTG 1080
QY 1102 QCQCMFGGRTCSECOELFWGDPDVECRACDCDPRGIETPQCDQSTGQCVCEGVEGPR 1161
Db 1081 QCQCMFGGRTCSECOELFWGDPDVECRACDCDPRGIETPQCDQSTGQCVCEGVEGPR 1140
QY 1162 CDKCTRGYSGVFPDCTPCHQCFALWDVIIAELTNRTHRFLEKAKALKISGVIQPYRETVD 1221
Db 1141 CDKCTRGYSGVFPDCTPCHQCFALWDVIIAELTNRTHRFLEKAKALKISGVIQPYRETVD 1200
QY 1222 SVERKYSEIKDILAQSPAAPPLKNIGNLFEEAEKLIKDVTEMAQVEVKLSDTTSQSNST 1281
Db 1201 SVERKYSEIKDILAQSPAAPPLKNIGNLFEEAEKLIKDVTEMAQVEVKLSDTTSQSNST 1260
QY 1282 AKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTTE 1341
Db 1261 AKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTTE 1320
QY 1342 PNSTVEQSALMRDRVEDVMMERESQFKEQEEQARLLDELAKLQSLDSAAAEMTCGTP 1401

Db 1321 PNSTVEQSALMRDRVEDVMMERESQFKEQEQEARLLDELAKQLQSLDLSAAEMTCGTP 1380
QY 1402 PGASCSETECGPNCRTDEGERKCGGPGCGGLVTVVAHNAWQKAMDLDQDVLALAEVEQL 1461
Db 1381 PGASCSETECGPNCRTDEGERKCGGPGCGGLVTVVAHNAWQKAMDLDQDVLALAEVEQL 1440
QY 1462 SKMVEAKLRADAEAKQSAEDILLKTNATKEKMDKSNELRNLIKQIRNFLTQDSADLDSI 1521
Db 1441 SKMVEAKLRADAEAKQSAEDILLKTNATKEKMDKSNELRNLIKQIRNFLTQDSADLDSI 1500
QY 1522 EAVANEVLKMEMPTPQQLQNLTERIRVESLSQVEVILQHSAAADIARAEMLLEAKRA 1581
Db 1501 EAVANEVLKMEMPTPQQLQNLTERIRVESLSQVEVILQHSAAADIARAEMLLEAKRA 1560
QY 1582 SKSATDVKTADVMVKEALEEAQKAAQVAAEKAQKQADEDIQGTQNLTSISSETAASEETL 1641
Db 1561 SKSATDVKTADVMVKEALEEAQKAAQVAAEKAQKQADEDIQGTQNLTSISSETAASEETL 1620
QY 1642 FNASQRISSELRNVEELKRKAQNSGEAEYIEKVVTYVKSQSAEDVKKTLTGELDEKYYKV 1701
Db 1621 FNASQRISSELRNVEELKRKAQNSGEAEYIEKVVTYVKSQSAEDVKKTLTGELDEKYYKV 1680
QY 1702 ENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLLKDLERKYEDNQBYLEDKAQEL 1761
Db 1681 ENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLLKDLERKYEDNQBYLEDKAQEL 1740
QY 1762 ARLEGEVRSLLKDISQKVAVYSTCL 1786
Db 1741 ARLEGEVRSLLKDISQKVAVYSTCL 1765

RESULT 11

ABB81591
ID ABB81591 standard; protein; 1765 AA.

XX ABB81591;

DT 19-SEP-2002 (first entry)

DE Human laminin 10 second chain protein sequence SEQ ID NO:8.

XX Laminin alpha 5; laminin 10; vulnerary; cell growth; differentiation;
KW tissue repair development; laminin; healing; vascular tissue;
KW re-endothelialisation; vascular injury; cell attachment; cell stasis;
KW proliferation; migration.

XX Homo sapiens.

OS WO200250111-A2.

PN 27-JUN-2002.

XX 21-DEC-2001; 2001WO-US051035.

XX 21-DEC-2000; 2000US-0257449P.

PR 28-MAR-2001; 2001US-0279282P.

PR 13-NOV-2001; 2001US-00279282.

XX (BIOS-) BIOSTRATUM INC.

XX Tryggvason K, Doi M, Thyboll J;

XX WPI; 2002-557650/59.

DR N-PSDB; ABQ72909.

XX New human laminin-10 proteins, useful for accelerating the healing of
PT vascular tissue, improving the biocompatibility of grafts, or for
PT promoting re-endothelialization at the site of vascular injuries.

XX Claim 9; Page 126-132; 231pp; English.

XX The present invention describes human laminin alpha 5. Also described is
CC an isolated laminin 10. Laminin 10 has vulnerary activity. Laminins are

CC useful in maintaining cell/tissue phenotype as well as promoting cell
CC growth and differentiation in tissue repair development. Specifically,
CC laminin 10 can be used for accelerating the healing injuries of vascular
CC tissue, improving the biocompatibility of grafts useful for treating such
CC injuries, for promoting re-endothelialisation at the site of vascular
CC injuries, and promote cell attachment and subsequent cell stasis,
CC proliferation, differentiation, and/or migration. The present sequence
CC represents a second chain protein of laminin 10, from the present
CC invention

XX SQ Sequence 1765 AA;

Query Match 99.0%; Score 9654; DB 5; Length 1765;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 QEPFSGYCAEGSCYPATGDLILIGRAQKLSVTSTCGLHKPEPPIVSHLQEDKKCFICNS 81

Db 1 QEPFSGYCAEGSCYPATGDLILIGRAQKLSVTSTCGLHKPEPPIVSHLQEDKKCFICNS 60

QY 82 QDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENVTIQLDLEAEFFHFLIMTFK 141

Db 61 QDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENVTIQLDLEAEFFHFLIMTFK 120

QY 142 TFRPAAMLIERSDDFGKTGWVYRYFAYDCEASFPPISTGPMKKVDDIICDSRYSDIEPST 201

Db 121 TFRPAAMLIERSDDFGKTGWVYRYFAYDCEASFPPISTGPMKKVDDIICDSRYSDIEPST 180

QY 202 EGEVIFRALDPAFKIEDPSPRIQNLKLTNLRKFVXLHTLGDNLDSRMEIREKYYA 261

Db 181 EGEVIFRALDPAFKIEDPSPRIQNLKLTNLRKFVXLHTLGDNLDSRMEIREKYYA 240

QY 262 VYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGHCMCRHNTKGLNCELMDPYHDLPW 321

Db 241 VYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGHCMCRHNTKGLNCELMDPYHDLPW 300

QY 322 RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGVCDCCQHTMTGRNCEQCKPFY 381

Db 301 RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGVCDCCQHTMTGRNCEQCKPFY 360

QY 382 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFDSTGLIAGQCRCKLNVEGEHCDVCK 441

Db 361 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFDSTGLIAGQCRCKLNVEGEHCDVCK 420

QY 442 EGFYDLSSDDPFGCKSCACNPLGTPGPNPCDSETGHCYCKRLVTGQHCDCQCLPEHWGLS 501

Db 421 EGFYDLSSDDPFGCKSCACNPLGTPGPNPCDSETGHCYCKRLVTGQHCDCQCLPEHWGLS 480

QY 502 NDLGCRPCDCDLGGALNNSCFABSGQCSRPHMIGRQNEVEPGYYFATLDHYLYEABE 561

Db 481 NDLGCRPCDCDLGGALNNSCFABSGQCSRPHMIGRQNEVEPGYYFATLDHYLYEABE 540

QY 562 ANLPGVSIIVERQYIQDRIPSWTGAQFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 621

Db 541 ANLPGVSIIVERQYIQDRIPSWTGAQFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 600

QY 622 DHWEKAVITVQRPGRIPRTSSRCNTIPDDDNQVVSLSFGSRYVVLPRPVCCEKGTNYTVR 681

Db 601 DHWEKAVITVQRPGRIPRTSSRCNTIPDDDNQVVSLSFGSRYVVLPRPVCCEKGTNYTVR 660

QY 682 LELPQYTSDDSDVESPYTLIDSLVMPYCKSLDIFTVGGSGDGVVNTNSAWETFORYRCLE 741

Db 661 LELPQYTSDDSDVESPYTLIDSLVMPYCKSLDIFTVGGSGDGVVNTNSAWETFORYRCLE 720

QY 742 NSRSVVKTPMTDVCNRIIFSISALLHOTGLACECDPQGLSSVCDPNGGQCCQCPNVVGR 801

Db 721 NSRSVVKTPMTDVCNRIIFSISALLHOTGLACECDPQGLSSVCDPNGGQCCQCPNVVGR 780

QY 802 TCNRCAPGTFFGPGSGCKPCCEHLQGSVNAFCNPVTGQCHCFQGVYARQCDCCLPGHWGF 861

Db 781 TCNRCAPGTFFGPGSGCKPCCEHLQGSVNAFCNPVTGQCHCFQGVYARQCDCCLPGHWGF 840

QY 862 PSCQPCQCNHADDCCDPVTGECINQDQYTMGNCRCLAGYGDPIIGSGDHCRPCPCPD 921

Db 841 PSCQPCQCNHADDGDPVTGECNCDYTWGNCERCLAGYGDPIGSGDHCRCPCPD 900
QY 922 GPDSGRQFARSCYQDPVTLQLACVCDPGYIGSRCDCCASGYFGNPNSEVGGSCQPCQCHNN 981
Db 901 GPDSGRQFARSCYQDPVTLQLACVCDPGYIGSRCDCCASGYFGNPNSEVGGSCQPCQCHNN 960
QY 982 IDTTDPEACDKETGRCLKCLYHTEGEHCQCFRFGYGDALRQDCRKVCNLYLGTVEHCN 1041
Db 961 IDTTDPEACDKETGRCLKCLYHTEGEHCQCFRFGYGDALRQDCRKVCNLYLGTVEHCN 1020
QY 1042 GSDCQCDKATGQCLCLPNVIGQNCDCRCAPNTWQLASGTGCDPCNCAHSGFSPSCNEFTG 1101
Db 1021 GSDCQCDKATGQCLCLPNVIGQNCDCRCAPNTWQLASGTGCDPCNCAHSGFSPSCNEFTG 1080
QY 1102 QCQCMGFGGRTCTSECQELFWGDDPVECRACDQDPRGIETPQCDQSTGQCVCEVGEVGP 1161
Db 1081 QCQCMGFGGRTCTSECQELFWGDDPVECRACDQDPRGIETPQCDQSTGQCVCEVGEVGP 1140
QY 1162 CDKCTRGYSVGFDPCTPCHQCFALWDVIIAELTNRTHRFLEKAKALKISGVIGPYRETVD 1221
Db 1141 CDKCTRGYSVGFDPCTPCHQCFALWDVIIAELTNRTHRFLEKAKALKISGVIGPYRETVD 1200
QY 1222 SVRKVSEIKDILAQSPAAPLKNIGNLFEEAEKLIKDVTEMAQVEVKLSDDTTSQSNST 1281
Db 1201 SVRKVSEIKDILAQSPAAPLKNIGNLFEEAEKLIKDVTEMAQVEVKLSDDTTSQSNST 1260
QY 1282 AKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAERVNASTTE 1341
Db 1261 AKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAERVNASTTE 1320
QY 1342 PNSTVEQSALMRDRVEDVMMERESQFKEQEEQARLLDELAKGLQSLDLSAAEMTCGTP 1401
Db 1321 PNSTVEQSALMRDRVEDVMMERESQFKEQEEQARLLDELAKGLQSLDLSAAEMTCGTP 1380
QY 1402 PGASCSETECGGPNCRTEDEGERKCGGPGGLVTVAHNAWQKAMDLDQDVLSALAEVEQL 1461
Db 1381 PGASCSETECGGPNCRTEDEGERKCGGPGGLVTVAHNAWQKAMDLDQDVLSALAEVEQL 1440
QY 1462 SKVSEAKLRADAEAKQSAEDILLKTNATKEKMDKSNELRNLIKQIRNFLTQDSADLDSI 1521
Db 1441 SKVSEAKLRADAEAKQSAEDILLKTNATKEKMDKSNELRNLIKQIRNFLTQDSADLDSI 1500
QY 1522 EAVANEVLKMEPSTPQQLNLTEDIRERVESLSQVEVILQHSAAADIARAEMLLLEEAKRA 1581
Db 1501 EAVANEVLKMEPSTPQQLNLTEDIRERVESLSQVEVILQHSAAADIARAEMLLLEEAKRA 1560
QY 1582 SKSATDVKVTADMVKEALEEAEKQAAVAAEKAQKQADEDIQGTQNLTSIESETAASEETL 1641
Db 1561 SKSATDVKVTADMVKEALEEAEKQAAVAAEKAQKQADEDIQGTQNLTSIESETAASEETL 1620
QY 1642 FNASQRISSELRNVEELKRKAQNSGEAEYIEKVVTYVQSAEDVKKTLGDELDEKYKV 1701
Db 1621 FNASQRISSELRNVEELKRKAQNSGEAEYIEKVVTYVQSAEDVKKTLGDELDEKYKV 1680
QY 1702 ENLIAKTEESADARRKAEMLQNEAKTLLAQANSKQLLKDLEKRYEDNQRYLEDKAQEL 1761
Db 1681 ENLIAKTEESADARRKAEMLQNEAKTLLAQANSKQLLKDLEKRYEDNQRYLEDKAQEL 1740
QY 1762 ARLEGEVRSLLKDISQKVAVYSTCL 1786
Db 1741 ARLEGEVRSLLKDISQKVAVYSTCL 1765

RESULT 12
AAB19799
ID AAB19799 standard; protein; 1786 AA.

XX AAB19799;

AC AAB19799;
XX 05-MAR-2001 (first entry)

XX Mouse laminin 2 beta-1 chain.

XX Laminin 2; mouse; nerve regeneration; angiogenic; cell adhesion;
KW degenerative muscle disorder; muscular dystrophy; cell therapy.
XX Mus musculus.
OS Key Location/Qualifiers
FH Peptide 1..21
FT /label= Signal_peptide
FT Protein 22..1786
FT /label= Mature_protein
XX WO200066730-A2.
PN 09-NOV-2000.
XX 28-APR-2000; 2000WO-US011378.
PF 30-APR-1999; 99US-0131720P.
PR 15-JUN-1999; 99US-0139198P.
PR 12-JUL-1999; 99US-0143289P.
PR 24-SEP-1999; 99US-0155945P.
XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
PA Yurchenco P;
XX WPI; 2000-687537/67.
XX N-PSDB; AAA88899.
DR Purified laminin 2 protein, useful for research and therapeutic purposes
DR including peripheral nerve regeneration, treatment of degenerative muscle
XX disorders, angiogenesis regulation, and ex vivo cell therapy.
PT Claim 5; Page 212-218; 305pp; English.
PT The present sequence is that of the beta-1 chain of mouse laminin 2.
XX Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1
CC (100 kDa) chains. It is thought to be specifically required for
CC stabilizing myotubes during skeletal muscle development, and for
CC preventing apoptosis. Genetic defects in human laminin 2 structure or
CC expression are associated with a major type of congenital muscular
CC dystrophy. Laminin 2 is also thought to be important in Schwann
CC cell/basal lamina interactions. The invention provides laminin 2 alpha-2,
CC beta-1 and gamma-1 chain polypeptides (see AAB19791-806) and the
CC polynucleotides encoding them (see AAA88891-906), methods for making
CC recombinant laminin 2, cells that express recombinant laminin 2, and
CC methods for using purified laminin 2 for research and therapeutic
CC purposes including peripheral nerve regeneration, treatment of
CC degenerative muscle disorders, angiogenesis regulation, promoting cell
CC attachment and migration, ex vivo cell therapy, improving the take of
CC grafts, improving the biocompatibility of medical devices and preparing
CC improved culture devices and media
XX Sequence 1786 AA;
SQ

Query Match 93.7%; Score 9144; DB 3; Length 1786;
Best Local Similarity 92.7%; Pred. No. 0;
Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;

QY 1 MGLLQLLAFSFLALCRARVRAQEPPEFSYGCAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60
Db 1 MGLLQVFAFGVLALWGTRVCAQEPPEFSYGCAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60
QY 61 PEPYCIIVSHLQEDKKCFICNSQDPYHETLNPDLSHLIENVVTFAPNRLKIWWQSENGVEN 120
Db 61 PEPYCIIVSHLQEDKKCFICDSRDPYHETLNPDLSHLIENVVTFAPNRLKIWWQSENGVEN 120
QY 121 VTIQDLLEAEFHTHLIMTFKTRFPAAMLIERSDDFGKWTGVTYFAYDCEASFPGISTG 180
Db 121 VTIQDLLEAEFHTHLIMTFKTRFPAAMLIERSDDFGKWTGVTYFAYDCEASFPGISTG 180
QY 181 PMKKVDDIICDSRYSIEPSTEGETEVIFFALDPAFKIEDPYSPIQNLLKITNLRIFVKL 240

PS	Claim 5; Page 176-182; 245pp; English.		
XX	The present sequence is a laminin 8 polypeptide chain. Laminins are a family of heterotrimeric glycoproteins that function via binding interactions with neighbouring cell receptors and by forming laminin networks. They are signalling molecules which influence cellular function. Laminin 8 is useful for treating injuries to tissue of mesenchymal origin, such as bone, cartilage, tendon, and ligament, treating injuries to vascular tissue, promoting cell attachment and migration, ex vivo cell therapy, improving the biocompatibility of medical devices, and preparing improved cell culture devices and media. Laminin 8 is also useful for promoting re-endothelialisation at the site of vascular injuries, improving the take of grafts, improving the biocompatibility of medical devices, treating neural injuries (neural regeneration), regulating angiogenesis, and promoting cell attachment and migration		
XX			
SQ	Sequence 1786 AA;		
	Query Match 93.7%; Score 9144; DB 3; Length 1786;		
	Best Local Similarity 92.7%; Pred. No. 0;		
	Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;		
QY	1 MGLLQLLAFSLALCRARVRAQEPESYGAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60		
Db	1 MGLLQVFAFGVLAALWGTRVCAQEPESYGAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60		
QY	61 PEPYCIYVSHLQEDKKCFICNSQDPYHETLNPDLSHLIENVVTFAPNRLKIWQSENGVEN 120		
Db	61 PEPYCIYVSHLQEDKKCFICDSRDPYHETLNPDLSHLIENVVTFAPNRLKIWQSENGVEN 120		
QY	121 VTIQLDLAEHFHETHLIMTFKTRPAAMLIERSDFGKTGWVRYFAYDCEASFPGISTG 180		
Db	121 VTIQLDLAEHFHETHLIMTFKTRPAAMLIERSDFGKTGWVRYFAYDCESSFPGISTG 180		
QY	181 PMKKVDDIIICSRYSYDIEPSTEGEVIIFRALDPAFKIEDPYSPIQNLLKITNLRIFVKL 240		
Db	181 PMKKVDDIIICSRYSYDIEPSTEGEVIIFRALDPAFKIEDPYSPIQNLLKITNLRIFVKL 240		
QY	241 HTLGDNLLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGCMC 300		
Db	241 HTLGDNLLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMC 300		
QY	301 RHNTKGLNCELMDPYHDLWPRAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGG 360		
Db	301 RHNTKGLNCELMDPYHDLWPRAEGRNSNACKKNCNEHSSCHFDMAVFLATGNVSGG 360		
QY	361 VCDCCQHTNMGRCBOCKPFYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSG 420		
Db	361 VCDNCQHTNMGRCBOCKPFYQHPERDIRDPNLCEPCTCDPAGSNGGICDGYTDFSVG 420		
QY	421 LIAGQCRCKLHVEGEHCDVCKEGFYDLSSDDPFGCKSCACNPLGTIPGPNPCDSETGHY 480		
Db	421 LIAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGPNPCDSETGYC 480		
QY	481 CKRLVTGQHCDCQLPEHGLSNDLDGCRPCDCLGGALNNSCFABSGQSCSRPHMIGRQC 540		
Db	481 CKRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCLGGALNNSCSEDSGQCSCLPHMIGRQC 540		
QY	541 NEVEPGYYFATLDHYLYEAEEANLPGVSVIVERQYIQDRIPSWTGAGFVRVPEGAYLEFF 600		
Db	541 NEVESGYFTTLDHYLYEAEEANLPGVVVVERQYIQDRIPSWTGTGFRVVRVPEGAYLEFF 600		
QY	601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPTRSSRCNGTIPDDNQVVSLSPG 660		
Db	601 IDNIPYSMEYEILIRYEPQLPDHWEKAVITVQRPKIPASSRCNGTIPDDNQVVSLSPG 660		
QY	661 SRYVVLPRPVCFEKGTNYTVRLELPQYTSDDSDVESPYTLIDSVLMPYCKSLDIFTVGG 720		
Db	661 SRYVVLPRPVCFEKGMNVTYRLELPQYTAGSDVESPYTFIDSVLMPYCKSLDIFTVGG 720		
QY	721 SGDGVTNSAWETFORYRCLNSRSRVKTPMTDVCRNIIFISALIHQTLGACEDCPQS 780		

721	SGDGEVTNSAWETFORYRCLNSRSRVKTPMTDVCRNIIFISALIHQTLGACEDCPQS	780
QY	781 LSSVCDPNGGQCQCRPNVVGRTCNRCAPGTFGFGSPGCKPCECHLQGSVNAFCNPVTGQC	840
Db	781 LSSVCDPNGGQCQCRPNVVGRTCNRCAPGTFGFGPNGCKPCDCHLQGSASAFCDAITGQC	840
QY	841 HCFQGVYARQCDRCLPGHWGFPSPCQPCQCNHGADDCDPVTGECNLNQDYYTMHNCERCLA	900
Db	841 HCFQGIYARQCDRCLPGYWGFSPCQPCQCNHGALDCDVTGECNLCQDYYTTHNCERCLA	900
QY	901 GYGDPPIIGSGDHCRCPCPCDPDPSGRQFARSCYQDPVTIQLACVCDPGYIGSRCDDCAS	960
Db	901 GYGDPPIIGSGDHCRCPCPCDPDPSGRQFARSCYQDPVTIQLACVCDPGYIGSRCDDCAS	960
QY	961 GYFNPSEVGGSCQPCQCHNNIDTTDPEACDKETGRCLUKCLYHTEGEHCQCFRFGYIGDA	1020
Db	961 GFFGNPSDFGGSCQPCQCHNNIDTTDPEACDKDTGRCLUKCLYHTEGDHCQLCQYGYIGDA	1020
QY	1021 LRQDCRKVCVNYLGTVQEHNGSGDCQCDKATGQCCLCPNVIGQNCDCRCAPNTWQLASGTG	1080
Db	1021 LRQDCRKVCVNYLGTVKEHNGSGDCHCDKATGQCSCLPNVIGQNCDCRCAPNTWQLASGTG	1080
QY	1081 CDPCCNAAHSFGPSCNEFTGQCQCMFPGFGGRTCSQCQELFWGDDPVECRACDCDPRGIE	1140
Db	1081 CGPCNCNAAHSFGPSCNEFTGQCQCMFPGFGGRTCSQCQELFWGDDPVECRACDCDPRGIE	1140
QY	1141 TPQCDOSTGQCVCVEGVEGPRCDKCTRGYSGVFPDCTPCHQCFALWDVIIAELTNRTHRF	1200
Db	1141 TPQCDOSTGQCVCVEGVEGPRCDKCTRGYSGVFPDCTPCHQCFALWDVIIIGELTNRTHKF	1200
QY	1201 LEKAKALKISGVIGPYRETVDVSVERKVSEIKDILAQSPAEPPLKNIGNLFEEAEKLIKDV	1260
Db	1201 LEKAKALKISGVIGPYRETVDVSVEKKVNEIKDILAQSPAEPPLKNIGILFEEAEKLIKDV	1260
QY	1261 TEMMAQVEVKLSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDS	1320
Db	1261 TEKMAQVEVKLTDTASQSNSTAGELGALQAEAESLDKTVKELAEQLEFIKNSDIQGALDS	1320
QY	1321 ITKYFQMSLEAEERVNASATTPEPNSVTEQSALMRDRVEDVMMERESQFKEQEEQARLLDE	1380
Db	1321 ITKYFQMSLEAEKRVNASATTDPNSTVEQSALTRDRVEDLMLERESPFFKEQEEQARLLDE	1380
QY	1381 LAGKLSLDLSAAAEWTCGTPPGASCSETECGGPNCRCTDEGRKCGGPGCGGLVTVAHNA	1440
Db	1381 LAGKLSLDLSAAQMTGCTPPGADCSSECGGPNCRCTDEGKKCGGPGCGGLVTVAHSA	1440
QY	1441 WQKAMDLDQDVLALAEVEQLSKMVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNEEL	1500
Db	1441 WQKAMDFDRDVLALAEVEQLSKMVSEAKVRADEAKQNAQDVLKTNATKEKVDKSNEDL	1500
QY	1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKMWMPSTPQOLQNLNLTEDIRERVEISLSQVEVI	1560
Db	1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKSGNASTPQOLQNLNLTEDIRERVEITLSQVEVI	1560
QY	1561 LQHSAAADIARAEMLLEAEAKRASKSATDVKVTADMVKEALEEAEAKQVAAEKAIQOADEDI	1620
Db	1561 LQQSAADIARAEMLLEAEAKRASKSATDVKVTADMVKEALEEAEAKQVAAEKAIQOADEDI	1620
QY	1621 QGTQNLNLTISSETAAASEETLFNASQRISELERNVVEELKRKAQNSGEABEYIEKVYTVK	1680
Db	1621 QGTQNLNLTISSETAAASEETLTNASQRIKSLERNVEELKRKAQNSGEABEYIEKVYSVK	1680
QY	1681 QSAEDVKKTLDGELDEKIKVENLIAKKTTEESADARRKAEMLQNEAKTLLAQANSKLQLL	1740
Db	1681 QNADDVKKTLDGELDEKIKKVESLIAQKTEESADARRKAELLQNEAKTLLAQANSKLQLL	1740
QY	1741 KDLEKRYEDNQRYLEDKAQELARLEGEVRSLLKDISQKAVYSTCL 1786	
Db	1741 EDLEKRYEDNQRYLEDKAQELVRLEGEVRSLLKDISKAVYSTCL 1786	
	RESULT 14	
	ABB81592	

RESULT 14
ABB81592

ID ABB81592 standard; protein; 1786 AA.
XX ABB81592;
AC ABB81592;
DT 19-SEP-2002 (first entry)
XX Mouse laminin 10 second chain protein sequence SEQ ID NO:10.
DE
XX Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;
KW tissue repair development; laminin; healing; vascular tissue;
KW re-endothelialisation; vascular injury; cell attachment; cell stasis;
KW proliferation; migration.
XX Mus musculus.
OS
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT /label= signal
FT Protein 22..1786
FT /label= laminin_10_second_chain
XX WO200250111-A2.
PN
XX
PD 27-JUN-2002.
XX
PF 21-DEC-2001; 2001WO-US051035.
XX
PR 21-DEC-2000; 2000US-0257449P.
PR 28-MAR-2001; 2001US-0279282P.
PR 13-NOV-2001; 2001US-00279282.
XX
PA (BIOS-) BIOSTRATUM INC.
XX
PI Tryggvason K, Doi M, Thyboll J;
XX
DR WPI; 2002-557650/59.
DR N-PSDB; ABQ72910.
XX
PT New human laminin-10 proteins, useful for accelerating the healing of
PT vascular tissue, improving the biocompatibility of grafts, or for
PT promoting re-endothelialization at the site of vascular injuries.
XX
PS Claim 9; Page 140-145; 231pp; English.
XX
CC The present invention describes human laminin alpha 5. Also described is
CC an isolated laminin 10. Laminin 10 has vulnerary activity. Laminins are
CC useful in maintaining cell/tissue phenotype as well as promoting cell
CC growth and differentiation in tissue repair development. Specifically,
CC laminin 10 can be used for accelerating the healing injuries of vascular
CC tissue, improving the biocompatibility of grafts useful for treating such
CC injuries, for promoting re-endothelialisation at the site of vascular
CC injuries, and promote cell attachment and subsequent cell stasis,
CC proliferation, differentiation, and/or migration. The present sequence
CC encodes a second chain protein of laminin 10, from the present invention
XX
SQ Sequence 1786 AA;
Query Match 93.7%; Score 9144; DB 5; Length 1786;
Best Local Similarity 92.7%; Pred. No. 0;
Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;
QY 1 MGLLQLLAFSFLACRARVRAQEPFSGYCAEGSCYPATGDLILGRAQKLSVTSTCGLHK 60
Db 1 MGLLQVFAFGVLALWGTRVCAQEPFSGYCAEGSCYPATGDLILGRAQKLSVTSTCGLHK 60
QY 61 PEPYCIIVSHLQEDKKCFICNSQDPYHETLNPDHSHLIENVVTFAPNRLKIWQSENGVEN 120
Db 61 PEPYCIIVSHLQEDKKCFICDSRDPYHETLNPDHSHLIENVVTFAPNRLKIWQSENGVEN 120
QY 121 VTIQDLLEAEFFHFLIMTFKTRPAAMLIERSDDFGKTGWGVYRYFAYDCEASFPGISTG 180
Db 121 VTIQDLLEAEFFHFLIMTFKTRPAAMLIERSDDFGKTGWGVYRYFAYDCESSFPGISTG 180

QY 181 PMKKVDDIIICDSRYSDIEPSTEGEVIFFRALDPAFKIEDPYSPIQNLLKITNLRIKFVKL 240
Db 181 PMKKVDDIIICDSRYSDIEPSTEGEVIFFRALDPAFKIEDPYSPIQNLLKITNLRIKFVKL 240
QY 241 HTLGDNLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGCMC 300
Db 241 HTLGDNLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGCMC 300
QY 301 RHNTKGLNCELWDFYHDLPMRPAEGRNSNACKKCNENHSISCHDFMAVYLATGNVSGG 360
Db 301 RHNTKGLNCELWDFYHDLPMRPAEGRNSNACKKCNENHSISCHDFMAVYLATGNVSGG 360
QY 361 VDDCCQHNMTMGRNCEQCKPFYFQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTG 420
Db 361 VDDCCQHNMTMGRNCEQCKPFYFQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTG 420
QY 421 LIAGQCRCKLNVGEHCDVCKEGFYDLSSDDPFGCKSCACNPLGTIPGNGPCDSETGHY 480
Db 421 LIAGQCRCKLNVGEHCDVCKEGFYDLSSDDPFGCKSCACNPLGTIPGNGPCDSETGHY 480
QY 481 CKRLVTGQHCDOCLPEHWGLSNDLDGCRPCDCLGGALNNSCFAESGQSCSRPHMIGRQC 540
Db 481 CKRLVTGQHCDOCLPEHWGLSNDLDGCRPCDCLGGALNNSCFAESGQSCSRPHMIGRQC 540
QY 541 NEVEPGYFFATLDHYLYEAEANLPGVSVIVERQYIQRIPSWTGAQFVRVPEGAYLEFF 600
Db 541 NEVEPGYFFATLDHYLYEAEANLPGVSVIVERQYIQRIPSWTGAQFVRVPEGAYLEFF 600
QY 601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVORPGRIPTSRRSGNTIPDDNQVWSLSPG 660
Db 601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVORPGRIPTSRRSGNTIPDDNQVWSLSPG 660
QY 661 SRYVVLPRPVCFEKGTNYTVRLELPQYTSDDSDVESPYTLIDSLVLMYPYCKSLDIFTVGG 720
Db 661 SRYVVLPRPVCFEKGTNYTVRLELPQYTSDDSDVESPYTLIDSLVLMYPYCKSLDIFTVGG 720
QY 721 SGDGVTNSAWETFORRCLENSRSVVKTPMTDVCNIIIFSISALLHQTGLACECDPQGS 780
Db 721 SGDGVTNSAWETFORRCLENSRSVVKTPMTDVCNIIIFSISALLHQTGLACECDPQGS 780
QY 781 LSSVCDPNGGQCCRPNVGRTCNRCAPGTGFGPSGCKPCCECHLQGSVNAFCNPVTGQC 840
Db 781 LSSVCDPNGGQCCRPNVGRTCNRCAPGTGFGPSGCKPCCECHLQGSVNAFCNPVTGQC 840
QY 841 HCFQGVYARQCRLPGHWGFPSCQPCQCNHADDCCDPVTGECLNCDYTMGHNCERCLA 900
Db 841 HCFQGVYARQCRLPGHWGFPSCQPCQCNHADDCCDPVTGECLNCDYTMGHNCERCLA 900
QY 901 GYGDPIIGSGDHCRPCPCPDGSDGRQFARSCYQDPVTQLQACVCDPVGYSRCDCCAS 960
Db 901 GYGDPIIGSGDHCRPCPCPDGSDGRQFARSCYQDPVTQLQACVCDPVGYSRCDCCAS 960
QY 961 GYFQNPSEVGGSCQPCQCHNNDITDPEACDKETGRCLKCLYHTEGHCQFCRFGYGDG 1020
Db 961 GYFQNPSEVGGSCQPCQCHNNDITDPEACDKETGRCLKCLYHTEGHCQFCRFGYGDG 1020
QY 1021 LRQDCRKCVCNYLGTVQEHCHNGSDCCQCKATGQCLCLPNVIGONCDRCAPNTWOLASGTG 1080
Db 1021 LRQDCRKCVCNYLGTVQEHCHNGSDCCQCKATGQCLCLPNVIGONCDRCAPNTWOLASGTG 1080
QY 1081 CDPNCNAAHSFGSCNEFTGQCQCMFPGGRTCTSECQELFWGDDPVECRACDCDPRGIE 1140
Db 1081 CDPNCNAAHSFGSCNEFTGQCQCMFPGGRTCTSECQELFWGDDPVECRACDCDPRGIE 1140
QY 1141 TPQCDQSTGQCVCVEGVEGPRCDKCTRGYSGVFPDCTPCHQCQFALWDVIAELTNRTHRF 1200
Db 1141 TPQCDQSTGQCVCVEGVEGPRCDKCTRGYSGVFPDCTPCHQCQFALWDVIAELTNRTHRF 1200
QY 1201 LEKAKALKISGVIGPYRETVDSEVERKVSSEIKDILAQSPAAEPLKNIGNLFEAEKLIKDV 1260
Db 1201 LEKAKALKISGVIGPYRETVDSEVERKVSSEIKDILAQSPAAEPLKNIGNLFEAEKLIKDV 1260
QY 1261 TEMMAQVEVKLSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDS 1320


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Db 1261 TERMAQVEVKLTDTASQSNSTAGELGALQAEASLDKTVKELAEQLEFIKNSDIQGALDS 1320
QY 1321 ITRKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVMMERESQFKEQEBEQARLLDE 1380
Db 1321 ITRKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLESFPFKEQEBEQARLLDE 1380
QY 1381 LACKIQLSLDLASAAEMTCGTPPGASCSETECGGPNCRDTDEGERKCGGPGCGGLVTVAHNA 1440
Db 1381 LAGKIQSLDLASAAQMTCTGTPPGADCSSECGGPNCRDTDEGEKKCGGPGCGGLVTVAHSA 1440
QY 1441 WQKAMDLDQDVLASALAEVEQLSKMVSEAKURADEAKQSAEDILLKTNATKMKDKSNEEL 1500
Db 1441 WQKAMDLDQDVLASALAEVEQLSKMVSEAKURADEAKQSAEDILLKTNATKMKDKSNEEL 1500
QY 1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKXMPSTPQOLQNLTEDIRERVESLSQVEVI 1560
Db 1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKXMPSTPQOLQNLTEDIRERVESLSQVEVI 1560
QY 1561 LQHSAAADIAEAEMLLLEAKRASKSATDVKVTADMVKEALEEAEKAQVAEKAQKQADEDI 1620
Db 1561 LQHSAAADIAEAEMLLLEAKRASKSATDVKVTADMVKEALEEAEKAQVAEKAQKQADEDI 1620
QY 1621 QGTQNLTSISETAASEETLFPNASQRISELERNVVEELKRAAQNKGAEYIEKVYTVK 1680
Db 1621 QGTQNLTSISETAASEETLFPNASQRISELERNVVEELKRAAQNKGAEYIEKVYTVK 1680
QY 1681 QSAEDVKKTLDGELDEKYYKVENLIKAKTEESADARRKAEMLQNEAKTLLAQANSKLQLL 1740
Db 1681 QSAEDVKKTLDGELDEKYYKVENLIKAKTEESADARRKAEMLQNEAKTLLAQANSKLQLL 1740
QY 1741 KDLERKYEDNQRYLEDKAQELARLEGEVRSLLKXDISQVAVYSTCL 1786
Db 1741 EDLERKYEDNQRYLEDKAQELARLEGEVRSLLKXDISQVAVYSTCL 1786
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RESULT 15
AAW50894
ID AAW50894 standard; protein; 1776 AA.
XX AC AAW50894;
XX DT 07-DEC-1998 (first entry)
XX DE Mouse laminin B1 chain.
XX LX Laminin; mouse; beta-amyloid; amyloidosis; Alzheimer's disease;
XX KW Down's syndrome; hereditary cerebral haemorrhage; inflammation;
XX KW malignancy; Familial Mediterranean Fever; multiple myeloma;
XX KW type II diabetes; prion disease; Creutzfeldt-Jacob disease; CJD;
XX KW Gertsmann-Straussler syndrome; kuru; scrapie; haemodialysis;
XX KW carpal tunnel syndrome; senile cardiac amyloid polynuropathy;
XX KW Familial Amyloidotic Polynuropathy; thyroid carcinoma; diagnosis;
XX KW therapy.
XX XX Mus sp.
XX OS WO9815179-A1.
XX PN 16-APR-1998.
XX PD 08-OCT-1997; 97WO-US018145.
XX PR 08-OCT-1996; 96US-0027981P.
XX XX (UNIW ) UNIV WASHINGTON.
XX PA Castillo G, Snow AD;
XX PI WPI; 1998-240534/21.
XX DR Use of laminin and fragments - for developing products for use in the
XX PT diagnosis and treatment of amyloid disease, e.g. Alzheimer's disease or
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PT CJD.
XX Claim 15; Page 90-93; 132pp; English.
XX This is the amino acid sequence of the mouse laminin B1 chain. The
CC primary object of the invention is to use laminin, laminin-derived
CC protein fragments and/or laminin-derived polypeptides as potent
CC inhibitors of amyloid formation, deposition, accumulation and/or
CC persistence in Alzheimer's disease and other amyloidoses. The laminin
CC products (see AAW50888-98) may include mouse or human laminin A or A1
CC chain, laminin B1 or B2 chain, laminin A2 chain (merosin), laminin G1
CC chain, the globular repeats of the laminin A1 chain and the beta-amyloid
CC binding domain of the laminin A chain. A claimed method for treating an
CC amyloid disease comprises administering a polypeptide having a
CC conformational similarity to a fragment of a laminin protein. A method
CC for diagnosing an amyloid disease involves determining levels of laminin
CC in a sample. Production of laminin or its fourth globular repeat in vivo
CC provides a method for in vivo inhibition of beta-amyloid amyloidosis. The
CC products and methods can be used for the diagnosis, prognosis, monitoring
CC and treatment of amyloidoses such as Alzheimer's disease, Down's syndrome
CC and hereditary cerebral haemorrhage with amyloidosis of the Dutch type
CC (where the specific amyloid is the beta-amyloid protein), the amyloidosis
CC associated with chronic inflammation, various forms of malignancy and
CC Familial Mediterranean Fever (AA amyloid or inflammation-association
CC amyloidosis), the amyloidosis associated with multiple myeloma and other
CC B-cell abnormalities (AL amyloid), the amyloidosis associated with type
CC II diabetes (amylin or islet amyloid), the amyloidosis associated with
CC prion diseases including Creutzfeldt-Jacob disease, Gertsmann-Straussler
CC syndrome, kuru and animal scrapie (Prp amyloid), the amyloidosis
CC associated with long-term haemodialysis and carpal tunnel syndrome (beta
CC 2-microglobulin amyloid), the amyloidosis associated with senile cardiac
CC amyloid and Familial Amyloidotic Polynuropathy (prealbumin or
CC transthyretin amyloid), and the amyloidosis associated with endocrine
CC tumours such as medullary carcinoma of the thyroid (variant of
CC procalsitonin)
XX SQ Sequence 1776 AA;
Query Match 93.2%; Score 9087; DB 2; Length 1776;
Best Local Similarity 92.5%; Pred. No. 0;
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Db 61 PEPYCIIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVEN 120
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Db 181 PMKKVDDIICDSRYSYDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLLKITNLRKFVKL 240
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QY 421 LIAGQCRCKLNVEGEHCDVCKEGFYDLSSDDPFGCKSCACNPLGTIPGPNPCDSETHCY 480
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QY	721	SGDGVVNTSAWETFQYRCLENSRSVVKTPMTDVCRNIIIFSISALLHOTGLACEDPQGS	780
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Db	901	GYGDP IIGSGDHCRPCPCPDGPDGSRGFARSCYQDPVTQLACVCDPGYIGSRCDDCAS	960
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QY	1021	LRQDCRKVCNYLGTVEHCNGSDCQCDKATGQCLCLPNVIGQNCDCRCAEPTWQLASGTG	1080
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OM protein - protein search, using sw model

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Title: US-10-037-182-6
Perfect score: 9754
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	9754	100.0	1786	4 US-09-562-702A-14	Sequence 14, Appl
2	9754	100.0	1786	4 US-09-561-818A-14	Sequence 14, Appl
3	9754	100.0	1786	4 US-09-561-709B-9	Sequence 9, Appl
4	9654	99.0	1765	4 US-09-562-702A-16	Sequence 16, Appl
5	9654	99.0	1765	4 US-09-561-818A-16	Sequence 16, Appl
6	9144	93.7	1786	4 US-09-562-702A-18	Sequence 18, Appl
7	9144	93.7	1786	4 US-09-561-818A-18	Sequence 18, Appl
8	8873	91.0	1725	4 US-09-562-702A-20	Sequence 20, Appl
9	8873	91.0	1725	4 US-09-561-818A-20	Sequence 20, Appl
10	6051.5	62.0	1196	1 US-08-144-121-4	Sequence 4, Appl
11	6051.5	62.0	1196	2 US-08-735-893-4	Sequence 4, Appl
12	5051.5	51.8	1799	4 US-09-845-583A-6	Sequence 6, Appl
13	4926.5	50.5	1798	4 US-09-561-709B-11	Sequence 11, Appl
14	4921.5	50.5	1798	4 US-09-845-583A-8	Sequence 8, Appl
15	3832.5	39.3	1761	4 US-09-561-709B-1	Sequence 1, Appl
16	3076.5	31.5	1101	4 US-09-561-709B-5	Sequence 5, Appl
17	2940.5	30.1	1342	4 US-09-561-709B-13	Sequence 13, Appl
18	1682	17.2	1605	4 US-09-562-702A-30	Sequence 30, Appl
19	1682	17.2	1605	4 US-09-561-818A-26	Sequence 26, Appl
20	1680.5	17.2	1609	4 US-09-562-702A-22	Sequence 22, Appl
21	1680.5	17.2	1609	4 US-09-561-818A-22	Sequence 22, Appl
22	1680.5	17.2	1617	4 US-09-562-702A-26	Sequence 26, Appl
23	1677	17.2	1572	4 US-09-562-702A-32	Sequence 32, Appl
24	1677	17.2	1572	4 US-09-561-818A-28	Sequence 28, Appl
25	1673	17.2	279	1 US-08-152-019A-29	Sequence 29, Appl
26	1673	17.2	1576	4 US-09-562-702A-24	Sequence 24, Appl
27	1673	17.2	1576	4 US-09-561-818A-24	Sequence 24, Appl

28	1673	17.2	1584	4 US-09-562-702A-28	Sequence 28, Appl
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39	1558.5	16.0	1172	4 US-09-919-172-16	Sequence 16, Appl
40	1543.5	15.8	1170	4 US-09-561-709B-12	Sequence 12, Appl
41	1539	15.8	3106	4 US-09-562-702A-10	Sequence 10, Appl
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45	1515.5	15.5	1587	4 US-09-845-583A-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-562-702A-14
; Sequence 14, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-14

Query Match 100.0%; Score 9754; DB 4; Length 1786;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 14, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortessmaa, Jarrko
; APPLICANT: Tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-818A-14

Query Match 100.0%; Score 9754; DB 4; Length 1786;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MGLLQLLAFSFLALCRARVRAQEPFSGCAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60
QY 61 PEPYCIIVSHLQEDKKCFICNSQDPYHETLNPD SHLIENVVTTFAPNRLKIWWQSENGVEN 120
DB 61 PEPYCIIVSHLQEDKKCFICNSQDPYHETLNPD SHLIENVVTTFAPNRLKIWWQSENGVEN 120
QY 121 VTIQDLLEAEFFHFTLIMTFTFRPAAMLIERSDDFGKTGWVYRYPAYDCEASPPGISTG 180
DB 121 VTIQDLLEAEFFHFTLIMTFTFRPAAMLIERSDDFGKTGWVYRYPAYDCEASPPGISTG 180
QY 181 PMKKVDDIIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPRIONLLKITNLRKFKVL 240
DB 181 PMKKVDDIIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPRIONLLKITNLRKFKVL 240
QY 241 HTLGDNLLDSRMEIREKYYIAYVDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGCMC 300
DB 241 HTLGDNLLDSRMEIREKYYIAYVDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGCMC 300
QY 301 RHNTKGLNCELQWDFYHDL PWRPAEGRNSNACKKCNCHSISCHFDMAVYLATGNVSGG 360

Db 301 RHNTKGLNCELCMDFYHDLPRWPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGG 360

QY 361 VCDDCQHNTMGRNCEOCKPFYYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSG 420

Db 361 VCDDCQHNTMGRNCEOCKPFYYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSG 420

QY 421 LIAGQCRCKLNVEGEHCDVCKEGFYDLSSDPFGCKSCACNPLGTIPGPNPCDSETGHY 480

Db 421 LIAGQCRCKLNVEGEHCDVCKEGFYDLSSDPFGCKSCACNPLGTIPGPNPCDSETGHY 480

QY 481 CKRLVTGQHCDCQCLPEHWGLSNDLDGCRPCDCLGALNNSCFAESGQCSRPHMIGRQC 540

Db 481 CKRLVTGQHCDCQCLPEHWGLSNDLDGCRPCDCLGALNNSCFAESGQCSRPHMIGRQC 540

QY 541 NEVEPGYYFATLDHYLYEAEEANLPGVSIVERQYIQDRIPSWTGAGFVRVPEGAYLEFF 600

Db 541 NEVEPGYYFATLDHYLYEAEEANLPGVSIVERQYIQDRIPSWTGAGFVRVPEGAYLEFF 600

QY 601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPTSRRCNGTIPDDNQVWSLSPG 660

Db 601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPTSRRCNGTIPDDNQVWSLSPG 660

QY 661 SRYVVLPRPVCFEKGTNYTVRLELPQYTTSSDSVESPYTLIDSLVLMPYCKSLDIFTVGG 720

Db 661 SRYVVLPRPVCFEKGTNYTVRLELPQYTTSSDSVESPYTLIDSLVLMPYCKSLDIFTVGG 720

QY 721 SGDGVVTNSAWETFORYRCLENSRSVVKTPMTDVCNIIIFSISALLHOTGLACECDPOGS 780

Db 721 SGDGVVTNSAWETFORYRCLENSRSVVKTPMTDVCNIIIFSISALLHOTGLACECDPOGS 780

QY 781 LSSVCDPNGGQCQCRPNVVRTCNRCAPGTFGFGSGCKPCECHLQGSVNAFCNPVTGQC 840

Db 781 LSSVCDPNGGQCQCRPNVVRTCNRCAPGTFGFGSGCKPCECHLQGSVNAFCNPVTGQC 840

QY 841 HCFQGVYARQCDRCLPGHWGFPSCQPCQCNCGHADDCDPVTGECNLCQDYTMHNCERCLA 900

Db 841 HCFQGVYARQCDRCLPGHWGFPSCQPCQCNCGHADDCDPVTGECNLCQDYTMHNCERCLA 900

QY 901 GYGDPIIGSDHCRPCPCDGPDSGRQFARSCYQDPVTQLACVCDPGYIGSRCDDCAS 960

Db 901 GYGDPIIGSDHCRPCPCDGPDSGRQFARSCYQDPVTQLACVCDPGYIGSRCDDCAS 960

QY 961 GYFGNPSVGGSCQPCQCHNIDTTPDPEACDKETGRCLKCLYHTEGEHCQCRFGYYGDA 1020

Db 961 GYFGNPSVGGSCQPCQCHNIDTTPDPEACDKETGRCLKCLYHTEGEHCQCRFGYYGDA 1020

QY 1021 LRQDCRKVCNYLGTVOEHONGSDCQCDKATGQCLCPNVIGQNCDRCAPTWQLASGTG 1080

Db 1021 LRQDCRKVCNYLGTVOEHONGSDCQCDKATGQCLCPNVIGQNCDRCAPTWQLASGTG 1080

QY 1081 CDPNCNAAHSFGPSCNEFTGQCQCMFPGGRTCSQELFWGDPDVECRACDCDPRGIE 1140

Db 1081 CDPNCNAAHSFGPSCNEFTGQCQCMFPGGRTCSQELFWGDPDVECRACDCDPRGIE 1140

QY 1141 TPQCDQSTGQCVCVEGVEGPRCDKCTRGYSVFPDCTPCHQCFCALWDVIAELTNRTHRF 1200

Db 1141 TPQCDQSTGQCVCVEGVEGPRCDKCTRGYSVFPDCTPCHQCFCALWDVIAELTNRTHRF 1200

QY 1201 LEKAKALKISGVIGPYRETVDVSVERKVSEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDV 1260

Db 1201 LEKAKALKISGVIGPYRETVDVSVERKVSEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDV 1260

QY 1261 TENMAQVEVKLSDTTQSNSSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDS 1320

Db 1261 TENMAQVEVKLSDTTQSNSSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDS 1320

QY 1321 ITKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVMMERESQFKEKEEQARLLDE 1380

Db 1321 ITKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVMMERESQFKEKEEQARLLDE 1380

QY 1381 LACKLQSLDLSAAAEWTCGTPPGASCSETECGGPNCTDEGERKCGGPGCGGLVTVAHNA 1440

Db 1381 LACKLQSLDLSAAAEWTCGTPPGASCSETECGGPNCTDEGERKCGGPGCGGLVTVAHNA 1440

RESULT 3

US-09-561-709B-9
; Sequence 9, Application US/09561709B
; Patent No. 6682911
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Champliand, Marie-France
; APPLICANT: Olson, Pamela
; APPLICANT: Koch, Manuel
; APPLICANT: Brunken, William
; TITLE OF INVENTION: LAMININS AND USES THEREOF
; FILE REFERENCE: 10287-060001
; CURRENT APPLICATION NUMBER: US/09/561,709B
; CURRENT FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 09/168,949
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: US 60/061,609
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-709B-9

Query Match 100.0%; Score 9754; DB 4; Length 1786;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLLQLLAFSFLALCRARVRAQAEPEFSYGAEGSCYPATGDLIGRAQKLSVTSTCLHK 60

Db 1 MGLLQLLAFSFLALCRARVRAQAEPEFSYGAEGSCYPATGDLIGRAQKLSVTSTCLHK 60

Qy 61 PEPYCTVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVVTTFAPNRLKIWWQSENGVEN 120

Db 61 PEPYCTVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVVTTFAPNRLKIWWQSENGVEN 120

Qy 121 VTIQDLEAEFHFTHLIMFTKTRPAAMLIERSDFGKTGWVYRYFAYDCEASFPGISTG 180

Db 121 VTIQDLEAEFHFTHLIMFTKTRPAAMLIERSDFGKTGWVYRYFAYDCEASFPGISTG 180

Qy 181 PMKKVDDIICDSRYSYDIEPSTGEVIFRALDPAFKIEDPYPRIQNLKLTNLRKIFVKL 240

Db 181 PMKKVDDIICDSRYSYDIEPSTGEVIFRALDPAFKIEDPYPRIQNLKLTNLRKIFVKL 240

Qy 241 HTLGDNLDSRMEIREKYYYAVYDMVVRGNCFCYGHASECAPVDGFNEEVGMVHGCMC 300

Db 241 HTLGNLLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGCMC 300
QY 301 RHNTKGLNCEL CMDFYHDL PWRPAEGRNSNACKKCNNEHS1SCHFDMAYLATGNVSGG 360
Db 301 RHNTKGLNCEL CMDFYHDL PWRPAEGRNSNACKKCNNEHS1SCHFDMAYLATGNVSGG 360
QY 361 VCDDCQHNTMGRNCEQCKPFYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFSTG 420
Db 361 VCDDCQHNTMGRNCEQCKPFYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFSTG 420
QY 421 LIAGQCRCKLNVEGEHCDCVKEGFYDLSSSEDPFGCKSCACNPLGTIPGGNPCDSETHCY 480
Db 421 LIAGQCRCKLNVEGEHCDCVKEGFYDLSSSEDPFGCKSCACNPLGTIPGGNPCDSETHCY 480
QY 481 CKRLVTGQHCDOCLPEHWGLSNDLDGCRPCDCLGGALNNSCFABSGQSCSRPHMIGRQC 540
Db 481 CKRLVTGQHCDOCLPEHWGLSNDLDGCRPCDCLGGALNNSCFABSGQSCSRPHMIGRQC 540
QY 541 NEVEPGYYFATLDHYLYEAEANLGPVGSIVERQYIQDRIPSWTGAGFVRVPEGAYLEFF 600
Db 541 NEVEPGYYFATLDHYLYEAEANLGPVGSIVERQYIQDRIPSWTGAGFVRVPEGAYLEFF 600
QY 601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPRTSSRCGNTIPDDDNQVVSLSPG 660
Db 601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPRTSSRCGNTIPDDDNQVVSLSPG 660
QY 661 SRYVVLPRPVCPEKGTNYTVRLELPQYTSSDSVESPYTLIDSLVLMYPYCKSLDIFTVGG 720
Db 661 SRYVVLPRPVCPEKGTNYTVRLELPQYTSSDSVESPYTLIDSLVLMYPYCKSLDIFTVGG 720
QY 721 SGDGVTNSAWETFORYRCLENSRSVVKTPMTDVCRNIIIFSISALLHQTGLACECDPQGS 780
Db 721 SGDGVTNSAWETFORYRCLENSRSVVKTPMTDVCRNIIIFSISALLHQTGLACECDPQGS 780
QY 781 LSSVCDPNNGGQCQCRPNVVGRTCNRCAPGTGFGPSGCKPCECHLQGSVNAFCNPVTGQC 840
Db 781 LSSVCDPNNGGQCQCRPNVVGRTCNRCAPGTGFGPSGCKPCECHLQGSVNAFCNPVTGQC 840
QY 841 HCFQGVYARQCRLCPGHGWFPPSCQPCQCNHGADDCDPTVTECLNCQDVTMGNRCERCLA 900
Db 841 HCFQGVYARQCRLCPGHGWFPPSCQPCQCNHGADDCDPTVTECLNCQDVTMGNRCERCLA 900
QY 901 GYGDPPIIGSDHCRPCPCPDGPDGSGRQFARSCYQDPVTQLACVCDPGYIGSRCDDCAS 960
Db 901 GYGDPPIIGSDHCRPCPCPDGPDGSGRQFARSCYQDPVTQLACVCDPGYIGSRCDDCAS 960
QY 961 GYFGNPSEVGSGCQPCQCHNNIDTTDPEACDKETGRCLKCLYHTEGEHCQCFRFGYIGDA 1020
Db 961 GYFGNPSEVGSGCQPCQCHNNIDTTDPEACDKETGRCLKCLYHTEGEHCQCFRFGYIGDA 1020
QY 1021 LRQDCRKVCNYLGTVQEHGNCGSDCQCDKATGQCLCLPNVIGONCDRCAPNTWQLASGTG 1080
Db 1021 LRQDCRKVCNYLGTVQEHGNCGSDCQCDKATGQCLCLPNVIGONCDRCAPNTWQLASGTG 1080
QY 1081 CDPNCNAAHSFGPSCNEFTGQCQCMPFGGRTCECQELFWGDPDVECRACDCDPRGIE 1140
Db 1081 CDPNCNAAHSFGPSCNEFTGQCQCMPFGGRTCECQELFWGDPDVECRACDCDPRGIE 1140
QY 1141 TPQCDQSTGQCVCEGVGPRCDKCTRGYSGVFPDCTPCHQCQFALWDVIIAELTNRTHRF 1200
Db 1141 TPQCDQSTGQCVCEGVGPRCDKCTRGYSGVFPDCTPCHQCQFALWDVIIAELTNRTHRF 1200
QY 1201 LEKAKALKISGVIGPYRETVDVSVERKVBBIKDILAQSPAAPLKNIGNLFEEAEKLIKDV 1260
Db 1201 LEKAKALKISGVIGPYRETVDVSVERKVBBIKDILAQSPAAPLKNIGNLFEEAEKLIKDV 1260
QY 1261 TEMMAQVEVKLSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDS 1320
Db 1261 TEMMAQVEVKLSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDS 1320
QY 1321 ITKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVMMERESQFKEKEEQEARLLDE 1380

Db 1321 ITKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVMMERESQFKEKEEQEARLLDE 1380
QY 1381 LAGKQLSLDLASAAEMTCGTPPGASCSETECGGPNCRCTDEGERKCGGPGGGLVTVAHNA 1440
Db 1381 LAGKQLSLDLASAAEMTCGTPPGASCSETECGGPNCRCTDEGERKCGGPGGGLVTVAHNA 1440
QY 1441 WQKAMDLDQDVL SALAEVEQLSKMVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNEEL 1500
Db 1441 WQKAMDLDQDVL SALAEVEQLSKMVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNEEL 1500
QY 1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKWMEMPSTPQQLQNLTEDIRERVE SLSQVEVI 1560
Db 1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKWMEMPSTPQQLQNLTEDIRERVE SLSQVEVI 1560
QY 1561 LOHSAADIAAEMLIEEAKRASKSATDVKVTADMVKEALEEAEKAAQVAEAKAIKQADEDI 1620
Db 1561 LOHSAADIAAEMLIEEAKRASKSATDVKVTADMVKEALEEAEKAAQVAEAKAIKQADEDI 1620
QY 1621 QGTQNL LTSIESETAA SEETLFNASQRISELERNVVEELKRKAAQNSGEAEYIEKVVTYTK 1680
Db 1621 QGTQNL LTSIESETAA SEETLFNASQRISELERNVVEELKRKAAQNSGEAEYIEKVVTYTK 1680
QY 1681 QSAEDVKKTLDGELDEKYYKKVENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLL 1740
Db 1681 QSAEDVKKTLDGELDEKYYKKVENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLL 1740
QY 1741 KDLERKYEDNQRYLEDKAQELARLEGEVRSLLKDISOQKAVYSTCL 1786
Db 1741 KDLERKYEDNQRYLEDKAQELARLEGEVRSLLKDISOQKAVYSTCL 1786

RESULT 4

US-09-562-702A-16
; Sequence 16, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 1765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-16

Query Match 99.0%; Score 9654; DB 4; Length 1765;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 QEPEFSYGCAEGSCYPATGDL LIGRAQKLSVTSTCGLHKPEPYCIVSHLOEDKKCFICNS 81
Db 1 QEPEFSYGCAEGSCYPATGDL LIGRAQKLSVTSTCGLHKPEPYCIVSHLOEDKKCFICNS 60
QY 82 QDPYHETLNPDSHLIENVTTFAPNRLKIWWQSENGVENVTIQLDLEAEFHFTHLIMTFK 141
Db 61 QDPYHETLNPDSHLIENVTTFAPNRLKIWWQSENGVENVTIQLDLEAEFHFTHLIMTFK 120
QY 142 TFRPAAMLIERSDDFGKTGWGVRYRYFAYDCEASFPGISTGPMKKVDDIICDSRYSDIEPST 201
Db 121 TFRPAAMLIERSDDFGKTGWGVRYRYFAYDCEASFPGISTGPMKKVDDIICDSRYSDIEPST 180

QY 202 EGEVIFRALDPAFKIEDPYSPRIQNLLK1TNLR1K1FVKLH1TLG1DNL1DSR1ME1REK1YYA 261
DB 181 EGEVIFRALDPAFKIEDPYSPRIQNLLK1TNLR1K1FVKLH1TLG1DNL1DSR1ME1REK1YYA 240
QY 262 VYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHCHCMCRHNTKGLNCEL1CWD1FYH1DL1PW 321
DB 241 VYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHCHCMCRHNTKGLNCEL1CWD1FYH1DL1PW 300
QY 322 RPAEGRNSNACKKNCNEHS1SCHFDMAV1LATGNVSGGV1CDD1CQHNTWGRNCE1QCK1PFY 381
DB 301 RPAEGRNSNACKKNCNEHS1SCHFDMAV1LATGNVSGGV1CDD1CQHNTWGRNCE1QCK1PFY 360
QY 382 YQHPERDIRDPNFCERCTCDPAGSQNEG1CDSYTD1FSTGL1AGQCRCKLNVEGEH1CDV1CK 441
DB 361 YQHPERDIRDPNFCERCTCDPAGSQNEG1CDSYTD1FSTGL1AGQCRCKLNVEGEH1CDV1CK 420
QY 442 EGFYDLSSSEDPFGCKSCACNPLGT1PGGNPCDSETHCYCKRLVTG1QHCDQCL1PEHW1GLS 501
DB 421 EGFYDLSSSEDPFGCKSCACNPLGT1PGGNPCDSETHCYCKRLVTG1QHCDQCL1PEHW1GLS 480
QY 502 NDL1D1GCRPCD1D1G1GALNNS1CFAES1GQCS1CRPHM1GRQCNEVE1PGY1FAT1D1H1LYE1AEE 561
DB 481 NDL1D1GCRPCD1D1G1GALNNS1CFAES1GQCS1CRPHM1GRQCNEVE1PGY1FAT1D1H1LYE1AEE 540
QY 562 AN1L1GPGV1S1VERQY1QDRI1PSWTGAGFVRV1PEGAY1LEFF1IDN1PYSMEYD1IL1RYEP1QLP 621
DB 541 AN1L1GPGV1S1VERQY1QDRI1PSWTGAGFVRV1PEGAY1LEFF1IDN1PYSMEYD1IL1RYEP1QLP 600
QY 622 DHWEKAVITVQRPGR1PTSSRCGNT1PDDDNQVVS1SPGSRYV1VLP1R1PVC1PEK1GTNY1TVR 681
DB 601 DHWEKAVITVQRPGR1PTSSRCGNT1PDDDNQVVS1SPGSRYV1VLP1R1PVC1PEK1GTNY1TVR 660
QY 682 LELPQYTS1SDSDVESPY1TL1D1SLV1LMPY1CKSLD1FTV1GSG1D1GV1TNS1AWET1FQY1RCLE 741
DB 661 LELPQYTS1SDSDVESPY1TL1D1SLV1LMPY1CKSLD1FTV1GSG1D1GV1TNS1AWET1FQY1RCLE 720
QY 742 NSRSVVK1T1PMTD1VCRN1I1FS1S1ALL1H1QT1GLACE1D1PQ1G1SL1SSV1CD1PNG1G1CQ1CR1PNV1VGR 801
DB 721 NSRSVVK1T1PMTD1VCRN1I1FS1S1ALL1H1QT1GLACE1D1PQ1G1SL1SSV1CD1PNG1G1CQ1CR1PNV1VGR 780
QY 802 TCNRCAP1GTF1GFG1PSG1CKP1CECH1LQGS1VNAFC1NPVT1G1OCH1CFQ1GVY1AR1QC1DR1CL1PGH1WGF 861
DB 781 TCNRCAP1GTF1GFG1PSG1CKP1CECH1LQGS1VNAFC1NPVT1G1OCH1CFQ1GVY1AR1QC1DR1CL1PGH1WGF 840
QY 862 PSC1QC1QC1NGH1AD1D1CPVT1G1E1C1N1CQ1DY1TM1GHN1C1ER1C1LAG1Y1GD1PI1G1SG1DH1CR1PC1CPD 921
DB 841 PSC1QC1QC1NGH1AD1D1CPVT1G1E1C1N1CQ1DY1TM1GHN1C1ER1C1LAG1Y1GD1PI1G1SG1DH1CR1PC1CPD 900
QY 922 GPD1SG1RQ1FAR1SCY1QDP1VT1LQ1ACV1CD1PGY1IG1SRC1DD1CAS1GY1F1GN1P1SEV1G1SG1CQ1PC1CHN 981
DB 901 GPD1SG1RQ1FAR1SCY1QDP1VT1LQ1ACV1CD1PGY1IG1SRC1DD1CAS1GY1F1GN1P1SEV1G1SG1CQ1PC1CHN 960
QY 982 ID1TTD1PE1AC1DK1ET1GR1CL1K1LY1H1TE1GE1HC1Q1CFR1FGY1YG1D1AL1R1Q1D1CR1KC1VC1NY1L1GT1V1QE1HCN 1041
DB 961 ID1TTD1PE1AC1DK1ET1GR1CL1K1LY1H1TE1GE1HC1Q1CFR1FGY1YG1D1AL1R1Q1D1CR1KC1VC1NY1L1GT1V1QE1HCN 1020
QY 1042 GSD1CQ1DK1AT1GQ1CL1P1NV1G1QNC1DR1CAP1NTW1Q1AS1GT1G1CD1PC1NC1N1AA1HS1FG1PS1C1NE1FTG 1101
DB 1021 GSD1CQ1DK1AT1GQ1CL1P1NV1G1QNC1DR1CAP1NTW1Q1AS1GT1G1CD1PC1NC1N1AA1HS1FG1PS1C1NE1FTG 1080
QY 1102 QC1CQ1MP1G1F1GG1RT1C1SEC1Q1EL1FW1G1D1PD1VE1CR1AC1D1C1D1PR1G1ET1P1Q1D1Q1ST1G1QC1VC1VE1G1EG1PR 1161
DB 1081 QC1CQ1MP1G1F1GG1RT1C1SEC1Q1EL1FW1G1D1PD1VE1CR1AC1D1C1D1PR1G1ET1P1Q1D1Q1ST1G1QC1VC1VE1G1EG1PR 1140
QY 1162 CD1K1CT1RG1SY1GV1FP1D1CT1P1CH1QC1FAL1WD1V1I1A1EL1TN1R1TH1R1F1LE1K1AK1K1IS1G1V1G1PY1RET1VD 1221
DB 1141 CD1K1CT1RG1SY1GV1FP1D1CT1P1CH1QC1FAL1WD1V1I1A1EL1TN1R1TH1R1F1LE1K1AK1K1IS1G1V1G1PY1RET1VD 1200
QY 1222 SV1ER1KV1S1B1K1D1I1LAQ1SPA1AE1PL1KN1GN1LF1EE1AE1K1I1KD1V1T1EM1MA1Q1VE1K1L1SD1T1S1Q1SN1ST 1281
DB 1201 SV1ER1KV1S1B1K1D1I1LAQ1SPA1AE1PL1KN1GN1LF1EE1AE1K1I1KD1V1T1EM1MA1Q1VE1K1L1SD1T1S1Q1SN1ST 1260
QY 1282 AK1ELD1SLQ1TE1AES1LD1NTV1K1EL1AE1Q1LEF1IK1NSD1IR1GALD1S1ITKY1FQ1MS1LE1AE1ERV1N1AST1TE 1341

DB 1261 AK1ELD1SLQ1TE1AES1LD1NTV1K1EL1AE1Q1LEF1IK1NSD1IR1GALD1S1ITKY1FQ1MS1LE1AE1ERV1N1AST1TE 1320
QY 1342 PN1STVE1QS1ALMR1DR1VED1VM1MER1ES1QF1KE1QE1Q1AR1LL1DE1LAG1K1Q1SLD1S1AAA1EM1TC1G1TP 1401
DB 1321 PN1STVE1QS1ALMR1DR1VED1VM1MER1ES1QF1KE1QE1Q1AR1LL1DE1LAG1K1Q1SLD1S1AAA1EM1TC1G1TP 1380
QY 1402 PG1ASC1SE1TE1CG1GP1NC1RT1DE1GER1K1CG1G1PG1CG1GL1VT1VAH1N1AQ1K1AMD1LD1Q1DV1LS1AL1AE1VE1QL 1461
DB 1381 PG1ASC1SE1TE1CG1GP1NC1RT1DE1GER1K1CG1G1PG1CG1GL1VT1VAH1N1AQ1K1AMD1LD1Q1DV1LS1AL1AE1VE1QL 1440
QY 1462 SK1MV1SE1AK1RA1DE1AK1Q1SA1ED1ILL1KT1NAT1K1EM1DK1S1NE1EL1RN1LI1K1Q1IR1N1FL1T1Q1DS1AD1L1DSI 1521
DB 1441 SK1MV1SE1AK1RA1DE1AK1Q1SA1ED1ILL1KT1NAT1K1EM1DK1S1NE1EL1RN1LI1K1Q1IR1N1FL1T1Q1DS1AD1L1DSI 1500
QY 1522 E1AV1ANE1VL1KM1EP1ST1PQ1OL1QN1LT1ED1IR1ER1VES1LS1Q1VE1V1L1QH1SA1ADI1ARA1E1ML1LE1E1AK1RA 1581
DB 1501 E1AV1ANE1VL1KM1EP1ST1PQ1OL1QN1LT1ED1IR1ER1VES1LS1Q1VE1V1L1QH1SA1ADI1ARA1E1ML1LE1E1AK1RA 1560
QY 1582 SK1SAT1DV1KV1T1AD1MV1KE1AL1EE1AE1KA1Q1VA1EA1K1QA1D1ED1IQ1GT1QN1LL1TS1IE1SE1TA1A1SE1ETL 1641
DB 1561 SK1SAT1DV1KV1T1AD1MV1KE1AL1EE1AE1KA1Q1VA1EA1K1QA1D1ED1IQ1GT1QN1LL1TS1IE1SE1TA1A1SE1ETL 1620
QY 1642 FN1AS1Q1RI1SE1L1ERN1VE1EL1KR1K1AA1Q1NS1GE1AE1Y1IE1KV1V1TV1K1Q1SA1ED1VK1T1D1G1EL1DE1KY1KV 1701
DB 1621 FN1AS1Q1RI1SE1L1ERN1VE1EL1KR1K1AA1Q1NS1GE1AE1Y1IE1KV1V1TV1K1Q1SA1ED1VK1T1D1G1EL1DE1KY1KV 1680
QY 1702 EN1LIA1K1K1TE1ES1AD1ARR1KA1EM1L1Q1NE1AK1T1LL1AQ1ANS1K1L1Q1LL1K1DL1ER1KY1ED1NQ1RY1LED1KA1QEL 1761
DB 1681 EN1LIA1K1K1TE1ES1AD1ARR1KA1EM1L1Q1NE1AK1T1LL1AQ1ANS1K1L1Q1LL1K1DL1ER1KY1ED1NQ1RY1LED1KA1QEL 1740
QY 1762 AR1LE1GE1VR1SL1LL1KD1IS1Q1K1VA1V1ST1CL 1786
DB 1741 AR1LE1GE1VR1SL1LL1KD1IS1Q1K1VA1V1ST1CL 1765

RESULT 5

US-09-561-818A-16
; Sequence 16, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortessmaa, Jarrko
; APPLICANT: Tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,204-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 1765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-818A-16

Query Match 99.0%; Score 9654; DB 4; Length 1765;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 QEPERSYCAEGSCYPATGDL1LIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCF1CNS 81
DB 1 QEPERSYCAEGSCYPATGDL1LIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCF1CNS 60
QY 82 QDPYHET1N1PDSH1EN1V1T1T1PAP1N1RL1KI1WQ1SEN1GV1ENV1T1Q1LD1LE1AF1H1F1TH1L1M1TF1K 141
DB 61 QDPYHET1N1PDSH1EN1V1T1T1PAP1N1RL1KI1WQ1SEN1GV1ENV1T1Q1LD1LE1AF1H1F1TH1L1M1TF1K 120
QY 142 TFRPAAMLIERS1S1DFG1KT1GW1V1RY1PAY1D1CE1AS1FP1G1S1T1G1PM1KK1V1DD1I1C1DS1RY1S1D1IE1P1ST 201
DB 121 TFRPAAMLIERS1S1DFG1KT1GW1V1RY1PAY1D1CE1AS1FP1G1S1T1G1PM1KK1V1DD1I1C1DS1RY1S1D1IE1P1ST 180
QY 202 EGEVIFRALDPAFKIEDPYSPRIQNLLK1TNLR1K1FVKLH1TLG1DNL1DSR1ME1REK1YYA 261

Db 181 EGEVIFRALDPAFKIEDPSPRIQNLLKITNLR1KFVKLHTLGDNLDSRMEIREKYYVA 240
QY 262 VYDMVVRGNCFCYGHASECAPVDGFNEEVGMVHGHCRCRNTKGLNCELMDFFYHDLPW 321
Db 241 VYDMVVRGNCFCYGHASECAPVDGFNEEVGMVHGHCRCRNTKGLNCELMDFFYHDLPW 300
QY 322 RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGVCDCCQHNMTGRNCEQCKPFY 381
Db 301 RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGVCDCCQHNMTGRNCEQCKPFY 360
QY 382 YQHPERDIRDPNFCBRCCTCDPAGSQNEGICDSYDFSTGLIAGQCCKLNVEGEHCDVCK 441
Db 361 YQHPERDIRDPNFCBRCCTCDPAGSQNEGICDSYDFSTGLIAGQCCKLNVEGEHCDVCK 420
QY 442 EGFYDLSSDPFGCKSCACNPLGTIPGGNPNCDSETGHCHYCKRLVTGQCHDQCLPEHWGLS 501
Db 421 EGFYDLSSDPFGCKSCACNPLGTIPGGNPNCDSETGHCHYCKRLVTGQCHDQCLPEHWGLS 480
QY 502 NDLGGRPCDCDLGGALNNSCFAESGQSCRPHEMIGRQCNEVEPGYYPATLDHYLYEAE 561
Db 481 NDLGGRPCDCDLGGALNNSCFAESGQSCRPHEMIGRQCNEVEPGYYPATLDHYLYEAE 540
QY 562 ANLPGVSIIVERQYIQRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 621
Db 541 ANLPGVSIIVERQYIQRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 600
QY 622 DHWEKAVITVQRPGRIPTRSSRCGNTIPDDDNQVVSLSPGSRVYVLPVPCFEKGTNYTVR 681
Db 601 DHWEKAVITVQRPGRIPTRSSRCGNTIPDDDNQVVSLSPGSRVYVLPVPCFEKGTNYTVR 660
QY 682 LELPOYTSSDSDVESPYTLIDSLVLMPCYCKSLDIFTVGGSGDGVVNTNSAWETFORYRCLE 741
Db 661 LELPOYTSSDSDVESPYTLIDSLVLMPCYCKSLDIFTVGGSGDGVVNTNSAWETFORYRCLE 720
QY 742 NSRSVVKTPMTDVCNRIIFISALLHOTGLACECDPQGSLSVSCDPPNGGQCQCRPNVVR 801
Db 721 NSRSVVKTPMTDVCNRIIFISALLHOTGLACECDPQGSLSVSCDPPNGGQCQCRPNVVR 780
QY 802 TCNRCAPGTGFGPGSGCKPCECHLQGSVNAPFCNPVTGQCHCFQGVYARQCDCRCLPGHWGF 861
Db 781 TCNRCAPGTGFGPGSGCKPCECHLQGSVNAPFCNPVTGQCHCFQGVYARQCDCRCLPGHWGF 840
QY 862 PSCQPCQCNHADDCCDPTVTECLNCQDYTMGHNCERCLAGYGDPIIGSGDHCRCPCPD 921
Db 841 PSCQPCQCNHADDCCDPTVTECLNCQDYTMGHNCERCLAGYGDPIIGSGDHCRCPCPD 900
QY 922 GPDSGRQFARSCYQDPVTIQLACVCDPGYIGSRDDCASGYFGNPSVGGSCQPCQCHNN 981
Db 901 GPDSGRQFARSCYQDPVTIQLACVCDPGYIGSRDDCASGYFGNPSVGGSCQPCQCHNN 960
QY 982 IDTTDPEACDKETGRCLKLYHTEGEHCQFCRFGYGDALRQDCRKCVCNYLGTVQEHCN 1041
Db 961 IDTTDPEACDKETGRCLKLYHTEGEHCQFCRFGYGDALRQDCRKCVCNYLGTVQEHCN 1020
QY 1042 GSDCQCDKATGQCLCPNVIGQNCDCRCAPNTWOLASGTGCDPCNCNAHSPGSPSCNEFTG 1101
Db 1021 GSDCQCDKATGQCLCPNVIGQNCDCRCAPNTWOLASGTGCDPCNCNAHSPGSPSCNEFTG 1080
QY 1102 QCQCMFGGRTCSECEQLFWGDDPVECRACDDPRGIETPQCDQSTGQCVCVEGVEGPR 1161
Db 1081 QCQCMFGGRTCSECEQLFWGDDPVECRACDDPRGIETPQCDQSTGQCVCVEGVEGPR 1140
QY 1162 CDKTRGYSGVFPDCTPCHQCFALWDVIIAELTNRTHRFLEKAKALKISGVIQPYRETVD 1221
Db 1141 CDKTRGYSGVFPDCTPCHQCFALWDVIIAELTNRTHRFLEKAKALKISGVIQPYRETVD 1200
QY 1222 SVERKVSSEIKDILAQSPAAEPLKNIGNLFEAEKLIKDVTEMAQVEVKLSDTTSQSNST 1281
Db 1201 SVERKVSSEIKDILAQSPAAEPLKNIGNLFEAEKLIKDVTEMAQVEVKLSDTTSQSNST 1260
QY 1282 AKELDSLQTEAESLDNTVKELAQLEFIKNSDIRGALDSITKYFQMSLEAERVNASTTE 1341
Db 1261 AKELDSLQTEAESLDNTVKELAQLEFIKNSDIRGALDSITKYFQMSLEAERVNASTTE 1320

QY 1342 PNSTVEQSALMRDRVEDVMMERESQFKQEBEQARLLDELQGLQSLDLSAAAAEMTCGTP 1401
Db 1321 PNSTVEQSALMRDRVEDVMMERESQFKQEBEQARLLDELQGLQSLDLSAAAAEMTCGTP 1380
QY 1402 PGASCSETECGGPNCRTDGERKCGGPGCGGLVTVVAHNQWKAMDLDQDVLSALAEVEQL 1461
Db 1381 PGASCSETECGGPNCRTDGERKCGGPGCGGLVTVVAHNQWKAMDLDQDVLSALAEVEQL 1440
QY 1462 SKMVSEAKLRADAKQSAEDILLKTNATKEMDKSNEELRNLIKQIRNFLTQDSADLDSI 1521
Db 1441 SKMVSEAKLRADAKQSAEDILLKTNATKEMDKSNEELRNLIKQIRNFLTQDSADLDSI 1500
QY 1522 EAVANEVLKMEMPSPTPQQLQNLTEDIRERVESLSQVEVILQHSAAADIARAEMLLEAAKRA 1581
Db 1501 EAVANEVLKMEMPSPTPQQLQNLTEDIRERVESLSQVEVILQHSAAADIARAEMLLEAAKRA 1560
QY 1582 SKSATDVKVTADMVKEALEEAEKAQVAAEKAQKQADEDIQGTQNLTSIESETAASEETL 1641
Db 1561 SKSATDVKVTADMVKEALEEAEKAQVAAEKAQKQADEDIQGTQNLTSIESETAASEETL 1620
QY 1642 FNASQRISELERNVVEELKRKAQNSGEAEYIEKVYVTVKQSAEDVKKTLDBELDEKYYKV 1701
Db 1621 FNASQRISELERNVVEELKRKAQNSGEAEYIEKVYVTVKQSAEDVKKTLDBELDEKYYKV 1680
QY 1702 ENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLOLLKDLERKYEDNORYLEDKAQEL 1761
Db 1681 ENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLOLLKDLERKYEDNORYLEDKAQEL 1740
QY 1762 ARLEGEVRSLDKDISQKVAVYSTCL 1786
Db 1741 ARLEGEVRSLDKDISQKVAVYSTCL 1765

RESULT 6

US-09-562-702A-18
; Sequence 18, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-562-702A-18

Query Match 93.7%; Score 9144; DB 4; Length 1786;
Best Local Similarity 92.7%; Pred. No. 0;
Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;
QY 1 MGLLQLLAFSFLALCRARVRAQEPFESYGCAGSCYPATGDLIGRAQKLSVTSTCGLHK 60
Db 1 MGLLQVFAFGVLALWGTRVCAQEPFESYGCAGSCYPATGDLIGRAQKLSVTSTCGLHK 60
QY 61 PEPYCIIVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVVTTTFAPNRLKIWWQSENGVEN 120
Db 61 PEPYCIIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVVTTTFAPNRLKIWWQSENGVEN 120
QY 121 VTIQDLAEAEHFTHLIMTFKTRPAAMLIERSDDFGKWTGVRYFYAYDCEASFPGISTG 180

Db 121 VTIQLDLAEAFHFTLINTFKTRPAAMLIERSSDFGKTGWYRYFAYDCSSFPGISTG 180
QY 181 PMKVVDDIICDSRYSIDIEPSTEGEVI FRALDPAPKIEDPYPRIQNLKXTNRIKFKVL 240
Db 181 PMKVVDDIICDSRYSIDIEPSTEGEVI FRALDPAPKIEDPYPRIQNLKXTNRIKFKVL 240
QY 241 HTLGDNLLDSRMEIREKYYIAYVDMVVRGNCFCHASACAPVDGFEVEGVHGHCMC 300
Db 241 HTLGDNLLDSRMEIREKYYIAYVDMVVRGNCFCHASACAPVDGFEVEGVHGHCMC 300
QY 301 RHNTKGLNCELMDFYHDLPLWRPAEGRNSNACKKNCNEHSSCHFDMAVFLATGNVSGG 360
Db 301 RHNTKGLNCELMDFYHDLPLWRPAEGRNSNACKKNCNEHSSCHFDMAVFLATGNVSGG 360
QY 361 VCDCCQHNMTGRNCEQCKPFPYQHPERDIROPNFCERCTCDPAGSQNEGICDSYDFSTG 420
Db 361 VCDNCQHNTMGRNCEQCKPFPYQHPERDIROPNFCERCTCDPAGSENGGICDGYTDFSVG 420
QY 421 LIAGQCRCKLHVEGERCDVCKEGFYDLSSDDPFGCKSCACNPLGTIPGGNPCDSETGHY 480
Db 421 LIAGQCRCKLHVEGERCDVCKEGFYDLSSDDPFGCKSCACNPLGTIPGGNPCDSETGYCY 480
QY 481 CKRLVTGQHCDCQLPEHGLSNDLDGCRPCDCLGGLNNSCFAESGQCSCRPHMIGRQC 540
Db 481 CKRLVTGQRCDQCLPQHGLSNDLDGCRPCDCLGGLNNSCSEDSGQCSCLPHMIGRQC 540
QY 541 NEVEPGYFATLDHYLYEAEANLPGVSI VERQYIQDRIPSWTGA GFVRVPEGAYLEFF 600
Db 541 NEVESGYFTTLDHYLYEAEANLPGVSI VERQYIQDRIPSWTGA GFVRVPEGAYLEFF 600
QY 601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPTSRRCNGTIPDDNQVSLSPG 660
Db 601 IDNIPYSMEYEILIRYEPQLPDHWEKAVITVQRPGRIPASSRRCNGTVPDDNQVSLSPG 660
QY 661 SRYVVLPRPVCFEKGTNYTVLELPQYTSDDSVESPYTLIDSLVLMPCYCKSLDIFTVGG 720
Db 661 SRYVVLPRPVCFEKGMNYTVLELPQYTAGSDSVESPYTFIDSLVLMPCYCKSLDIFTVGG 720
QY 721 SGDGVTNSAWETFORYRCLENSRSVVKTPMTDVCNIIIFSISALLHQTGLACECDPQGS 780
Db 721 SGDEVTNSAWETFORYRCLENSRSVVKTPMTDVCNIIIFSISALIHOTGLACECDPQGS 780
QY 781 LSSVCDPNGGQCQCRPNVVGRTCNRCAPGTGFGPSPCKPCECHLQGSVNAPCNVPTGQC 840
Db 781 LSSVCDPNGGQCQCRPNVVGRTCNRCAPGTGFGPSPCKPCECHLQGSASAFCAITGQC 840
QY 841 HCFQGIYARQCRCCLPBGHWGFPSCQPCQCNHADDCTVPTGECNLCQDYTMHNCERCLA 900
Db 841 HCFQGIYARQCRCCLPBGHWGFPSCQPCQCNHADDCTVPTGECNLCQDYTMHNCERCLA 900
QY 901 GYGDPIIGSGDHCRPCPCPDGSDGRQFARSCYQDPVTLQACVCDPFGYIGSRCDDCAS 960
Db 901 GYGDPIIGSGDHCRPCPCPDGSDGRQFARSCYQDPVTLQACVCDPFGYIGSRCDDCAS 960
QY 961 GYFGNPSEVGGSCQPCQCHNIDTDDPEACDKETGRCLKLYHTEGHCQFCRFGYYGDA 1020
Db 961 GYFGNPSEVGGSCQPCQCHNIDTDDPEACDKETGRCLKLYHTEGHCQFCRFGYYGDA 1020
QY 1021 LRQDCRKVCNYLGTVQEHNGSDCQCDKATGQCLPNNVIGQNCDCRCAPNTWQLASGTG 1080
Db 1021 LRQDCRKVCNYLGTVQEHNGSDCQCDKATGQCSCLPNNVIGQNCDCRCAPNTWQLASGTG 1080
QY 1081 CDPNCNAAHSPGSPCNFTGQCQCMPPGFGRTCTSECQELFWGDDPVECRACDPRGIE 1140
Db 1081 CDPNCNAAHSPGSPCNFTGQCQCMPPGFGRTCTSECQELFWGDDPVECRACDPRGIE 1140
QY 1141 TPQCDOSTGQCVCVEGVEGPRCDKCTRGYSVGFDPCTPCHQCFCALWDVITABELNTRTHF 1200
Db 1141 TPQCDOSTGQCVCVEGVEGPRCDKCTRGYSVGFDPCTPCHQCFCALWDVITABELNTRTHF 1200
QY 1201 LEKAKALKISGVI GPYRETVDVSVEKKNVEIKDILAQSPAAEPLKNIGILFEEAEKLTQDV 1260

Db 1201 LEKAKALKISGVI GPYRETVDVSVEKKNVEIKDILAQSPAAEPLKNIGILFEEAEKLTQDV 1260
QY 1261 TENMAQVEVKLSDDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDS 1320
Db 1261 TENMAQVEVKLTDTSQSNSTAGELGALQAEASLDKTVKELAEQLEFIKNSDIQALDS 1320
QY 1321 ITKYFQMSLEAEERVNASTTEPNSTVEQSALMRDVEDVMMERESQFKEQEQAARLLDE 1380
Db 1321 ITKYFQMSLEAEERVNASTTEPNSTVEQSALTRDRVEDMLERESPFEKEQEQAARLLDE 1380
QY 1381 LAGKLSLDSAAAAEMTCGTPPGASCSETCCGPNCRCTDEGERKCGGPGCGGLVTVAHNA 1440
Db 1381 LAGKLSLDSAAAAEMTCGTPPGADCESECCGPNCRCTDEGEKKCGGPGCGGLVTVAHSA 1440
QY 1441 WQKAMDLDQDVL SALAEVQLSKMVSEAKLRADAEAKQSAEDILLKTNATKEKMDKSNEDL 1500
Db 1441 WQKAMDLDQDVL SALAEVQLSKMVSEAKLRADAEAKQSAEDILLKTNATKEKMDKSNEDL 1500
QY 1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKMEMPTPQOLQNLNLTEDIRERVESLSQVEVI 1560
Db 1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKSGNASTPQOLQNLNLTEDIRERVETLSQVEVI 1560
QY 1561 LQHSAAADIAEAEMLEEAASKASKSATDVKVTADMVKEALAEAEAKAQAQADEDI 1620
Db 1561 LQHSAAADIAEAEMLEEAASKASKSATDVKVTADMVKEALAEAEAKAQAQADEDI 1620
QY 1621 QGTQNLNLTISSETAASEETLFNASQRISELRNVNVEELKRKAQNSGEAEYIEKVYTVK 1680
Db 1621 QGTQNLNLTISSETAASEETLFNASQRISELRNVNVEELKRKAQNSGEAEYIEKVYTVK 1680
QY 1681 QSAEDVKKTLDGELDEKYYKVENLI AKKTEESADARRKAEMLQNEAKTLLAQANSKLQLL 1740
Db 1681 QSAEDVKKTLDGELDEKYYKVENLI AKKTEESADARRKAEMLQNEAKTLLAQANSKLQLL 1740
QY 1741 KDLERKYEDNQRYLEDKAQELARLEGEVRSLLKXDISOKVAVYSTCL 1786
Db 1741 KDLERKYEDNQRYLEDKAQELARLEGEVRSLLKXDISOKVAVYSTCL 1786

RESULT 7

US-09-561-818A-18
; Sequence 18, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortese, Jarro
; APPLICANT: Tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99/274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 18
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-561-818A-18

Query Match 93.7%; Score 9144; DB 4; Length 1786;
Best Local Similarity 92.7%; Pred. No. 0;
Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;

QY 1 MGLLQLLAFSFLALCRARVRAQEPPEFSYGAEGSCYPATGDLIGRAQKLSVTSTGLHK 60
Db 1 MGLLQVFAFGVLWGTRVCAQEPPEFSYGAEGSCYPATGDLIGRAQKLSVTSTGLHK 60
QY 61 PEPYCIVSHLQEDKCKFCINCSQDPYHETLNPDNSHLIENVVTTTFAPNRLKIWWQSENGVEN 120
Db 61 PEPYCIVSHLQEDKCKFCINCSQDPYHETLNPDNSHLIENVVTTTFAPNRLKIWWQSENGVEN 120
QY 121 VTIQLDLAEAFHFTLINTFKTRPAAMLIERSSDFGKTGWYRYFAYDCASFPGISTG 180
Db 121 VTIQLDLAEAFHFTLINTFKTRPAAMLIERSSDFGKTGWYRYFAYDCASFPGISTG 180

QY 181 PMKKVDDIICDSRYSYDIEPSTEGEVIFRALDPAFKIEDPYSPRIQNLLKITNLRIFVKL 240
Db 181 PMKKVDDIICDSRYSYDIEPSTEGEVIFRALDPAFKIEDPYSPRIQNLLKITNLRIFVKL 240
QY 241 HTLGNLDSRMEIREKYYYAYYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGCWC 300
Db 241 HTLGNLDSRMEIREKYYYAYYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCWC 300
QY 301 RHNTKGLNCELWDFYHDLPRPAPAEGRNSNACKKCNNEHSTSCHEFDMAYLATGNVSGG 360
Db 301 RHNTKGLNCELWDFYHDLPRPAPAEGRNSNACKKCNNEHSSCHDFMAVFLATGNVSGG 360
QY 361 VCDQCQHNMTGRNCEQCKPFYFQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFSTG 420
Db 361 VCDNCQHNMTGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVG 420
QY 421 LIAGQCRCKLNVBEGHCDVCKEGFYDLSSDDPFPGCKSCACNPLGTIPGPNPCDSETGHCY 480
Db 421 LIAGQCRCKLNVBEGHCDVCKEGFYDLSSDDPFPGCKSCACNPLGTIPGPNPCDSETGYCY 480
QY 481 CKRLVTGQHCDOCLPEHWGLSNDLDGCRPCDCLGGALNNSCFBESGQCSRPHMIGRQC 540
Db 481 CKRLVTGQRCDOCLPQHWGLSNDLDGCRPCDCLGGALNNSCSDSGQCSCLPHMIGRQC 540
QY 541 NEVEPGYYFATLDHYLYEAEANLPGVSVIVERQYIQDRIPSWTGAGFVRVPEGAYLEFF 600
Db 541 NEVESGYFTTLDHYLYEAEANLPGVVVVERQYIQDRIPSWTGPGFVRVPEGAYLEFF 600
QY 601 IDNIPYSMEYDILIRYEPOLPDHWEKAVITVORPGRIPRTSSRCNGNTPDDDNQVVSLSPG 660
Db 601 IDNIPYSMEYEILIRYEPOLPDHWEKAVITVORPGKIPASSRCNGNTPDDDNQVVSLSPG 660
QY 661 SRYVVLPRPVCFEKGTNYTVRLELPQYTSDDSDVESPYTLIDSLVLMYPYCKSLDIFTVGG 720
Db 661 SRYVVLPRPVCFEKGMNYTVRLELPQYTAGSDVESPYTFIDSLVLMYPYCKSLDIFTVGG 720
QY 721 SGDGVVNTSAWETFORYRCLENRSRVVKTMTDVCNRNIIIFSISALLHQTGLACECDPQGS 780
Db 721 SGDGEVNTSAWETFORYRCLENRSRVVKTMTDVCNRNIIIFSISALLHQTGLACECDPQGS 780
QY 781 LSSVCDPNGGQCCQCRPNVVGRTCNRCAPGTGFGPGSGCKPCBCHLQGSVNAFCNPVTGQC 840
Db 781 LSSVCDPNGGQCCQCRPNVVGRTCNRCAPGTGFGPGNGCKPCDCHLQGSASAFCDAITGQC 840
QY 841 HCFQGVYARQCDRLPGYWGFPSPCQPCQCNHADDCCDPTVTECLNCQDYTMGHNCERCLA 900
Db 841 HCFQGIYARQCDRLPGYWGFPSPCQPCQCNHADDCCDPTVTECLSCQDYTTGHNCERCLA 900
QY 901 GYGDPIIGSGDHCRCPCPDGPDGSDGRQFARSCYQDPVTQLACVCDPGYIGSRCDDCAS 960
Db 901 GYGDPIIGSGDHCRCPCPDGPDGSDGRQFARSCYQDPVTQLACVCDPGYIGSRCDDCAS 960
QY 961 GYFGNPSVGGSCQPCQCHNNIDTTPDPEACDKETGRCLKCLYHTEGHCQCFRFGYYGDA 1020
Db 961 GYFGNPSDFGSGCQPCQCHNNIDTTPDPEACDKETGRCLKCLYHTEGHCQCLCQYGYGDA 1020
QY 1021 LRQDCRKVCNYLGTVBHCNGSDCCQDKATGQCLCLPNVIGQNCDCRCAPNTWQLASGTG 1080
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QY 1081 CDPNCNAAHSFGPSCNBEFTGQCQCMFGGRTGTCSECQELFWGDPDVECRACDCDPRGIE 1140
Db 1081 CGPCNCAAHSGPSCNBEFTGQCQCMFGGRTGTCSECQELFWGDPDVECRACDCDPRGIE 1140
QY 1141 TPQDQSTGQCVCEGVGPRCDKCTRGYSVGFDPCTPCHQCFCALWDVIAELTNRTHRF 1200
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Db 1201 LEXAKALKISGVIQPYRETVDVSVERKVSEIKDILAQSPAAEPLKNIGNLFEAEKLIKDV 1260

QY 1261 TEMMAQVEVKLSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDS 1320
Db 1261 TEKMAQVEVKLTDTSQSNSTAGELGALQAEASLDKTVKELAEQLEFIKNSDIQALDS 1320
QY 1321 ITKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVMMERESQFKEQEEOQARLLDE 1380
Db 1321 ITKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLERESPFKEQEEOQARLLDE 1380
QY 1381 LAGKLSLDLSAAAAEMTCGTPPGASCSETECGGPNCRNTEGERKCGGPGCGGLVTVAHNA 1440
Db 1381 LAGKLSLDLSAAAAQMTGTPPGADCSSECGGPNCRNTEGEKCGGPGCGGLVTVAHSA 1440
QY 1441 WQKAMDLDQDVLASALAEVEQLSKMVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNEEL 1500
Db 1441 WQKAMDFDRDVLASALAEVEQLSKMVSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDL 1500
QY 1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKMEMPSTPQQLQNLTFEDIRERVESLSQVEVI 1560
Db 1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKSGNASTPQQLQNLTFEDIRERVETLSQVEVI 1560
QY 1561 LQHSAAADIARAEMLLEAKRASKSATDVKVTADVMVKEALEEAEKAQVAAEKAIKQADEDI 1620
Db 1561 LQSSAAADIARAELLLEAKRASKSATDVKVTADVMVKEALEEAEKAQVAAEKAIKQADEDI 1620
QY 1621 QGTQNLTSIESETAASEETLFNASQRISELERNVVEELKRKAQNSGEAEYIEKVYTVK 1680
Db 1621 QGTQNLTSIESETAASEETLFNASQRISELERNVVEELKRKAQNSGEAEYIEKVYSVK 1680
QY 1681 QSAEDVKKTLDGELDEKYKKVENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLL 1740
Db 1681 QNADDVKKTLDGELDEKYKKVESLIAQKTESADARRKAELLQNEAKTLLAQANSKLQLL 1740
QY 1741 KDLEKRYEDNQRYLEDKAQELARLEGEVRSLLKDISQKAVVYSTCL 1786
Db 1741 EDLEKRYEDNQRYLEDKAQELVRLEGEVRSLLKDISEKAVVYSTCL 1786

RESULT 8

US-09-562-702A-20
; Sequence 20, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20:
; LENGTH: 1725
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-562-702A-20

Query Match 91.0%; Score 8873; DB 4; Length 1725;
Best Local Similarity 92.9%; Pred. No. 0;
Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

QY 62 EPYCIIVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVVTTTAPNRLKIWQSENGVENV 121
Db 1 EPYCIIVSHLQEDKKCFICSDRDPYHETLNPDSHLIENVVTTTAPNRLKIWQSENGVENV 60
QY 122 TTQLDLAEAFHFTHLIMTFKTRPAAMLIERSDFGKTGWYRYFAYDCEASFPGISTGP 181

Db 61 TIQLDLAEAFHFTLIMTFKTRPAAMLIERSSDFGKTGWVRYFYAYDCESSFPFGISTGP 120

QY 182 MKKVDDIIICDSRYSDIEPSTEGEVIIFRALDPAPKIEDPYSPRIQNLLKITNLRIFVKLH 241

Db 121 MKKVDDIIICDSRYSDIEPSTEGEVIIFRALDPAPKIEDPYSPRIQNLLKITNLRIFVKLH 180

QY 242 TLGDNLLDSRMEIREKYYIAYVDMVVRGNCFYGHASECAPVDGFNEVEGMVGHCMCR 301

Db 181 TLGDNLLDSRMEIREKYYIAYVDMVVRGNCFYGHASECAPVDGVNEVEGMVGHCMCR 240

QY 302 HNTKGLNCELCMDFYHDLPRWPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGGV 361

Db 241 HNTKGLNCELCMDFYHDLPRWPAEGRNSNACKKNCNEHSSSCHFDMAVYLATGNVSGGV 300

QY 362 CDDCQHNTMGRNCEQCKPFYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSL 421

Db 301 CDDCQHNTMGRNCEQCKPFYQHPERDIRDPNFCERCTCDPAGSENGGICDGYTDFSVGL 360

QY 422 IAGQCRCKLNVEGEHCDVCKEGFYDLSSDPFGCKSCACNPLGTIPGGNCPDSETGHYCYC 481

Db 361 IAGQCRCKLNVEGEHCDVCKEGFYDLSSDPFGCKSCACNPLGTIPGGNCPDSETGYCYC 420

QY 482 KRLVTGQHDQCLPEHWGLSNDLDGCRPCDCDLGGALNNSCFAESGQCSCRPHMIGRQCN 541

Db 421 KRLVTGQHDQCLPEHWGLSNDLDGCRPCDCDLGGALNNSCSEDSGQCSCLPHMIGRQCN 480

QY 542 EVERGYVFATLDHLYYEAEBANLPGVSIIVERQYIQDRIPSWTGAQFVRVPEGAYLEFFI 601

Db 481 EVERGYVFATLDHLYYEAEBANLPGVSIIVERQYIQDRIPSWTGAQFVRVPEGAYLEFFI 540

QY 602 DNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPSTSSRCGNTIPDDNQQVSLSPGS 661

Db 541 DNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPSTSSRCGNTIPDDNQQVSLSPGS 600

QY 662 RYVVLPRPVCFEKGTNYTVRLPELPOYTSDDSDVESPYTLIDSLVLMPCYKSLDIFTVGS 721

Db 601 RYVVLPRPVCFEKGTNYTVRLPELPOYTSDDSDVESPYTLIDSLVLMPCYKSLDIFTVGS 660

QY 722 GDGVVITNSAWETFORYRCLENSRSVVKTPMTDVCRNIIFSIALLHQTGLACEDPQGS 781

Db 661 GDGVVITNSAWETFORYRCLENSRSVVKTPMTDVCRNIIFSIALLHQTGLACEDPQGS 720

QY 782 SSVCDENGQCCQCRPNVVGRTNRCAPGTGFGPSGCKCECHLQGSVNAFCNPVTGQCH 841

Db 721 SSVCDENGQCCQCRPNVVGRTNRCAPGTGFGPSGCKCECHLQGSVNAFCNPVTGQCH 780

QY 842 CFQGVYARQCDRLPGHWGFPSCQPCQCNHADDGDPVTGECNLCQDYMTHGNCHERCLAG 901

Db 781 CFQGVYARQCDRLPGHWGFPSCQPCQCNHADDGDPVTGECNLCQDYMTHGNCHERCLAG 840

QY 902 YGDPPIIGSGDHRPCPCPDGDSGRQFARSQYQDPVTLQACVCDPQYIGSRCDDCASG 961

Db 841 YGDPPIIGSGDHRPCPCPDGDSGRQFARSQYQDPVTLQACVCDPQYIGSRCDDCASG 900

QY 962 YFGNPSVEGSGCQPCQCHNNDITDPEACDKETGRCLKLYHTEGEHCQFCRFGYGDAL 1021

Db 901 YFGNPSVEGSGCQPCQCHNNDITDPEACDKETGRCLKLYHTEGEHCQFCRFGYGDAL 960

QY 1022 RQDCKVCNYLGTVOEHGNGSDCCQDKATGQCLLPNVICQNCDCRCAFNWQLASGTGC 1081

Db 961 RQDCKVCNYLGTVOEHGNGSDCCQDKATGQCLLPNVICQNCDCRCAFNWQLASGTGC 1020

QY 1082 DPCNCNAAHSFGPSCNEFTGQCQCMFGGRTCSCEQELFWGDPDVECRACDCDPRGIET 1141

Db 1021 DPCNCNAAHSFGPSCNEFTGQCQCMFGGRTCSCEQELFWGDPDVECRACDCDPRGIET 1080

QY 1142 PQCDQSTGQCVCEGVEGPRCDKCTFGYSGVFPDCTPCHQCFALWDVIIAELTNRTHRFL 1201

Db 1081 PQCDQSTGQCVCEGVEGPRCDKCTFGYSGVFPDCTPCHQCFALWDVIIAELTNRTHRFL 1140

QY 1202 EKAKALKISGVIGPYRETVDVSVERKVSEIKDILAQSPAAEPLKNIGNLFEEAEKLDKVT 1261

Db 1141 EKAKALKISGVIGPYRETVDVSVERKVSEIKDILAQSPAAEPLKNIGNLFEEAEKLDKVT 1200

QY 1262 ENMAQVEVKLSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSI 1321

Db 1201 ENMAQVEVKLTDITASQSNSTAGELGALQAEASLDKTVKELAEQLEFIKNSDIQALDSI 1260

QY 1322 TKYFQMSLEAEERVNASTEPNSTVEQSALMRDRVEDVMMERESQFKEQEQEARLLDEL 1381

Db 1261 TKYFQMSLEAEERVNASTEPNSTVEQSALMRDRVEDVMMERESQFKEQEQEARLLDEL 1320

QY 1382 AGKQSLDLASAAAEWTCGTPPGASCSETCECGGPNCRDEGERKCGGPGCGGLTVVAHNAW 1441

Db 1321 AGKQSLDLASAAAEWTCGTPPGASCSETCECGGPNCRDEGERKCGGPGCGGLTVVAHNAW 1380

QY 1442 QKAMDLDQDVLASALAEVEQLSKMSVSEAKLRADAEAKQSAEDILLKTNATKEKMDKSNEELR 1501

Db 1381 QKAMDLDQDVLASALAEVEQLSKMSVSEAKLRADAEAKQSAEDILLKTNATKEKMDKSNEELR 1440

QY 1502 NLIQIRNFLTQDSADLDSIEAVANEVLKMPSTPQOLQNLTEDIRERVESLSQVEVIL 1561

Db 1441 NLIQIRNFLTQDSADLDSIEAVANEVLKMPSTPQOLQNLTEDIRERVESLSQVEVIL 1500

QY 1562 QHSAADIAEAEMLLLEAKRASKSATDVKTADVMVKEALEEAEAKQVAAEKAIKQADEDIQ 1621

Db 1501 QHSAADIAEAEMLLLEAKRASKSATDVKTADVMVKEALEEAEAKQVAAEKAIKQADEDIQ 1560

QY 1622 GTONLLTSIESETAASEETLNASQRISELERNVUELKRKAAQNSGEAEYIEKVVTYVKQ 1681

Db 1561 GTONLLTSIESETAASEETLNASQRISELERNVUELKRKAAQNSGEAEYIEKVVTYVKQ 1620

QY 1682 SAEDVKKTLDGELDEKYKVENLAKKTESADARRKAEMLQNEAKTLLAQANSKLQLLX 1741

Db 1621 SAEDVKKTLDGELDEKYKVENLAKKTESADARRKAEMLQNEAKTLLAQANSKLQLLX 1680

QY 1742 DLERKYEDNQRYLEDKAQELVLEGEVRSLLKDISQKAVYSTCL 1786

Db 1681 DLERKYEDNQRYLEDKAQELVLEGEVRSLLKDISQKAVYSTCL 1725

RESULT 9

US-09-561-818A-20
; Sequence 20, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortessmaa, Jarkko
; APPLICANT: Tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99.274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 1725
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-561-818A-20

Query Match 91.0%; Score 8873; DB 4; Length 1725;
Best Local Similarity 92.9%; Pred. No. 0;
Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

QY 62 EPYCIIVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVVTFAPNRLKIWWQSENGVENV 121

Db 1 EPYCIIVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVVTFAPNRLKIWWQSENGVENV 60

QY 122 TIQLDLAEAFHFTLIMTFKTRPAAMLIERSSDFGKTGWVRYFYAYDCESSFPFGISTGP 181

Db 61 TIQLDLAEAFHFTLIMTFKTRPAAMLIERSSDFGKTGWVRYFYAYDCESSFPFGISTGP 120

QY 182 MKKVDDIIICDSRYSDIEPSTEGEVIIFRALDPAPKIEDPYSPRIQNLLKITNLRIFVKLH 241

Db 121 MKKVDDIIICDSRYSDIEPSTEGEVIIFRALDPAPKIEDPYSPRIQNLLKITNLRIFVKLH 180

QY 242 TLGDNLLDSRMEIREKYYYAYVDMVRGNCFCYGHASECAPVDGFEVEEVEGMVGHCMCR 301
Db 181 TLGDNLLDSRMEIREKYYYAYVDMVRGNCFCYGHASECAPVDGFEVEEVEGMVGHCMCR 240
QY 302 HNTKGLNCELMDPYHDLWPRPAEGRNSNACKKCNNEHSTSCHEFDMAVYLATGNVSGGV 361
Db 241 HNTKGLNCELMDPYHDLWPRPAEGRNSNACKKCNNEHSSCHFDMAVFLATGNVSGGV 300
QY 362 CDDQHNTMGRNCEOCKPFYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFSTGL 421
Db 301 CDNCQHNTMGRNCEOCKPFYQHPERDIRDPNFCERCTCDPAGSENGGICDGYTDFSVGL 360
QY 422 IAGQCRCKLHVEGERCDVCKEGFYDLSSSEDPFGCKSCACNPLGTIPGGNPNCDSETHCYC 481
Db 361 IAGQCRCKLHVEGERCDVCKEGFYDLSSSEDPFGCKSCACNPLGTIPGGNPNCDSETHCYC 420
QY 482 KRLVTGQHCDCQLPEHGWGLSNDLDCGCPDCLGGLNNSCFASGQSCRPHEMIGRQCN 541
Db 421 KRLVTGQHCDCQLPEHGWGLSNDLDCGCPDCLGGLNNSCFASGQSCRPHEMIGRQCN 480
QY 542 EPEGYYPATLDHYLYEAEANLPGVSVIVERQYIQDRIPSWTGAQFVRVPEGAYLEFFI 601
Db 481 EPEGYYPATLDHYLYEAEANLPGVSVIVERQYIQDRIPSWTGAQFVRVPEGAYLEFFI 540
QY 602 DNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPSTRSCGNTIPDDNNQVLSLPGS 661
Db 541 DNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPSTRSCGNTIPDDNNQVLSLPGS 600
QY 662 RYVWLPVPVCEKGMNYTVRLELPQYTSDDSDVESPYTIDSLVMPYCKSLDIFTVGS 721
Db 601 RYVWLPVPVCEKGMNYTVRLELPQYTSDDSDVESPYTIDSLVMPYCKSLDIFTVGS 660
QY 722 GDGVVNTSAWETFORYRCLENSRSVVKTPMTDVCNIIIPSIALLHOTGLACECDPQGS 781
Db 661 GDGVVNTSAWETFORYRCLENSRSVVKTPMTDVCNIIIPSIALLHOTGLACECDPQGS 720
QY 782 SSVCDPNGGQOCQCPNVRGTCNRCAPGTGFGPGSGCKPCBCHLQGSVNAFCNPVTGOCH 841
Db 721 SSVCDPNGGQOCQCPNVRGTCNRCAPGTGFGPGSGCKPCBCHLQGSVNAFCNPVTGOCH 780
QY 842 CFQGVYARQCDRCLPGHWGFPSCQPCQNGHADDCTVTEGLNCCQDYTMHNCERCLAG 901
Db 781 CFQGVYARQCDRCLPGHWGFPSCQPCQNGHADDCTVTEGLNCCQDYTMHNCERCLAG 840
QY 902 YGDPPIIGSDHCRPCPCPDGSDGRQFARSCYQDPVTQLACVCDPPIGSRCDCCASG 961
Db 841 YGDPPIIGSDHCRPCPCPDGSDGRQFARSCYQDPVTQLACVCDPPIGSRCDCCASG 900
QY 962 YFGNPSVSGSCQPCQCHNNDITDPEACDKETGRCLKCLYHTEGHCQCFRFGYGDAL 1021
Db 901 YFGNPSVSGSCQPCQCHNNDITDPEACDKETGRCLKCLYHTEGHCQCFRFGYGDAL 960
QY 1022 RQDCRKCVCNLYGTVOEHGNSGDCQCDKATGQCLCPNVIGQNCDCRCAPNWQLASGTGC 1081
Db 961 RQDCRKCVCNLYGTVOEHGNSGDCQCDKATGQCLCPNVIGQNCDCRCAPNWQLASGTGC 1020
QY 1082 DPCNCAHSGFSPSCNEFTGQCCQMPGFGGRTSCQCBELFWGDPDVECRACDCDPRGIET 1141
Db 1021 DPCNCAHSGFSPSCNEFTGQCCQMPGFGGRTSCQCBELFWGDPDVECRACDCDPRGIET 1080
QY 1142 PQCDQSTGQCVCEGVEGPRCDKTRGYSVGFPPDCTPCHQCFALWDVILAEITNRTHREL 1201
Db 1081 PQCDQSTGQCVCEGVEGPRCDKTRGYSVGFPPDCTPCHQCFALWDVILAEITNRTHREL 1140
QY 1202 EKAKALKISGVIGPYRETVDVSEKVKSEIKDILAQSPAAEPLKNIIGNLFEAEKLIKDV 1261
Db 1141 EKAKALKISGVIGPYRETVDVSEKVKSEIKDILAQSPAAEPLKNIIGNLFEAEKLIKDV 1200
QY 1262 EMMAQVEVKLSDTTSQSNSTAKELDSLOTEAESLDNTVKELAEQLEFINKSDIRGALDSI 1321
Db 1201 EMMAQVEVKLSDTTSQSNSTAKELDSLOTEAESLDNTVKELAEQLEFINKSDIRGALDSI 1260
QY 1322 TKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVMMVERESQFKEKEEQARLLDEL 1381

Db 1261 TKYFQMSLEAEERVNASTTEPNSTVEQSALTRDRVEDLMERESPFEQEEQARLLDEL 1320
QY 1382 AGKLQSLDLSAAAEEMTCGTPPGASCSETECGGPNCRCTDEGERKCGGPGCGGLVTVAHNAW 1441
Db 1321 AGKLQSLDLSAAAEEMTCGTPPGASCSETECGGPNCRCTDEGERKCGGPGCGGLVTVAHNAW 1380
QY 1442 QKAMDLDQDVLASAEVEQLSKVSEAKLRADEAKQSAEDILIKTNATKEKMDKSNEEELR 1501
Db 1381 QKAMDLDQDVLASAEVEQLSKVSEAKLRADEAKQSAEDILIKTNATKEKMDKSNEDLR 1440
QY 1502 NLIKQIRNFLTQDSADLDSIEAVANEVLKMEMPTPQQLQNLTEDIRERVESLSQVEVIL 1561
Db 1441 NLIKQIRNFLTQDSADLDSIEAVANEVLKMEMPTPQQLQNLTEDIRERVESLSQVEVIL 1500
QY 1562 QHSAADIARAEMLLLEAKRASKSATDVKVTADVMVKEALEEAEAKQAAEKAIKQADEDIQ 1621
Db 1501 QHSAADIARAEMLLLEAKRASKSATDVKVTADVMVKEALEEAEAKQAAEKAIKQADEDIQ 1560
QY 1622 GTQNLTSIESETAASEETLNASORISELERNVEELKRAQNSGEAEYIEKVVTYVKQ 1681
Db 1561 GTQNLTSIESETAASEETLNASORISELERNVEELKRAQNSGEAEYIEKVVTYVKQ 1620
QY 1682 SAEDVVKTLGDELDEKYKVENLIAKTEESADARRKAEMLQNEAKTLLAQANSKLQLE 1741
Db 1621 NADDVVKTLGDELDEKYKVENLIAKTEESADARRKAEMLQNEAKTLLAQANSKLQLE 1680
QY 1742 DLERKYEDNQRYLEDKAQELARLEGEVRSLLKDISQKAVYSTCL 1786
Db 1681 DLERKYEDNQRYLEDKAQELARLEGEVRSLLKDISQKAVYSTCL 1725

RESULT 10
US-08-144-121-4
; Sequence 4, Application US/08144121
; Patent No. 5610031
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert E.
; APPLICANT: Wagman, David W.
; TITLE OF INVENTION: BLK CHAIN OF LAMININ AND METHODS OF USE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: United States
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/144,121
; FILING DATE: 27-OCT-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: (MGH-0780.0) MGP-021
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1196 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Domain

APPLICANT: Wagman, David W.
TITLE OF INVENTION: BLK CHAIN OF LAMININ AND METHODS OF USE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: BOSTON
STATE: Massachusetts
COUNTRY: United States
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/735,893
FILING DATE: 18-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/144,121
FILING DATE: 27-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: (MGH-0780.1) MGP-021DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1196 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Domain
LOCATION: 1..250
FEATURE:
NAME/KEY: Domain
LOCATION: 251..437
FEATURE:
NAME/KEY: Domain
LOCATION: 438..807
FEATURE:
NAME/KEY: Domain
LOCATION: 808..840
FEATURE:
NAME/KEY: Domain
LOCATION: 841..1196

US-08-735-893-4

Query Match 62.0%; Score 6051.5; DB 2; Length 1196;
Best Local Similarity 67.7%; Pred. No. 0;
Matches 1195; Conservative 0; Mismatches 0; Indels 571; Gaps 2;
QY 22 QEPEFSYGAEGSCYPATGDLIGRAQKLSVTS-TCGLHKPEPYCIVSHLOEDKKCFICN 80
Db 1 QEPEFSYGAEGSCYPATGDLIGRAQKLSVTS-TCGLHKPEPYCIVSHLOEDKKCFICN 60
QY 81 SQDPYHETINPDASHLIENVVTFAPNRLKIWWQSENGVENVTIQLDLAEFFHFTLIMTF 140
Db 61 SQDPYHETINPDASHLIENVVTFAPNRLKIWWQSENGVENVTIQLDLAEFFHFTLIMTF 120
QY 141 KTFRPAAMLIERSDFGKTGWVYRYFAYDCEASFPGISGTPMKKVDIICDSRYSDIEPS 200
Db 121 KTFRPAAMLIERSDFGKTGWVYRYFAYDCEASFPGISGTPMKKVDIICDSRYSDIEPS 180
QY 201 TEGEVIFRALDPFAFKIEDPSPRIQNLKLTNLRIFVKLHTGLDNLDSRMEIREKYYY 260
Db 181 TEGEVIFRALDPFAFKIEDPSPRIQNLKLTNLRIFVKLHTGLDNLDSRMEIREKYYY 240

QY 261 AVYDMVVRGNCFYGHASECAPVDGFNEEVEGMVHGHCMCRHNTKGLNCEL CMDFYHDL P 320
Db 241 AVYDMVVRGNCFYGHASECAPVDGFNEEVEGMVHGHCMCRHNTKGLNCEL CMDFYHDL P 300
QY 321 WRPAEGRNSNACKKCNCHNEHSISCHFDMAVYLATGNVSGVCDCCQHTMGRNCEQCKPF 380
Db 301 WRPAEGRNSNACKKCNCHNEHSISCHFDMAVYLATGNVSGVCDCCQHTMGRNCEQCKPF 360
QY 381 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSTGLIAGQCRCKLNVEGHCDCVC 440
Db 361 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSTGLIAGQCRCKLNVEGHCDCVC 420
QY 441 KEGFYDLSSSEDPFGCKSCACNPLGTIPGGNPDSETGHYCKRLVTGQHCDCQCLPEHWGL 500
Db 421 KEGFYDLSSSEDPFGCKS----- 437
QY 501 SNLDGCRPCDCLGGALNNSCFAESGQCSRPHMIGRQCNEVEPGYFATLDHYLYEAE 560
Db 438 ----- 437
QY 561 EANLPGVSIYERQYIQRIPSWTGAGFVRVEGAYLEFFIDNIPYSMEYDILIRYEPQL 620
Db 438 ----- 437
QY 621 PDHWEKAVITVQRPGRIPRTSSRCNGTIPDDDNQVVSLSPGSRYVVLPRPVCFEKGTNTYV 680
Db 438 ----- 437
QY 681 RLELPQYTSSDSVESPYTLIDSLVLMFYCKSLDIFTVGGSGDGVVTSNAWETFQRYRCL 740
Db 438 ----- 437
QY 741 ENSRSVVKTPMTDVCRNIIPISALLHOTGLACECDPQGSLSVCDPNGGQCCQCRNVVG 800
Db 438 ----- 437
QY 801 RTCNRCAPGTGFGPFGSGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDRLPGHWG 860
Db 438 ----- 437
QY 861 FPGSCQPCNGHADDCCDPTVTECLNCQDYTMGNHCERCLAGYGDPIIGSGDHCRPCPCP 920
Db 438 ----- 437
QY 921 DGPDSGRQFARSCYQDPVTLQACVCDPFIYIGSRCDDCASGYFGNPSVGGSCQPCQCHN 980
Db 438 ----- 437
QY 981 NIDTTDPEACDKETGRCLKCLYHTEGHEHCQCFRFGYGDALRQDCRCKVCNVLGTVOEHC 1040
Db 438 -----CVCNVLGTVOEHC 450
QY 1041 NGSDCCQCKATGQCLCLPNVIGQNCDCRCAPNTWQLASGTGCDPCNCNAHSGFSPSCNEFT 1100
Db 451 NGSDCCQCKATGQCLCLPNVIGQNCDCRCAPNTWQLASGTGCDPCNCNAHSGFSPSCNEFT 510
QY 1101 GQCQCMPPGFGGRTCSCEQELFWGDPDVECRACDCDPRGIETPQCDQSTGQCVCVEGVEGP 1160
Db 511 GQCQCMPPGFGGRTCSCEQELFWGDPDVECRACDCDPRGIETPQCDQSTGQCVCVEGVEGP 570
QY 1161 RCDKCTRGYSYGVFPDCTPCHQCFALWDVIIAELTNRTHRFLEKAKALKISGVIGPYRET V 1220
Db 571 RCDKCTRGYSYGVFPDCTPCHQCFALWDVIIAELTNRTHRFLEKAKALKISGVIGPYRET V 630
QY 1221 DSVERKVSEIKDILAQSPAAPLKNIGNLFEAEKLIKDVTEMMAQVEVKLSDTTSQNS 1280
Db 631 DSVERKVSEIKDILAQSPAAPLKNIGNLFEAEKLIKDVTEMMAQVEVKLSDTTSQNS 690
QY 1281 TAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTT 1340
Db 691 TAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTT 750

QY 1341 EPNSTVEQSALMRDRVEDVMMERESQFKQEEQARLLDELAKLQSLDLSAAAEEMTCGT 1400
Db 751 EPNSTVEQSALMRDRVEDVMMERESQFKQEEQARLLDELAKLQSLDLSAAAEEMTCGT 810
QY 1401 PPGASCSETCGGPNCRTEDEGERKCGGPGGGLVTVAHNAWQKAMDLDQDVLSSALAEVEQ 1460
Db 811 PPGASCSETCGGPNCRTEDEGERKCGGPGGGLVTVAHNAWQKAMDLDQDVLSSALAEVEQ 870
QY 1461 LSKMWSEAKLRADAEKQSAEDILLKTNATKEMKDKSNEELNLIKQIRNFLTQDSADLDS 1520
Db 871 LSKMWSEAKLRADAEKQSAEDILLKTNATKEMKDKSNEELNLIKQIRNFLTQDSADLDS 930
QY 1521 IEAVANEVLKXEMPSPPQQLNLTEDIRERVESLSQVEVILQHSAAADIAAEMLLEBAKR 1580
Db 931 IEAVANEVLKXEMPSPPQQLNLTEDIRERVESLSQVEVILQHSAAADIAAEMLLEBAKR 990
QY 1581 ASKSATDVKVTADMVKEALEEAEKQAAEKAQKQADEDIQGTQNLTSIESETAASEET 1640
Db 991 ASKSATDVKVTADMVKEALEEAEKQAAEKAQKQADEDIQGTQNLTSIESETAASEET 1050
QY 1641 LFNASQRISELERNVSEELKRAAQNSEGEABYIEKVYTVKQSAEDVKKTLGDELDEKYK 1700
Db 1051 LFNASQRISELERNVSEELKRAAQNSEGEABYIEKVYTVKQSAEDVKKTLGDELDEKYK 1110
QY 1701 VENLIAKTEESADARRKAEMLQNEAKTLLAQANSKLQLLKDLERKYEDNQRYLEDKAE 1760
Db 1111 VENLIAKTEESADARRKAEMLQNEAKTLLAQANSKLQLLKDLERKYEDNQRYLEDKAE 1170
QY 1761 LARLEGEVRSLLKDISQKAVYSTCL 1786
Db 1171 LARLEGEVRSLLKDISQKAVYSTCL 1196

RESULT 12

US-09-845-583A-6
; Sequence 6, Application US/09845583A
; Patent No. 6635616
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Brunken, William Joseph
; APPLICANT: Champlaud, Marie-France
; APPLICANT: Hunter, Dale
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
; FILE REFERENCE: 10287-056001
; CURRENT APPLICATION NUMBER: US/09/845,583A
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/200,863
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1799
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-845-583A-6

Query Match 51.8%; Score 5051.5; DB 4; Length 1799;
Best Local Similarity 50.8%; Pred. No. 1.8e-285;
Matches 907; Conservative 304; Mismatches 560; Indels 15; Gaps 8;
QY 7 LAFSFLALCRARVRAQEPESY-GCAEGSCYPATGDLIGRAQKLSVTSTCGLHKPEPYC 65
Db 21 LRLGLLSVLAATLAQAPSLDVPGCSRGSCYPATGDLVGRADRLTASSTCGLHSPQPYC 80
QY 66 IVSHLQEDKKFCICNSQDPYHETLNPDSDHLIENVVTTTFAPNRLKIWQSENGVENVTIQL 125
Db 81 IVSHLQEDKKFCICNSQDPYHETLNPDSDHLIENVVTTTFAPNRLKIWQSENGVENVTIQL 140
QY 126 DLEAEFHFTLMTFKTRPAAMLIERSSDFGKTWGVYRFPAYDCEASFPGISTGPMKV 185
Db 141 DLEAEFHFTLMTFKTRPAAMLVERSDFGRTWHVYRFSYDCGADFPGIPAPRRW 200
QY 186 DDIICDSRYSIDIEPSTEGEVI FRALDPAFKIEDPYSPRIQNLKITNLRIKPVKLTGLD 245

Db 201 DDVVCESRYSEIEPSTEGEVIYRVLDPAIPDPYSSRIQNLKITNLRLTLHTLGD 260
QY 246 NLLDSRMEIREKYYAVYVDMVRGNCFCYCHASBAPVDGFNEEVEGVMCHCMCRHNTK 305
Db 261 NLLDSRMEIREKYYAVYVDMVRGNCFCYCHASBAPVDGFNEEVEGVMCHCMCRHNTK 320
QY 306 GLNCELMDFFYHDLPRPABGRNSNACKKCNCHSISCHFDMAVYLATGNVSGVGDCC 365
Db 321 GLNCEQODFYQDLPHFPAEDGHATHACRKECNGHSHCHFDMAVYLASGNVSGVGDCC 380
QY 366 QHNTMGRNCEQCKPFYQHPERDIRDPNFCERCCTCDPAGSQNEGICDSYTDSTGLIAGQ 425
Db 381 QHNTAGRHCFCRPFYRDTKMDRDPVCRPCDDCPMGSDGGRCDSHDDPVLGLVSGQ 440
QY 426 CRCKLNVEGEHCDVCKEGFDLSSEDPFGCKSCACNPLGTIPGGNPNCDSETGHYCKRLV 485
Db 441 CRCKEHVVGTRCQCRDGFGLSASDPGRCQRCQNSRGTVPGSSPCDSSSGTCFCCKRLV 500
QY 486 TGHGCDQCLPEHMGSLNDLDCRCPDCDGLGALNNSCFAESGQSCSRPHMIGRQCNVEP 545
Db 501 TGHGCDQCLPEHMGSLNDLDCRCPDCDGLGALNNSCFAESGQSCSRPHMIGRQCNVEP 560
QY 546 GYFATLDHLYEAEZANLPGVSIIVERQYIQDRIPSWTGAQFVRVPEGAYLEFFIDNIP 605
Db 561 GYFATLDHLYEAEZANLPGVSIIVERQYIQDRIPSWTGAQFVRVPEGAYLEFFIDNIP 619
QY 606 YSMEYDILIRYEPOLPDHWEKAVITVQRPGRPTSSRCGNTIPDDNQVVSLSPGSRVYV 665
Db 620 RAMDYDILLRWEPOVPEQWAELELMVQRPGPSAHSAPCGHVLKDDRIQGMHLPNTRVLV 679
QY 666 LPRPVCFEKGTNTYVRLPQYTSDDSDVESPYT--LIDSLVLMPCYKSLDIFTVGGSGD 723
Db 680 LPRPVCFEKGTNTYVRLPQYTSDDSDVESPYT--LIDSLVLMPCYKSLDIFTVGGSGD 734
QY 724 GVTNSAWETFORYRCLNRSRVVKTMTDVCNIIIFSISALLHQTGLACEDPQGSLS 783
Db 735 DAAALERTTTFERYRCHHEGLMPSKAPLSETCAPLLISVALIYNGALPCQCDPQGSLS 794
QY 784 VCDPNGGQCCQCRPNVVRTCNRCAPGTGFGPSGCKPCECHLQGSVNAFCNPVTGQCHCF 843
Db 795 ECSPHGGQCRCKPGVVGRRCDVCATGYGFGPAGCQACQCSPDGALSALCEGTSQGPCR 854
QY 844 QGVYARQCDRLPGHWGFPSCQPCQCNQGHADDCDPTVTECLNCQDYTMHNCERCLAGY 903
Db 855 PGAFGLRCDHCQRGQGWFPNCRPCVNCGRADDECDDTHTGACLGCRDVTGGEHCERCIAGFH 914
QY 904 GDFIIGSGDHCRCPCPCDGPDSGRQFARSCVQDPVTLQACVDFYIGSRCDDCASGYF 963
Db 915 GDFIIGSGDHCRCPCPCDGPDSGRQFARSCVQDPVTLQACVDFYIGSRCDDCASGYF 974
QY 964 GNPSEVGGSCQPCQCHRNIDTDDPEACDKETGRCLKCLYHTEGHCQCFRFGYGDALRQ 1023
Db 975 GNPSEVGGSCQPCQCHRNIDTDDPEACDKETGRCLKCLYHTEGHCQCFRFGYGDALRQ 1034
QY 1024 DCRKVCNVLGTVQEHNGSD-CQCDKATGQCLCLPNVIGQNCDCRCPNTWQLASGTGCD 1082
Db 1035 SCHRCTCNLLGTDPRCPSDLDLCHDPPSTGQCPCLPHVQGLNCDHCAPNFWNFTSGRGQ 1094
QY 1083 PCNCNAHSGFSPSCNEFTGQCCQMPGFGRTCSCEQLFWGDDPVECRACDPRGIETP 1142
Db 1095 PCACHPSRARGPTCNFTGQCHHAGFGRTCSCEQLFWGDDPVECRACDPRGIETP 1154
QY 1143 QCDQSTGQCVCEGVEGPRCDKCTRGYSVGFPPDCTPCHQCFALWDVIIAELTNRTHRLE 1202
Db 1155 QCHRSTGHCSRCPGSGVRCDCQCARGFSGVFPACHPCHACFGDWDVVDLAARTRRLEQ 1214
QY 1203 KAKALKISGVIGVIRETVDSVERKVSIEKIDILAQSPAAEPLKNICNLFFEEAEKL---IKD 1259
Db 1215 WAQELQOTGVLAGFESSFLNQKLMQVQAIMSARNAS--AATAKLVATEGLRHEIGK 1272
QY 1260 VTEMMAQVEVKLSDTTSQSNSTAKELDSLOTEAESLDNTVKELAEQLEFIKNSDIRGALD 1319

Db 1273 TTERLTQLEAELTAVQDENFNANHALSGLERDGFALNLTLRQLDQHLEILKHSNPLGAYD 1332
QY 1320 SITKYFQMSLEAERVNASTTEPNSTVEQSALMRDRVEDVNMERESQFKEKEQEQARLLD 1379
Db 1333 SIRHAHSQSTEAEERRANASTFAVPSVNSADTRRRTEVLMAQAQENFNQHLANQOALG 1392
QY 1380 ELAGKLSLDLSAAAEMTCGTPPGASCSETECGGPNCRTEDEGERKCGGPGCGGLVTVAHN 1439
Db 1393 RLSAHAHTLSLTGINELVCGAPDAPCATSPCGGAGCRDEDPQRCGGLGCSGAAAPADL 1452
QY 1440 AWQKAMDLDQDVLASALAEVQLSKMVSEAKLRADEAKQSAEDILLKTNATKEMDKSNEE 1499
Db 1453 ALGRARHSQAELOALVEGGGILSRVSETRRQAEAAQOQAALDKANASRGQVEQANQE 1512
QY 1500 LRNLIKQIRNFLTQDSADLDSIEAVANEVLKMEMPSTPQOLQNLTEDIRERVESLSQVEV 1559
Db 1513 LRELIONKDFLSQEGADPDSIEMVATRVLDISIPASPEIQRLASEIAERVSRLADVDT 1572
QY 1560 ILQSAADIAARAEMLLBEAKRASKSATDVKTADVMKEALEEAEKAAQVAAEKAQKQADE 1619
Db 1573 ILAHTMGDVRAEQLLQDAHRARAEGERQKAETVQAALEEAQRAQAAGAAQGAIRGAVVD 1632
QY 1620 IQGTQNLTSIESETAASEETLFNASQRISSELRNVEELKRAAQNSEGEAEYIEKVYTV 1679
Db 1633 TQNTQTLQVRQERMAGAEKSLNSAGERARQLDALLEALKLRAGNSLAETAETAGSA 1692
QY 1680 QSAEDVKKIDGELDEKIKYKVENLIAKKTESASADARRKAEMLQNEAKTLLAQANSKLQ 1739
Db 1693 QSRAREAEKQREQVGDQYQTVRALLAERKAEGVLAQAARAEQLRDEARDLLQAAQDKLQ 1752
QY 1740 LKDLERKYEDNQRYLEDKAQELARLEGEVRSLLKDISQKVAVYSTC 1785
Db 1753 LOELEGTYEENERALEGKAAQLDGLAEMRSVLQAINLQVQIYNTC 1798

RESULT 13

US-09-561-709B-11
; Sequence 11, Application US/09561709B
; Patent No. 6682911

GENERAL INFORMATION:

; APPLICANT: Burgeson, Robert
; APPLICANT: Champilaud, Marie-France
; APPLICANT: Olson, Pamela
; APPLICANT: Koch, Manuel
; APPLICANT: Brunken, William
; TITLE OF INVENTION: LAMININS AND USES THEREOF
; FILE REFERENCE: 10287-060001
; CURRENT APPLICATION NUMBER: US/09/561,709B
; CURRENT FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 09/168,949
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: US 60/061,609
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1798
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-709B-11

Query Match 50.5%; Score 4926.5; DB 4; Length 1798;

Best Local Similarity 49.6%; Pred. No. 3.4e-278;

Matches 886; Conservative 309; Mismatches 575; Indels 15; Gaps 7;

QY 7 LAFSFLALCRARVRAQEPFESYGCAEGSCYPATGDLIGRAQKLSVTSTCGLHKPEPYCI 66

Db 22 LLLSVLAATLAQAPADVP--GCSRGSCYPATADLLVGRADRLTASSTCGLNGRQPYCI 78

QY 67 VSHLQEDKKCFICNSQDPYHETLNPDSHLIENVYVTFAPNRLKIWQSENGVENVTIQLD 126

Db 79 VSHLQEDKKCFICNSQDPYHETLNPDSHLIENVYVTFAPNRLKIWQSENGVENVTIQLD 138

QY 127 LEAEFFHTLIMTFKTERPAAMLIERSSDFGKTGWVYRYFAYDCEASFPGISTGPMKKVD 186
Db 139 LEAEFFHTLIMTFKTERPAAMLIERSSDFGKTGWVYRYFAYDCEASFPGISTGPMKKVD 198
QY 187 DIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPRIQNLKITNLRIKFVKLHTLGDN 246
Db 199 DVVCESTRYSEIEPSTEGEVIVRLDPAIPIDPYSSRIQNLKITNLRIKFVKLHTLGDN 258
QY 247 LILDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGFNEVEGMVHGCMCHNFKG 306
Db 259 LILDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGFNEVEGMVHGCMCHNFKG 318
QY 307 LNCELCMDFYHDLPRWPAEGRNSNACKKCNNEHSISCHFDMAVYLATGNVSGGVCDQCQ 366
Db 319 LNCCEQCQDFYRDLPRWPAEGRNSNACKKCNNEHSISCHFDMAVYLATGNVSGGVCDQCQ 378
QY 367 HNTMGRNCEQCKPFYFYOHPERDIRDPNFCERCTCDPAGSONEGICDSYTDFTSTGLIAGQC 426
Db 379 HNTAYRHCELCRPFYFYOHPERDIRDPNFCERCTCDPAGSONEGICDSYTDFTSTGLIAGQC 438
QY 427 RCKLNVGEHCQVCKEGFYDLSSDEPFGCKSCACNPLGTIPGNNPCDSETHCYCKRLVT 486
Db 439 RCKEHVVGTRCQCRDGFGLSISDPGSCRRCCQCNARGTVPGSTPCDPNSGSCYCKRLVT 498
QY 487 GQHCDCQLPEHWSLNDLDCRCPDCLGGALNNSCFABSGQSCSRPHMIGRQCNEVEPG 546
Db 499 GRGCDRCLPGHWSLNDLDCRCPDCLGGALNNSCFABSGQSCSRPHMIGRQCNEVEPG 558
QY 547 YFATLHDYLYEAEANLPGVSIYERQYIQDRIPSWTGAQVVRVPEGAYLEFFIDNIPY 606
Db 559 YFRPFLDHLIWEAENR-GQVLDVVERLVTGETPSTGSGFVRVLEGQTLFPLVASVPN 617
QY 607 SMEYDILIRYEPQLPDHWEKAVTVQRPGRIPRTSSRCNTIPDDDNQVVSLSPGSRVVL 666
Db 618 AMDYDLLLLLEPQVPEQWAELELVQRPVPAHSLGHLVPRDDRIQGTLPQHARYLIF 677
QY 667 PRPVCFEKGTNYTVRLELPQYTSDDSDVESPYT----LIDSLVLMYPYCKSLDIFTVGGSG 722
Db 678 PNPVCLPEPGISYKHLKLV-RGSSAQPETPYSGPGLLIDSLVLLPRVLVLEMF----SG 732
QY 723 DGVVTVNSAWETFORYRCLENSRSVVTMTDVCRNIFISISALLHQTGLACECDPQGSLS 782
Db 733 GDAALERQATFERYQCHEGLVPSKTSPEACAPLLISLTLIYNGALPCQCNPPQGSLS 792
QY 783 SVCDPNGGQCCQCRPNVVRGTRCNRCAPGTGFGPSPGCKPCECHLQGSVNAFCNVPVTGQCHC 842
Db 793 SECNPHGGQCLCKPGVVRRCRDTCAPGYGFGPTGQACQCSPRGALSCLERTSGQCLC 852
QY 843 FQGVYARQCDRCCLPBGHWFPSCQPCQCNHADDCCDPVTGECNQCQDYMTHNCERCLAGY 902
Db 853 RTGAFGLRCDACQRGQWGFSPCRPCVCNCGHADECNTHTGACLCGRDHTGHEHCERCIAGF 912
QY 903 YGDPPIIGSGDHCRCPCPCPDGDSGRQFARSCYQDPVTQLACVCDPGYIGSRCDDCASGY 962
Db 913 HGDPRLPYGAQCRPCPCPEGSGQRHFATSCHQDEYSQQIVCHCRAGYTGURCEACAPGQ 972
QY 963 FGNPSEVGGSCQPCQCHNNIDTTPDPEACDKETGRCLKLYHTEGEHCQCFRFGYGDALR 1022
Db 973 FGDPSRPGRCQLCECSGNIDPMDPDACDPHPGQCLRLHHTGEPHCAHSKPGFHHGQAAR 1032
QY 1023 QDCRKCVCNYLGTVQEHCHNSD-CQCDKATGQCLCLPNVIGQNCDCRCAPTWQLASGTGC 1081
Db 1033 QSCHRTCNLLGTNPQQCPSPDQCHCDPSSGQCPCLPNVQALAVDRCAFPNFWNLTSGHGC 1092
QY 1082 DPCNCAHSAHSGPSCNEFTGQCCQCMFPGGRTGCTSECQELFWGDDPDVECRACDCDPRGIET 1141
Db 1093 QPCACLPSPPEEGPTCNFTGQCHCLCGFGGRTGCTSECQELFWGDDPDVECRACDCDPRGIET 1152
QY 1142 PQCDQSTGQCVCEVGEVGPBCKCTRGYSVGFDDTTPCHQCQFALWDVILAEILTNRTHRFL 1201
Db 1153 PQCHRTGHTCTCRPGVSGVRCDQACARGFSGIFPACHPCHACFGDWDVVDLAARTORLE 1212
QY 1202 EKAKALKISGVIGPYRETVDVSVERKVSEIKDIL-AQSPAAEPLKNIGNLFEAEKLIKDV 1260

Db	1213	QRAQELQOTGVLGAFESSFWHMQEKLGIVQGVICARNTSAASTAQLVEATEELRREIGE	1272
QY	1261	TEMMAQVEVKLSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKXNSDIRGALDS	1320
Db	1273	TEHLTQLEADLTVDQDENFNANHALSGLERDRLLNLTLRQLDQHLDLLKXSNFLGAYDS	1332
QY	1321	ITKYFQMSLEAEERVNASTTEPNSTVEQSAIMRDRVEDVMMERESQFKEKQEEQARLLDE	1380
Db	1333	IRHAHSQSAEAEERRANTSALAVPSPVSNASASARHTEALMDAQKEDFNSKHMANQRALGK	1392
QY	1381	LAKGLQSLDLSAAABMTCTGTPPGASCSETETCCGGPNCRDTDEGERKCGGPGGLVTVAHNA	1440
Db	1393	LSAHTHTLSLTDINELVCGAQGLHHDRITSPCGGAGCRDEDGQPRCGGLSCNGAATAADLA	1452
QY	1441	WQAMDLDDQVLSALAEVEQLSKWVSEAKLRADAEAKQSAEDILLKTNATKEMDKSNEEL	1500
Db	1453	LGRARHTQAEQLRALAEGGSILSRVAETRRQASEAQRAQAALDKANASRGQVEQANQEL	1512
QY	1501	RNLIKQIRNFLTQDSADLDSIEAVANEVLKXMPSTPQQLQNLTEDIRERVESLSQVEVI	1560
Db	1513	QELIQSVKDFLNEGADPDSIEMVATRVLELSIPASAEQIOHLAGAI AERVRSIADVDAI	1572
QY	1561	LQHSAAADIARAEMLLBEAKRASKSATDVKVTADMVKEALEEAEKAQVAAEKAIKQADEI	1620
Db	1573	LARTVGDVRRARQLQDARRARSWADEKQKAEIVQAALAEAQRAQGI AQGAIRGAVADT	1632
QY	1621	QGTQNLLTSISETAASEETLFNASQRISELERNVHEELKRKAAQNSGEAEYIEKVYTVTK	1680
Db	1633	RDTEQTLYQVQERMAGAEERALSSAGERARQLDALLEALKLKRAGNSLAASTAEETAGSAQ	1692
QY	1681	QSAEDVKKTLDGELDEKYKKVENLIAKKTTEESADARRKAEMLQNEAKTLLAQANSKLQLL	1740
Db	1693	GRAQAEQLLRGPLGDQYQTVKALAERKAQGVLAQAQVLAQAQAEQLPDEARDLLQAAQDKLQRL	1752
QY	1741	KDLERKYEDNQRYLXEDKAQELARLEGEVRSLLKDISQKVAVYSTC	1785
Db	1753	QELGTYEENERALESKAAQLDGLAERMRSVLQAINLQVQIYNTC	1797

RESULT 14

US-09-845-583A-8
: Sequence 8, Application US/09845583A

Patent No. 6635616

: GENERAL INFORMATION:

APPLICANT: Burgeson, Robert

APPLICANT: Brunken, William Joseph

APPLICANT: CHAMPLAUD, Marie-France

APPLICANT: Hunter, Dale

APPLICANT: HUNTER, DALE
: TITLE OF INVENTION: LAMININ 15 AND USES THEREOF

FILE OF INVENTION: FEMININ
: FILE REFERENCE: 10287-056001

FILE REFERENCE: 10287-030001
: CURRENT APPLICATION NUMBER: US/09/845,583A

: CURRENT FILING DATE: 2001-04-30
; CURRENT AFFILIATION NUMBER: 0070

CURRENT FILING DATE: 2001-04-30
: PRIOR APPLICATION NUMBER: US 60/200,863

; PRIOR APPLICATION NUMBER: 03
 : PRIOR FILING DATE: 2000-05-01

; PRIOR FILING DATE: 2000-
 : NUMBER OF SEQ ID NOS: 18

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NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0

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; SOFTWARE:
; SEQ ID NO 8

SEQ ID NO 8
LENGTH: 1798

LENGTH: 1
TYPE: PBT

TYPE: PRI
ORGANISM: Homo sapiens

ISS-09-845-583A-8

Query Match 50.5%; Score 4921.5; DB 4; Length 1798;

Best Local Similarity 49.6%: Pred. No. 6.6e-278;

Best Local Alignment	100.0%	100.0%	100.0%
Matches	885	Conservative	309
Mismatches	576	Indels	15
Gaps	7	Gaps	7

QV 7 LAFSFLALCRARVRAOEPEFSYGCAEGSCYPATGDL LIGRAQKLSVTSTCGLHKPEPYCI 66

22 LLSVLAA TL A O A P A P D V P - - - G C S R G S C Y P A T A D L L V G R A D R L T A S S T C G L N G R Q P Y C I 78

04 67 VSHI,0EDKKCFICNSODPYHETLNPDSHLIENVTTFAPNRLKIWOSENGVENVTIOLD 126

Dd	79	VSHLQDEKKCELCDSRRPFSARDNETHRIQNVVTSFAPQPRAAWQSONGIPAVTIQLD	138
Qy	127	LEAEFHFTHLINTFKTFRPAAMLIERSSDFKGTWGVYRYPAYDCEASFPGISTGPMKKVD	186
Dd	139	LEAEFHFTHLINTFKTFRPAAMLVERSADFGRTWHVYRYFSYHCCADFPVPLAPPRHWD	198
Qy	197	DIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPRIQNLLKITNLRIKFVKLHTLGDN	246
Dd	199	DWCESRYSEIEPSTEGEVIYRVLDPAIPIPDYSSRIQNLLKITNLRVNLTRLHTLGDN	258
Qy	247	LLDSRMEIREKYYAYVDMVVRGNCFYGHASECAPVDGFNEEVEGMVHGHCMCRHNTKG	306
Dd	259	LLDPRREIREKYYALYELVVRGNCFYGHASECAPAPAPAAEAGMVGACICKENTRG	318
Qy	307	LNCELCMDFYHDLPWPRPAEGRNSNACKKCNNEHSISCHFDMAVYLATGNVSGVCDCCQ	366
Dd	319	LNCEQCQDFYRDLPWPRPAEDGHSHACRCKDRHGHTHSCHFDMAVYLGSGNVSGVCDGCQ	378
Qy	367	HNTMGRNCEQCFFYYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFSTGLIAGQC	426
Dd	379	HNTAWRHCELCRFFFYRDPTKDLRDPVAVCRSCDCDPMGSDGGRCDSDHDDPALGLVSGQC	438
Qy	427	RCKLNVEGEHCDVCKEFGYDLSSDPFGCKSKACACNPLGTIPGGNPDSETGHCHYCKRLVT	486
Dd	439	RCKEHVGTRCQCRDGFGLSISDRSGCRRCCQCNARGTVPGSTPCDPSGSCYCKRLVT	498
Qy	487	GOHCDQCCLPEHWGLSNDLDGCRPCDCDLGGALNNSCFAESGQCSQRPHMIGRQCNEVEPG	546
Dd	499	GRGCDRCLPGHWGLSLDLLGCRPCDCDVGGALDPQCDEGTQCHCRQHVMVRRCEQVQPG	558
Qy	547	YYPATLDHYLYEAEEANLPGVSVIVERQYIQDRIPSWTGAGFVRVPEGAYLEFFIDNIPY	606
Dd	559	YFRPFLDLHWEAENTR-GQVLDVVERLVTGETPSWTSGSFVRLQEGQTFLEFLVASVPN	617
Qy	607	SMEYDILIRYEBQLPDHWEKAVITVQRPGRIPTSRRCGNTIPDDNQVVSLSPGSRVVL	666
Dd	618	AMDYDLLRLLEQVPEQWAELELIVORPGVPVAHSLCGHLVPRDDRIQGTLOPHARYLLF	677
Qy	667	PRPVCFEKGTNYTVRLELPQYTSSDSVESPYT---LIDSLVLMPYCKSLDIFTVGGSG	722
Dd	678	PNPVCLEPGISYKHLKLV-R-TGGSAQPETPYSGPGLLIDSLVLLPRVLVLEMF---SG	732
Qy	723	DGVVTNSAWETFORYRCLENSRSVVKTPMTDVCRNIIFSISALLHQTGLACEDPQGSLS	782
Dd	733	GDAALERQATFERYQCHEEGLVPSKTSPEACAPLLISLSTLIYNGALPCQCNPQGSLS	792
Qy	783	SVCDPNGGQCQCRPNVVGRTCNRCAPGTFGGPSGCKPCECHLQGSWAFNCNPVTQCHC	842
Dd	793	SECNPHGGQCLCKPGVVRRCDTCAPGYGFGPTGCACQCSPRGALSSLCERTSGQCLC	852
Qy	843	FQGVYARQCDRCLPGHWGFPSCQPCQCNGHADDCDPVTGECILNCQDYTMGHNCERLAGY	902
Dd	853	RTGAFGLRCDACQRGQWGFPSCRPCVCNCGHADECNTHTGACLGCRDLTGGEHCERCIAGF	912
Qy	903	YGDPIIGSGDHCRPCPCPDGPDGSGROFARSCYQDPVTLQACVCDPGYIGSRCDDCASGY	962
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Qy	963	FGNPSEVGGSCQPCQCHNNIDTTPDPAKDKETGRCLKCLYHTEGEHCQFCRFGYYGDALR	1022
Dd	973	FGDPSRPGGRQCLCECSGNIDPMDPDACDPHPGQCLRCLHHTEGPHCAHSKPGFHGQAAR	1032
Qy	1023	QDCRKCVCNVLGTVOEHCNGSD-CQCDKATGQCLCLPNVIGQNCDCRCAPNTWQLASGTGC	1081
Dd	1033	QSCHRCTCNLLGTNPQQCPSPDQCHCDPSSGQCPCLPNVQALAVDRCAPNFWNLTSGHGC	1092
Qy	1082	DPCNCNAHSFGPSCNEFTGQCQCMEFGGRTCSECOELFWGDDPVECRACDCDPRGIET	1141
Dd	1093	QPCACLPSPPEGPTCNEFTGQCHCLCGFGGRTCSECOELHWGDPGLQCHACDCDSRGIDT	1152
Qy	1142	PQCDQSTGQCVCEGVGPRCDKCTRGYSGVFPDCTPCHQCPCALWDVIIAELTNRTHRFL	1201
Dd	1153	PQCHRFTGHTCRPGVSGVRCDQCARGFSGIFPACHPCCHACFGDWDRVWQDLAARTORLE	1212

QY	1202	EKAKALKISGVIGPYRETVDVSVERKVSEIKDIL-AQSPAAEPLKNIGNLFTFEAEKLIKOV	1260
Db	1213	ORAQELQQTGVILGAFESSFWHMQEKLGIVOGIVGARNTSAASTAQLVEATEELRREIGEA	1272
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<p>; Patent No. 6682911</p>					
<p>; GENERAL INFORMATION:</p>					
<p>; APPLICANT: Burgeson, Robert</p>					
<p>; APPLICANT: Champlaud, Marie-France</p>					
<p>; APPLICANT: Olson, Pamela</p>					
<p>; APPLICANT: Koch, Manuel</p>					
<p>; APPLICANT: Brunken, William</p>					
<p>; TITLE OF INVENTION: LAMININS AND USES THEREOF</p>					
<p>; FILE REFERENCE: 10287-060001</p>					
<p>; CURRENT APPLICATION NUMBER: US/09/561,709B</p>					
<p>; CURRENT FILING DATE: 2000-05-01</p>					
<p>; PRIOR APPLICATION NUMBER: US 09/168,949</p>					
<p>; PRIOR FILING DATE: 1998-10-09</p>					
<p>; PRIOR APPLICATION NUMBER: US 60/061,609</p>					
<p>; PRIOR FILING DATE: 1997-10-10</p>					
<p>; NUMBER OF SEQ ID NOS: 13</p>					
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<p>; SEQ ID NO 1</p>					
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Db 1644 HA-----VNAKVQAESAQHOA-GSLEKEFVELKKQYAILQRTSTTGLTKETLGVKVKQ 1695

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QY 1782 YSTC 1785

Db 1756 YARC 1759

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Job time : 23.5107 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:56:24 ; Search time 45.4374 Seconds
(without alignments)
10937.572 Million cell updates/sec

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	9754	100.0	1786	9	US-09-938-275-6
3	9754	100.0	1786	14	US-10-037-182-6
4	9654	99.0	1765	14	US-10-037-182-8
5	9144	93.7	1786	9	US-09-938-275-7
6	9144	93.7	1786	14	US-10-037-182-10
7	8873	91.0	1725	14	US-10-037-182-12
8	6044.5	62.0	1196	16	US-10-443-349-4
9	5088.5	52.2	1801	9	US-09-938-275-8
10	5052.5	51.8	1798	9	US-09-938-275-9
11	5051.5	51.8	1799	9	US-09-845-583-6
12	4921.5	50.5	1798	9	US-09-845-583-8
13	3772.5	38.7	1808	15	US-10-369-493-5986
14	3076.5	31.5	1101	12	US-10-287-971-18
15	2348	24.1	527	12	US-09-925-298-703

16	2348	24.1	527	14	US-10-102-806-703	Sequence 703, Appl
17	1729.5	17.7	3672	15	US-10-369-493-6146	Sequence 6146, Ap
18	1696.5	17.4	1557	15	US-10-369-493-6816	Sequence 6816, Ap
19	1682	17.2	1605	14	US-10-037-182-18	Sequence 18, Appl
20	1680.5	17.2	1609	14	US-10-037-182-14	Sequence 14, Appl
21	1680.5	17.2	1609	14	US-10-299-058-12	Sequence 12, Appl
22	1677	17.2	1572	14	US-10-037-182-20	Sequence 20, Appl
23	1676.5	17.2	1609	9	US-09-938-275-11	Sequence 11, Appl
24	1676.5	17.2	1609	15	US-10-372-683-36	Sequence 36, Appl
25	1673	17.2	1576	14	US-10-037-182-16	Sequence 16, Appl
26	1658	17.0	1607	9	US-09-938-275-10	Sequence 10, Appl
27	1645.5	16.9	3712	12	US-10-037-417-48	Sequence 48, Appl
28	1645.5	16.9	3712	13	US-10-108-605-103	Sequence 103, Appl
29	1641.5	16.8	3712	12	US-10-037-417-51	Sequence 51, Appl
30	1605	16.5	3635	9	US-09-845-583-2	Sequence 2, Appl
31	1605	16.5	3635	12	US-10-037-417-47	Sequence 47, Appl
32	1605	16.5	3635	14	US-10-037-182-4	Sequence 4, Appl
33	1573.5	16.1	2743	14	US-10-037-182-36	Sequence 36, Appl
34	1573.5	16.1	3695	12	US-10-312-352-22	Sequence 22, Appl
35	1573.5	16.1	3695	14	US-10-037-182-2	Sequence 2, Appl
36	1569	16.1	3696	15	US-10-312-088-31	Sequence 31, Appl
37	1568.5	16.1	3690	12	US-10-112-944-347	Sequence 347, Appl
38	1566	16.1	3070	10	US-09-961-403-7	Sequence 7, Appl
39	1562.5	16.0	1174	15	US-10-603-725-22	Sequence 22, Appl
40	1562.5	16.0	3705	15	US-10-312-088-30	Sequence 30, Appl
41	1560.5	16.0	1186	15	US-10-603-725-18	Sequence 18, Appl
42	1558.5	16.0	1172	9	US-09-919-172-16	Sequence 16, Appl
43	1558.5	16.0	1172	9	US-09-974-298-56	Sequence 56, Appl
44	1552.5	15.9	1155	15	US-10-603-725-24	Sequence 24, Appl
45	1552.5	15.9	1167	15	US-10-603-725-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-09-873-676-113
; Sequence 113, Application US/09873676
; Patent No. US20020077289A1
; GENERAL INFORMATION:
; APPLICANT: MacDonald, Nicholas J.
; APPLICANT: Sim, Kim L.
; TITLE OF INVENTION: Angiostatin and Endostatin Binding Proteins and Methods of Use
; FILE REFERENCE: 05213-0378 (43170-259333)
; CURRENT APPLICATION NUMBER: US/09/873,676
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 60/209,065
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/289,387
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 113
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-873-676-113

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Sequence 6, Application US/09938275
; Patent No. US20020111309A1
; GENERAL INFORMATION:
; APPLICANT: Gerardo Castillo
; APPLICANT: Alan Snow
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications
; TITLE OF INVENTION: Of Laminin and Laminin-Derived Protein Fragments
; FILE REFERENCE: PROTEO.P03
; CURRENT APPLICATION NUMBER: US/09/938,275
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Swissprot P07942
; DATABASE ENTRY DATE: 1988-08-01
US-09-938-275-6

Query Match 100.0%; Score 9754; DB 9; Length 1786;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLLQLLAFSFLALCRARVRAQEPFESYGCABGSCYPATGDLIGRAQKLSVTSTCGLHK 60
Db 1 MGLLQLLAFSFLALCRARVRAQEPFESYGCABGSCYPATGDLIGRAQKLSVTSTCGLHK 60
QY 61 PEYCIVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVTTFAPNRLKIWWQSENGVEN 120
Db 61 PEYCIVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVTTFAPNRLKIWWQSENGVEN 120
QY 121 VTIQDLAEAEHFTHLINTFKTFRPAAMLIERSDDFGKTGWVRYFAYDCEASFPGISTG 180

Db 1201 LEKAKALKISGVIGPYRETVDVSVERKVSEIKDILAQSPAAPLKNIGNLFEEAEKLIKDV 1260
QY 1261 TEMMAQVEVKLSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDS 1320
Db 1261 TEMMAQVEVKLSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDS 1320
QY 1321 ITKYFQMSLEAEERVNASTTEPNSTVEQSALMEDRVEDVMMERESQFKEKEEQEARLLDE 1380
Db 1321 ITKYFQMSLEAEERVNASTTEPNSTVEQSALMEDRVEDVMMERESQFKEKEEQEARLLDE 1380
QY 1381 LAGKLSQSLDLSAAAEMTCGTPPGASCSETECGPNCRCTDEGERKCGGPGCGGLVTVAHNA 1440
Db 1381 LAGKLSQSLDLSAAAEMTCGTPPGASCSETECGPNCRCTDEGERKCGGPGCGGLVTVAHNA 1440
QY 1441 WQKAMDLDQDVLALAEVEQLSKMVSEAKLRADEAKQSAEDILLKTNATKEXMDKSNEEL 1500
Db 1441 WQKAMDLDQDVLALAEVEQLSKMVSEAKLRADEAKQSAEDILLKTNATKEXMDKSNEEL 1500
QY 1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKMEMPSPTPQQLQNLTEDIRERVESLSQVEVI 1560
Db 1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKMEMPSPTPQQLQNLTEDIRERVESLSQVEVI 1560
QY 1561 LQHSAADIAAEMLLEAKRASKSATDVKVTADMVKEALEEAEKAQVAAEKAIKQADEDI 1620
Db 1561 LQHSAADIAAEMLLEAKRASKSATDVKVTADMVKEALEEAEKAQVAAEKAIKQADEDI 1620
QY 1621 QGTQNLTSIESETAASEETLFNASQRISELERNVBELKRKAQNSGEAEYIEKVYVTVK 1680
Db 1621 QGTQNLTSIESETAASEETLFNASQRISELERNVBELKRKAQNSGEAEYIEKVYVTVK 1680
QY 1681 QSAEDVKKTLDGELDEKYKKVENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLL 1740
Db 1681 QSAEDVKKTLDGELDEKYKKVENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLL 1740
QY 1741 KDLEKVEDNQRYLEDKAQELARLEGEVRSLLKDISQKVAVYSTCL 1786
Db 1741 KDLEKVEDNQRYLEDKAQELARLEGEVRSLLKDISQKVAVYSTCL 1786

RESULT 3

US-10-037-182-6
; Sequence 6, Application US/10037182
; Publication No. US20030044899A1
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Doi, Masayuki
; APPLICANT: Thyboll, Jill
; TITLE OF INVENTION: Recombinant Laminin 10
; FILE REFERENCE: 99-274-F
; CURRENT APPLICATION NUMBER: US/10/037,182
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,449
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/279,282
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-037-182-6

Query Match : 100.0%; Score 9754; DB 14; Length 1786;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLLQLLAFSFLALCRARVRAQEPFESYGAEGSCYPATGDLIIGRAQKLSVTSTCGLHK 60
Db 1 MGLLQLLAFSFLALCRARVRAQEPFESYGAEGSCYPATGDLIIGRAQKLSVTSTCGLHK 60
QY 61 PEPYCIVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVVTTTFAPNRLKIWQSENGVEN 120

Db 121 VTIQDLLEAEFHTLIMTFKTRPAAMLIERSSDFGKTGWYRYPAYDCEASFPGISTG 180
QY 181 PMKKVDDIIICDSRYSDIEPSTEGEVI FRAIDPAFKIEDPSPRIQNLKITNLRIKFVKL 240
Db 181 PMKKVDDIIICDSRYSDIEPSTEGEVI FRAIDPAFKIEDPSPRIQNLKITNLRIKFVKL 240
QY 241 HTLGDNLLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGNEEVEGMVGHCMC 300
Db 241 HTLGDNLLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGNEEVEGMVGHCMC 300
QY 301 RHNTKGLNCELMDPFYHDL PWRPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGG 360
Db 301 RHNTKGLNCELMDPFYHDL PWRPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGG 360
QY 361 VDDDCQHNMTGRNCEQCKPFYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYDFSTG 420
Db 361 VDDDCQHNMTGRNCEQCKPFYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYDFSTG 420
QY 421 LIAGQCRCKLNVEGEHCDVCKEGFYDLSSDPFGCKSCACNPLGTIPGPNPCDSETGHY 480
Db 421 LIAGQCRCKLNVEGEHCDVCKEGFYDLSSDPFGCKSCACNPLGTIPGPNPCDSETGHY 480
QY 481 CKRLVTGQHCDCQLPEHWGLSNDLDGCRPCDCLGGALNNSCFAESGQCSRPHMIGRQC 540
Db 481 CKRLVTGQHCDCQLPEHWGLSNDLDGCRPCDCLGGALNNSCFAESGQCSRPHMIGRQC 540
QY 541 NEVEPGYYFATLDHYLYEAEANLPGVSI VERQYIQDRIPSWTGAGFVRVPEGAYLEFF 600
Db 541 NEVEPGYYFATLDHYLYEAEANLPGVSI VERQYIQDRIPSWTGAGFVRVPEGAYLEFF 600
QY 601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVORPGRIPTSSRCNGTIPDDNQVWSLSPG 660
Db 601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVORPGRIPTSSRCNGTIPDDNQVWSLSPG 660
QY 661 SRYVVLPRPVCFEKGTNYTVRLPQYTTSSDSVESPYTLIDSLVLMYPYCKSLDIFTVGG 720
Db 661 SRYVVLPRPVCFEKGTNYTVRLPQYTTSSDSVESPYTLIDSLVLMYPYCKSLDIFTVGG 720
QY 721 SGDGVVVNSAWETFORYRCLENSRSVVKTPMTDVCNRIIFSISALLHQTGLACECDPQGS 780
Db 721 SGDGVVVNSAWETFORYRCLENSRSVVKTPMTDVCNRIIFSISALLHQTGLACECDPQGS 780
QY 781 LSSVCDPNGGQCQCRPNVVGRTCNRCAPGTFGFGPSGCKPCECHLQGSVNAFCNPVTGQC 840
Db 781 LSSVCDPNGGQCQCRPNVVGRTCNRCAPGTFGFGPSGCKPCECHLQGSVNAFCNPVTGQC 840
QY 841 HCFQGVYARQCDCRLCPGHWGFPSQPCQCNHADDCTPVTGECLNCQDYTMHNCERCLA 900
Db 841 HCFQGVYARQCDCRLCPGHWGFPSQPCQCNHADDCTPVTGECLNCQDYTMHNCERCLA 900
QY 901 GYIGDPIIGSDHCRPCPCDPGDSGRQFARSCYQDPVTQLACVCDPFGYIGSRCDCCAS 960
Db 901 GYIGDPIIGSDHCRPCPCDPGDSGRQFARSCYQDPVTQLACVCDPFGYIGSRCDCCAS 960
QY 961 GYFGNPSEVGGSCQPCQCHNNIDTTDPEACDKETGRCLKCLYHTEGEHCQCFRFGYYGDA 1020
Db 961 GYFGNPSEVGGSCQPCQCHNNIDTTDPEACDKETGRCLKCLYHTEGEHCQCFRFGYYGDA 1020
QY 1021 LRQDCRKVCVNYLGTVQEHNGSDCCQCDKATGQCLCLPNVIGQNCDCRCAPNWTQLASGTG 1080
Db 1021 LRQDCRKVCVNYLGTVQEHNGSDCCQCDKATGQCLCLPNVIGQNCDCRCAPNWTQLASGTG 1080
QY 1081 CDPNCNAAHSFGPSCNEFTGQCQCMFPGFGRITCSECELFWDGDPDVECRACDCDPRGIE 1140
Db 1081 CDPNCNAAHSFGPSCNEFTGQCQCMFPGFGRITCSECELFWDGDPDVECRACDCDPRGIE 1140
QY 1141 TPQCDSGTQCVCVEGVEGPRCKCTRGYSVFPDCTPCHQCFCALWDVIIAELTNRTHRF 1200
Db 1141 TPQCDSGTQCVCVEGVEGPRCKCTRGYSVFPDCTPCHQCFCALWDVIIAELTNRTHRF 1200
QY 1201 LEKAKALKISGVIGPYRETVDVSVERKVSEIKDILAQSPAAPLKNIGNLFEEAEKLIKDV 1260

Db 61 PEPYCIVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVVTTFAPNRLKIWWQSENGVEN 120
QY 121 VTIQDLLEAEFHFTHLIMTFKTRPAAMLIERSSDFGKTGWVYRYFAYDCEASFPFGISTG 180
Db 121 VTIQDLLEAEFHFTHLIMTFKTRPAAMLIERSSDFGKTGWVYRYFAYDCEASFPFGISTG 180
QY 181 PMKKVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLLKITNLRIKFPVKL 240
Db 181 PMKKVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLLKITNLRIKFPVKL 240
QY 241 HTLGNLLDSRMEIREKYYYAVYDMVVRGNCFYGHASECAPVDGFNEEVEGMVHGHCMC 300
Db 241 HTLGNLLDSRMEIREKYYYAVYDMVVRGNCFYGHASECAPVDGFNEEVEGMVHGHCMC 300
QY 301 RHNTKGLNCEL CMDFYHDL PWRPAEGRNSNACKKNCNHSISCHFDMAVYLATGNVSGG 360
Db 301 RHNTKGLNCEL CMDFYHDL PWRPAEGRNSNACKKNCNHSISCHFDMAVYLATGNVSGG 360
QY 361 VCDCCOHNMTGRNCEQCKPFYIOHPERDIRDPNFCERCTCDPAGSQNEGICDSYDFSTG 420
Db 361 VCDCCOHNMTGRNCEQCKPFYIOHPERDIRDPNFCERCTCDPAGSQNEGICDSYDFSTG 420
QY 421 LIAGQCRCKLNVEGEHCDVCKEGFYDLSSDPFGCKSCACNPLGTIPGNGNPCDSETHCY 480
Db 421 LIAGQCRCKLNVEGEHCDVCKEGFYDLSSDPFGCKSCACNPLGTIPGNGNPCDSETHCY 480
QY 481 CKRLVTGQHCDQCLPEHWGLSNDLDGCRPCDCLGALNNSCPAESGCSCRPHMIGRQC 540
Db 481 CKRLVTGQHCDQCLPEHWGLSNDLDGCRPCDCLGALNNSCPAESGCSCRPHMIGRQC 540
QY 541 NEVEPGYYFATLDHYLYEAEANLPGVSIIVERQYIQDRIPSWTGAGFVRVPEGAYLEFF 600
Db 541 NEVEPGYYFATLDHYLYEAEANLPGVSIIVERQYIQDRIPSWTGAGFVRVPEGAYLEFF 600
QY 601 IDNIPYSMEVDILIRYEPOLPDHWEKAVITVQRPGRIPTSRSCGNTIPDDNQVVSLSPG 660
Db 601 IDNIPYSMEVDILIRYEPOLPDHWEKAVITVQRPGRIPTSRSCGNTIPDDNQVVSLSPG 660
QY 661 SRYVVLPRPVCFEKGTNYTVRLELPQYTSDDSDVESPYTLIDSLVLMPCYCKSLDIFTVGG 720
Db 661 SRYVVLPRPVCFEKGTNYTVRLELPQYTSDDSDVESPYTLIDSLVLMPCYCKSLDIFTVGG 720
QY 721 SGDGVTNSAWETFORYRCLENSRSVVKTPMTDVCRNIIIFSISALLHQTGLACECDPQS 780
Db 721 SGDGVTNSAWETFORYRCLENSRSVVKTPMTDVCRNIIIFSISALLHQTGLACECDPQS 780
QY 781 LSSVCDPNPGGQCCQCRPNVGRVTCNRCAFGTGFPGSGCKPCECHLQGSVNAFCNPVTGQC 840
Db 781 LSSVCDPNPGGQCCQCRPNVGRVTCNRCAFGTGFPGSGCKPCECHLQGSVNAFCNPVTGQC 840
QY 841 HCFQGVYARQCDRCLPGHWGFPSCQPCQNGHADDCTPVTGECNLCQDVTMGNRCERCLA 900
Db 841 HCFQGVYARQCDRCLPGHWGFPSCQPCQNGHADDCTPVTGECNLCQDVTMGNRCERCLA 900
QY 901 GYGDPIIGSGDHCRPCPCPDGPDSDGRQFARSCYQDPVTQLACVCDPFGYIGSRCDDCAS 960
Db 901 GYGDPIIGSGDHCRPCPCPDGPDSDGRQFARSCYQDPVTQLACVCDPFGYIGSRCDDCAS 960
QY 961 GYFGNPSVGGSCQPCQCHNNIDTTDPEACDKETGRCLKCLYHTEGEHCQFCRFGYYGDA 1020
Db 961 GYFGNPSVGGSCQPCQCHNNIDTTDPEACDKETGRCLKCLYHTEGEHCQFCRFGYYGDA 1020
QY 1021 LRQDCRKCVCNLYGVQEHCHNGSDCCQDKATGQCLCLPNVIGQNCDRCAPNTWQLASGTG 1080
Db 1021 LRQDCRKCVCNLYGVQEHCHNGSDCCQDKATGQCLCLPNVIGQNCDRCAPNTWQLASGTG 1080
QY 1081 CDPNCNAAHSFGPSCNEFTGQCQCMFGFGRTCTSECQELFWGDPDVECRACDCDPRGIE 1140
Db 1081 CDPNCNAAHSFGPSCNEFTGQCQCMFGFGRTCTSECQELFWGDPDVECRACDCDPRGIE 1140
QY 1141 TPQCDQSTGQCVCEGVGPRCDKCTRGYSGVFPDCTPCHQCQFALWDVIAELTNRTHRE 1200
Db 1141 TPQCDQSTGQCVCEGVGPRCDKCTRGYSGVFPDCTPCHQCQFALWDVIAELTNRTHRE 1200

QY 1201 LEKAKALKISGVI GPYRETVDSEVERKVSEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDV 1260
Db 1201 LEKAKALKISGVI GPYRETVDSEVERKVSEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDV 1260
QY 1261 TENMAQVEVKLSDDTTSSQNSSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDS 1320
Db 1261 TENMAQVEVKLSDDTTSSQNSSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDS 1320
QY 1321 ITKYFQMSLEAEERNVASTTEPNSTVEQSALMRDRVEDVMNERESQFKEKEQEEQARLLDE 1380
Db 1321 ITKYFQMSLEAEERNVASTTEPNSTVEQSALMRDRVEDVMNERESQFKEKEQEEQARLLDE 1380
QY 1381 LAGKLSLDLSAAAEAMTCGTPPGASCSETCGGPNCRITDEGERKCGGPGCGGLVTVAHNA 1440
Db 1381 LAGKLSLDLSAAAEAMTCGTPPGASCSETCGGPNCRITDEGERKCGGPGCGGLVTVAHNA 1440
QY 1441 WQKAMDLDQDVL SALAEVEQLSKMVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNEEL 1500
Db 1441 WQKAMDLDQDVL SALAEVEQLSKMVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNEEL 1500
QY 1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKMPSTPQQLQNLTEDIRERVESLSQVEVI 1560
Db 1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKMPSTPQQLQNLTEDIRERVESLSQVEVI 1560
QY 1561 LQHSAAADIARAEMLLEEAKRASKSATDVKVTADMVKEALEEAEKAQVAEKAIKQADEDI 1620
Db 1561 LQHSAAADIARAEMLLEEAKRASKSATDVKVTADMVKEALEEAEKAQVAEKAIKQADEDI 1620
QY 1621 QGTQNLTSIESETAASEETLFNASQRISELERNVVEELKRAAQNSEAEYIEKVVTYVK 1680
Db 1621 QGTQNLTSIESETAASEETLFNASQRISELERNVVEELKRAAQNSEAEYIEKVVTYVK 1680
QY 1681 QSAEDVKKTLDGELDEKYYKVENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLL 1740
Db 1681 QSAEDVKKTLDGELDEKYYKVENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLL 1740
QY 1741 KDLERKYEDNQRYLEDKAQELARLEGEVRSLKDISQKAVYSTCL 1786
Db 1741 KDLERKYEDNQRYLEDKAQELARLEGEVRSLKDISQKAVYSTCL 1786

RESULT 4

US-10-037-182-8
; Sequence 8, Application US/10037182
; Publication No. US20030044899A1
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Doi, Masayuki
; APPLICANT: Thyboll, Jill
; TITLE OF INVENTION: Recombinant Laminin 10
; FILE REFERENCE: 99-274-F
; CURRENT APPLICATION NUMBER: US/10/037,182
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,449
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/279,282
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 8
; LENGTH: 1765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-037-182-8

Query Match 99.0%; Score 9654; DB 14; Length 1765;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 QEPFESYGCAGSCYPATGDL LIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICNS 81
Db 1 QEPFESYGCAGSCYPATGDL LIGRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICNS 60

QY 82 QDPYHETLNPDShLIENVTTFAPNRLKIWQSENGVENVTIQLDLEAFHFTHLIMTFK 141
Db
QY 142 TFRPAAMLIERSSSDFGKTGWVYRYFAYDCEASFGISTGPMKKVDDIICDSRYSYDIEPST 201
Db 121 TFRPAAMLIERSSSDFGKTGWVYRYFAYDCEASFGISTGPMKKVDDIICDSRYSYDIEPST 180
QY 202 EGEVIFRALDPAFKIEDPSPRIQNLKLTNLRKFVKLHTLGLNLLDSRMEIREKYYA 261
Db 181 EGEVIFRALDPAFKIEDPSPRIQNLKLTNLRKFVKLHTLGLNLLDSRMEIREKYYA 240
QY 262 VYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGCMCRHNTKGLNCELMDFYHDLWP 321
Db 241 VYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGCMCRHNTKGLNCELMDFYHDLWP 300
QY 322 RPAEGRNSNACKKCNCHNEHSISCHFDMAVYLATGNVSGGVCDCCQHNTMGENCEQCKPFY 381
Db 301 RPAEGRNSNACKKCNCHNEHSISCHFDMAVYLATGNVSGGVCDCCQHNTMGENCEQCKPFY 360
QY 382 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSTGLIAGQCRCKLNVGEHCHDVCK 441
Db 361 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSTGLIAGQCRCKLNVGEHCHDVCK 420
QY 442 EGFYDLSSDDPFGCKSKACNPLGTIPGGNPNCDSETGHCYCKRLVTGQHCDCQCLPEHWGLS 501
Db 421 EGFYDLSSDDPFGCKSKACNPLGTIPGGNPNCDSETGHCYCKRLVTGQHCDCQCLPEHWGLS 480
QY 502 NDLGCRPCDCDLGALNNSCPAESGQCSCRPHMIGRCQNEVEPGYYFATLDHYLYEAE 561
Db 481 NDLGCRPCDCDLGALNNSCPAESGQCSCRPHMIGRCQNEVEPGYYFATLDHYLYEAE 540
QY 562 ANLGPVSIVERQYIQDRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 621
Db 541 ANLGPVSIVERQYIQDRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 600
QY 622 DHWEKAVITVQRPGRIPRTSSRCGNTIPDDNQVWSLSPGSRYVWLP RPVPCFEKGTNYTVR 681
Db 601 DHWEKAVITVQRPGRIPRTSSRCGNTIPDDNQVWSLSPGSRYVWLP RPVPCFEKGTNYTVR 660
QY 682 LELPQYTSDDSDVESPYTLIDSLVLMPCYCKSLDIFTVGSQDGVWNTNSAWETQRYRCLE 741
Db 661 LELPQYTSDDSDVESPYTLIDSLVLMPCYCKSLDIFTVGSQDGVWNTNSAWETQRYRCLE 720
QY 742 NSRSVVKTPMTDVCNRIIFSISALLHOTGLACECDPQGSLSVCDPNNGGQCQCRPNVVG 801
Db 721 NSRSVVKTPMTDVCNRIIFSISALLHOTGLACECDPQGSLSVCDPNNGGQCQCRPNVVG 780
QY 802 TCNRCAPGTFGFGPSGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDCRLPGHWGF 861
Db 781 TCNRCAPGTFGFGPSGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDCRLPGHWGF 840
QY 862 PSCQPCQCNHADDCCDPVTGECNLCQDYTMGHNCERCLAGYGDPIIGSGDHCHPCPCPD 921
Db 841 PSCQPCQCNHADDCCDPVTGECNLCQDYTMGHNCERCLAGYGDPIIGSGDHCHPCPCPD 900
QY 922 GPDSGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCAGYFGNPNSEVGGSCQPCQCHNN 981
Db 901 GPDSGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCAGYFGNPNSEVGGSCQPCQCHNN 960
QY 982 IDTTDPEACDKETGRCLKLYHTEGHCQCFRFGYYGDALRQDCRCKVCNLYLGTVEHCN 1041
Db 961 IDTTDPEACDKETGRCLKLYHTEGHCQCFRFGYYGDALRQDCRCKVCNLYLGTVEHCN 1020
QY 1042 GSDCQCDKATGQCLCLPNVIGQNCRCAPNTWQLASGTGCDPCNCAHSGFSPSCNEFTG 1101
Db 1021 GSDCQCDKATGQCLCLPNVIGQNCRCAPNTWQLASGTGCDPCNCAHSGFSPSCNEFTG 1080
QY 1102 QCQCMPPGGRGTCSECOELFWGDPDVECRACDCDPRGIETPQCDQSTGQCVCVEGEGPR 1161
Db 1081 QCQCMPPGGRGTCSECOELFWGDPDVECRACDCDPRGIETPQCDQSTGQCVCVEGEGPR 1140

QY 1162 CDKTRGYSGVFPDCTPCHQCFALWDVIIAELTNRTHRFLEKAKALKISGVIGPYRETVD 1221
Db 1141 CDKTRGYSGVFPDCTPCHQCFALWDVIIAELTNRTHRFLEKAKALKISGVIGPYRETVD 1200
QY 1222 SVERKVSEIKDILAQSPAAPLKNIGNLFEEAEKLIKDVTEMMAQVEVKLSDTTSQSNST 1281
Db 1201 SVERKVSEIKDILAQSPAAPLKNIGNLFEEAEKLIKDVTEMMAQVEVKLSDTTSQSNST 1260
QY 1282 AKELDSLQTEAESLDNTVKELAEQLEFIKNDSIRGALDSITKYFQMSLEAEERVNASTTE 1341
Db 1261 AKELDSLQTEAESLDNTVKELAEQLEFIKNDSIRGALDSITKYFQMSLEAEERVNASTTE 1320
QY 1342 PNSTVEQSALMRDRVEDVMERESQFKEQEAEQARLJLDELAKLQSLDLSAAAEWTCGTP 1401
Db 1321 PNSTVEQSALMRDRVEDVMERESQFKEQEAEQARLJLDELAKLQSLDLSAAAEWTCGTP 1380
QY 1402 PGASCSETECGGPNCRITDEGERKCGGPGCGGLVTVVAHNWQKAMDLDQDVLSALAEVEQL 1461
Db 1381 PGASCSETECGGPNCRITDEGERKCGGPGCGGLVTVVAHNWQKAMDLDQDVLSALAEVEQL 1440
QY 1462 SKMVSEAKLRADAEAKQSAEDILLKTNATKEKMDKSNELRNLIKQIRNFLTQDSADLDSI 1521
Db 1441 SKMVSEAKLRADAEAKQSAEDILLKTNATKEKMDKSNELRNLIKQIRNFLTQDSADLDSI 1500
QY 1522 EAVANEVLKMEMPSTPQQLQNLTEDIRERVESLSQVEVILQHSAAADIARAEMLLLEAKRA 1581
Db 1501 EAVANEVLKMEMPSTPQQLQNLTEDIRERVESLSQVEVILQHSAAADIARAEMLLLEAKRA 1560
QY 1582 SKSATDVKVTADVMKEALEEAEKQAAVAAEKAQADEDIQGTQNLTSIESEIAASEETL 1641
Db 1561 SKSATDVKVTADVMKEALEEAEKQAAVAAEKAQADEDIQGTQNLTSIESEIAASEETL 1620
QY 1642 FNASORISELERNVEELKRAAQNSEAEYIEKVVTVKQSAEDVKTLDGELDEKYYKV 1701
Db 1621 FNASORISELERNVEELKRAAQNSEAEYIEKVVTVKQSAEDVKTLDGELDEKYYKV 1680
QY 1702 ENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLLKDLERKYNQRYLEDKQAE 1761
Db 1681 ENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLLKDLERKYNQRYLEDKQAE 1740
QY 1762 ARLEGEVRSLLKDISQKAVYSTCL 1786
Db 1741 ARLEGEVRSLLKDISQKAVYSTCL 1765

RESULT 5

US-09-938-275-7

; Sequence 7, Application US/09938275

; Patent No. US20020111309A1

; GENERAL INFORMATION:

; APPLICANT: Gerardo Castillo

; APPLICANT: Alan Snow

; TITLE OF INVENTION: Therapeutic and Diagnostic Applications

; FILE REFERENCE: PROTEO.P03

; CURRENT APPLICATION NUMBER: US/09/938,275

; CURRENT FILING DATE: 2001-08-16

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 7

; LENGTH: 1786

; TYPE: PRT

; ORGANISM: Mus Musculus

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: Swissprot P02469

; DATABASE ENTRY DATE: 1989-07-01

US-09-938-275-7

Query Match

93.7%; Score 9144; DB 9; Length 1786;

Best Local Similarity 92.7%; Pred. No. 0;

Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;

QY 1 MGLLQLLAFSFLALCRARVRAQEPFESYGAEGSCYPATGDLILIGRAQKLSVTSTCGLHK 60

Db 1 MGLLQVFAFGLALMGTRVCAQEPESYGAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60
QY 61 PEPYCIIVSHLOEDKKCFICNSQDPYHETLNPDSHLIENVVTFAPNRLKIMWQSENGVEN 120
Db 61 PEPYCIIVSHLOEDKKCFICDSRDPYHETLNPDSHLIENVVTFAPNRLKIMWQSENGVEN 120
QY 121 VTIQDLLEAEFHTLIMTFTFRPAAMLIERSDDFGKTGWVYRFAYDCEASFPGISTG 180
Db 121 VTIQDLLEAEFHTLIMTFTFRPAAMLIERSDDFGKTGWVYRFAYDCESSFPGISTG 180
QY 181 PMKKVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPIQNLLKITNLRIFVKL 240
Db 181 PMKKVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPIQNLLKITNLRIFVKL 240
QY 241 HTLGDNLLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGCMC 300
Db 241 HTLGDNLLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMC 300
QY 301 RHNTKGLNCELMDFYHDLPRWPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGG 360
Db 301 RHNTKGLNCELMDFYHDLPRWPAEGRNSNACKKNCNEHSSSCHFDMAVFLATGNVSGG 360
QY 361 VDDCQHNTMGENCEQCKPFYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSG 420
Db 361 VCDNCQHNTMGRNCEQCKPFYQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVG 420
QY 421 LIAGQCRCKLNVEGEHCDVCKEGFYDLSEDDPFGCKSCACNPLGTIPGPNPCDSETGHY 480
Db 421 LIAGQCRCKLHVEGERCDVCKEGFYDLSEDDPFGCKSCACNPLGTIPGPNPCDSETGYCY 480
QY 481 CKRLVTGQHCDQCLPEHWGLSNDLDGCRPCDCLDGGALNNSCFABSGQCSRPHMIGRQC 540
Db 481 CKRLVTGQRCDQCLPQHGLSNDLDGCRPCDCLDGGALNNSCSEDSGQCSCLPHMIGRQC 540
QY 541 NEVEPGYYFATLDHYLYEAEANLGPVSVIVERQYIQDRIPSWTQAGFVRVPEGAYLEFF 600
Db 541 NEVESGYFTTLDHYLYEAEANLGPVVVVERQYIQDRIPSWTQAGFVRVPEGAYLEFF 600
QY 601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPRTSSRCNGTIPDDDNQVVSLSPG 660
Db 601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPASSRCNGTVPDDDNQVVSLSPG 660
QY 661 SRYVVLPRPVCFEKGTNYTVRLELPQYTSSDSVSPYTLIDSLVLMYPYCKSLDIFTVGG 720
Db 661 SRYVVLPRPVCFEKGMVTVRLELPQYTASGSVSPYTFIDSLVLMYPYCKSLDIFTVGG 720
QY 721 SGDGVVNTSAWETFQRYVCLNSRSVVKTPMTDVCNRIIFSISALHQTGLACECDPQGS 780
Db 721 SGDGEVNTSAWETFQRYVCLNSRSVVKTPMTDVCNRIIFSISALIHQTGLACECDPQGS 780
QY 781 LSSVCDPNGGQCQCRPNVVGRTCNRCAPGTFGFPGSGCKPCCECHLOGSVNAFCNPVTGQC 840
Db 781 LSSVCDPNGGQCQCRPNVVGRTCNRCAPGTFGFPGSGCKPCDCHLQGSASAFCDAITGQC 840
QY 841 HCFQGYVARQCDRCLPGHWGFPSCQPCQCNHADDCTPVTGECNCDYTMGHNCERCLA 900
Db 841 HCFQGIYARQCDRCLPGYWGFPSCQPCQCNHGLDCTVTGECNCDYTMGHNCERCLA 900
QY 901 GYGDPIIGSDHCRPCPCPDGPDGSGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCAS 960
Db 901 GYGDPIIGSDHCRPCPCPDGPDGSGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCAS 960
QY 961 GYFNPSEVGGSCQPCQCHNNIDTTDPEACDKETGRCLKCLYHTEGEHCQCFRFGYYGDA 1020
Db 961 GFFGNPSEVGGSCQPCQCHNNIDTTDPEACDKETGRCLKCLYHTEGEHCQCFRFGYYGDA 1020
QY 1021 LRQDCRKCVCNLYGTVOEHNGSDCQCDKATGQCLCLPNVIGQNCDCRCAFNWQLASGTG 1080
Db 1021 LRQDCRKCVCNLYGTVKEHNGSDCHCDKATGQCSCLPNVIGQNCDCRCAFNWQLASGTG 1080
QY 1081 CDPNCNAAHSFGPSCNEFTGQCQCMFPGGRTCTSECQELFWGDPDVECRACDCDPRGIE 1140

Db 1081 CGPCNCAHSGPSCNEFTGQCQCMFPGGRTCTSECQELFWGDPDVECRACDCDPRGIE 1140
QY 1141 TPOCDQSTGQCVCEGVEGPRCDKCTRGYSVGFPPDCTPCHQCFALWDVIIAELTNRTHRF 1200
Db 1141 TPOCDQSTGQCVCEGVEGPRCDKCTRGYSVGFPPDCTPCHQCFALWDIIIGELTNRTHKF 1200
QY 1201 LEKAKALKISGIVGIPYRETVDVSVERKVSEIKDILAQSPAAPLKNIGNLFEEAEKLIKDV 1260
Db 1201 LEKAKALKISGIVGIPYRETVDVSVEKKYNEIKDILAQSPAAPLKNIGNLFEEAEKLIKDV 1260
QY 1261 TEMMAQVEVKLSDDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIQALDS 1320
Db 1261 TEKMAQVEVKLTDTSQSNSTAGELGALQAEAESLDKTVKELAEQLEFIKNSDIQALDS 1320
QY 1321 ITKYFQMSLEAEERVNASTTEPNSTVQSALMRDRVEDVMMERESQFKEQEQAARLLDE 1380
Db 1321 ITKYFQMSLEAEERVNASTTEPNSTVQSALMRDRVEDVMMERESQFKEQEQAARLLDE 1380
QY 1381 LAGKLSLDLSAAAEEMTCGTPPGASCSETECGGPNCRCTDEGERKCGGPGCGGLVTVAHNA 1440
Db 1381 LAGKLSLDLSAAAEEMTCGTPPGADCSECECGGPNCRCTDEGERKCGGPGCGGLVTVAHNA 1440
QY 1441 WQKAMDLDQDVLALAEVEQLSKMWSEAKLRADAEAKQSAEDILLKTNATKEKMDKSNEEL 1500
Db 1441 WQKAMDLDQDVLALAEVEQLSKMWSEAKLRADAEAKQSAEDILLKTNATKEKMDKSNEEL 1500
QY 1501 RNLKIQIRNFLTQDSADLDSIEAVANEVLKVMEMPSTPQOLQNLTEDIRERVESLSQVEVI 1560
Db 1501 RNLKIQIRNFLTQDSADLDSIEAVANEVLKVMEMPSTPQOLQNLTEDIRERVESLSQVEVI 1560
QY 1561 LQHSAAADIARAEMLEAEAKRASKSATDVKVTADVMKEALEEAEAKQVAAEKAIKQADEDI 1620
Db 1561 LQHSAAADIARAEMLEAEAKRASKSATDVKVTADVMKEALEEAEAKQVAAEKAIKQADEDI 1620
QY 1621 QGTQNLTLTSIESETAASEETLNFNASQRISELERNVVEELKRKAQNSGEAEYIEKVYVTVK 1680
Db 1621 QGTQNLTLTSIESETAASEETLNFNASQRISELERNVVEELKRKAQNSGEAEYIEKVYVTVK 1680
QY 1681 QSAEDVKKTLTGDELDEKYYKKVENLIKKTESADARRKAEMLQNEAKTLAQANSKIQLL 1740
Db 1681 QNADDVKKTLTGDELDEKYYKKVENLIKKTESADARRKAEMLQNEAKTLAQANSKIQLL 1740
QY 1741 KDLERKYNQRYLEDKAQELARLEGEVRSLLKDISOQVAVYSTCL 1786
Db 1741 EDLERKYNQRYLEDKAQELARLEGEVRSLLKDISOQVAVYSTCL 1786

RESULT 6
US-10-037-182-10
; Sequence 10, Application US/10037182
; Publication No. US20030044899A1
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Doi, Masayuki
; APPLICANT: Thyboli, Jill
; TITLE OF INVENTION: Recombinant Laminin 10
; FILE REFERENCE: 99-274-F
; CURRENT APPLICATION NUMBER: US/10/037,182
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,449
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/279,282
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-037-182-10

Query Match 93.7%; Score 9144; DB 14; Length 1786;
Best Local Similarity 92.7%; Pred. No. 0;

Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;				
QY	1	MGLQLLAFSLALCRARVRAQEPFESYCAEGSCYATGDDLIGRAQKLSVTSTCGLHK	60	
Db	1	MGLQVFAFGVLALWGTVCAGQEPFESYCAEGSCYATGDDLIGRAQKLSVTSTCGLHK	60	
QY	61	PEPYCIVSHLQEDKKCFICNSQDPYHETLNPDSLHNIENVVTFAPNRLKIWQSENGVEN	120	
Db	61	PEPYCIVSHLQEDKKCFICDSRDPYHETLNPDSLHNIENVVTFAPNRLKIWQSENGVEN	120	
QY	121	VTIQDLLEAEFHFTHLIMTFKTRPAAMLIERSSDFGKTGWVRYRFAYDCEASFPGISTG	180	
Db	121	VTIQDLLEAEFHFTHLIMTFKTRPAAMLIERSSDFGKTGWVRYRFAYDCESSFPGISTG	180	
QY	181	PMKKVDDIICDSRYSIDIEPSTEGEVIFRALDPAFKIEDPYSPRIQNLLKITNLRKIFVKL	240	
Db	181	PMKKVDDIICDSRYSIDIEPSTEGEVIFRALDPAFKIEDPYSPRIQNLLKITNLRKIFVKL	240	
QY	241	HTLGDNLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGCMC	300	
Db	241	HTLGDNLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMC	300	
QY	301	RHNTKGLNCELMDFYHDLWPRAEGRNSNACKKCNNEHSISCHFDMAVYLATGNVSGG	360	
Db	301	RHNTKGLNCELMDFYHDLWPRAEGRNSNACKKCNNEHSSSHCHDFMAVFLATGNVSGG	360	
QY	361	VCDDCOHNTMGNCEQCKPFYQYHPRDIRDPNFCERCTCDPAGSQNEGICDSYTFSTG	420	
Db	361	VCDNCOHNTMGNCEQCKPFYQYHPRDIRDPNLCERCTCDPAGSENGGICDGYTDFSVG	420	
QY	421	LIAGQCRCKLVGEGERCDVCKEGFYDLSSDDPFPGCKSCACNPLGTIPGNGPCDSETHCY	480	
Db	421	LIAGQCRCKLVGEGERCDVCKEGFYDLSEAEDPYGCKSCACNPLGTIPGNGPCDSETHCY	480	
QY	481	CKRLVTGQHCDOCLPEHWGLSNDLDGCRPCDCLGGALNNSCPAESGQCSCRPHMIGRQC	540	
Db	481	CKRLVTGQRCDOCLPQHWSLNDLDGCRPCDCLGGALNNSCSHSDSGCSCLPHMIGRQC	540	
QY	541	NEVEPGYYFATLDHYLYEAEANLPGVYSIVERQYIQDRIPSWTGAQFVRVPEGAYLEFF	600	
Db	541	NEVESGYFFTLDDHYLYEAEANLPGVVVVERQYIQDRIPSWTGPFGVRVPEGAYLEFF	600	
QY	601	IDNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPRIPTSSRCNGTIPDDNQVVSLSPG	660	
Db	601	IDNIPYSMEYEILIRYEPQLPDHWEKAVITVQRPKIPASSRCNGTVPDDNQVVSLSPG	660	
QY	661	SRYVVLPRPVCBEKGTNYTVRLELPQYTSDDSDVESPYTLIDSLVLPYCKSLDIFTVGG	720	
Db	661	SRYVVLPRPVCBEKGMNYTVRLELPQYTAGSDSDVESPYTFIDSLVLPYCKSLDIFTVGG	720	
QY	721	SGDGVVTNSAWETFORYRCLENSRSVVKTPMTDVCNRIIFSISALLHOTGLACECDPQGS	780	
Db	721	SGDGEVTNSAWETFORYRCLENSRSVVKTPMTDVCNRIIFSISALIHOTGLACECDPQGS	780	
QY	781	LSSVCDPNGGQCQCRPNVVGRTCNRCAPGTGFGPGSGCKPCBCHLOGSVNAFCNPVTGQC	840	
Db	781	LSSVCDPNGGQCQCRPNVVGRTCNRCAPGTGFGPGNGCKPCDCHLQGSASAFCDAITGQC	840	
QY	841	HCFAQGYARQCDRLPGHWGFPSCQPCQCNHADDCTPVTGECNCDYTMGHNCERCLA	900	
Db	841	HCFAQGIYARQCDRLPGYWGFPSCQPCQCNHADDCTVTGECSCQDYTTGHNCERCLA	900	
QY	901	GYGDPPIIGSDHCRPCPCPDGPDGSGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCAS	960	
Db	901	GYGDPPIIGSDHCRPCPCPDGPDGSGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCAS	960	
QY	961	GYFGNPSVGGSCQPCQCHNIDTTDPEACDKETGRCLKCLYHTEGHCHQCFRFGYYGDA	1020	
Db	961	GFFGNPSDFGSCQPCQCHNIDTTDPEACDKDTGRCLKCLYHTEGHCHQCLCYGYYYGDA	1020	
QY	1021	LRQDCRKVCNYLGTVOEHCHNGSDCQCCKATGQCLCLPNVIGONCDRCAPNTWQLASGTG	1080	
Db	1021	LRQDCRKVCNYLGTVKEHCHNGSDCHCDKATGQCSCLPNVIGONCDRCAPNTWQLASGTG	1080	

QY	1081	CDPCNCNAAHSFGPSCNEFTGQCQCMPPGFGGRTCTSECQBLFWGDPDVECRACDCDPRGIE	1140	
Db	1081	CGPCNCNAAHSFGPSCNEFTGQCQCMPPGFGGRTCTSECQELFWGDPDVECRACDCDPRGIE	1140	
QY	1141	TPQCDQSTGQCVCVEGVEGPRCDKCTRGYSYGVFPDCTPCHQCFALWDVIIAELTNRTHRF	1200	
Db	1141	TPQCDQSTGQCVCVEGVEGPRCDKCTRGYSYGVFPDCTPCHQCFALWDIIIGELTNRTHKF	1200	
QY	1201	LEKAKALKISGVIGPYRETVDVSVERKVSEIKDILAQSPAAPLKNIGNLFEEAEKLIKDV	1260	
Db	1201	LEKAKALKISGVIGPYRETVDVSVEKKVNEIKDILAQSPAAPLKNIGILFEEAEKLTADV	1260	
QY	1261	TEMMAQVEVKLSDDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDS	1320	
Db	1261	TEKMAQVEVKLTDTASQSNSTAGELGALQAEASLDKTVKELAEQLEFIKNSDIQALDS	1320	
QY	1321	ITKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVMMERESQFKEQEEQARLLDE	1380	
Db	1321	ITKYFQMSLEAEKRVNASTTDPNSIVEQSALTRDRVEDMLERESPFEQEEQARLLDE	1380	
QY	1381	LAGKLSLDLSAAAEMTCGTPPGASCSETECGGPNCRITDEGERKCGPGCGGLVTVAHNA	1440	
Db	1381	LAGKLSLDLSAAAQMTCTGTPPGADCSSECGGPNCRITDEGEKKCGPGCGGLVTVAHSA	1440	
QY	1441	WQKAMDLDQVLSALAEVEQLSKMVSEAKLRADAEAKQSAEDILLKTNATKEKMDKSNEEL	1500	
Db	1441	WQKAMDFDRDVLALAEVEQLSKMVSEAKVRADAEAKQADVLLKTNATKEKVDKSNEDL	1500	
QY	1501	RNLIKQIRNFLTQDSADLDSIEAVANEVLKMEMPSTPQQLQNLTEDIRERVESLSQVEVI	1560	
Db	1501	RNLIKQIRNFLTQDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVI	1560	
QY	1561	LQHSAAADIARAEMLLEAEAKRASKSATDVKVTADMVKEALEEAEAKQVAAEKAIKQADEI	1620	
Db	1561	LQOSAADIARAELLLEAEAKRASKSATDVKVTADMVKEALEEAEAKQVAAEKAIKQADEI	1620	
QY	1621	QGTQNLITSIESETAASEETLFNASQRISELERNVVEELKRKAQNSGEAEYIEKVYTVK	1680	
Db	1621	QGTQNLITSIESETAASEETLTNASQRISELERNVVEELKRKAQNSGEAEYIEKVYSVK	1680	
QY	1681	QSAEDVKKTLDGELDEKYKKVENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLL	1740	
Db	1681	QNAEDVKKTLDGELDEKYKKVESLIAQKTESADARRKAELLQNEAKTLLAQANSKLQLL	1740	
QY	1741	KDLERKYEDNQRYLEDKAQELARLEGEVRSLLKDISQKAVYSTCL	1786	
Db	1741	EDLERKYEDNQRYLEDKAQELVRLEGEVRSLLKDISQKAVYSTCL	1786	

RESULT 7
US-10-037-182-12
; Sequence 12, Application US/10037182
; Publication No. US20030044899A1
; GENERAL INFORMATION:
; APPLICANT: Tryggsavon, Karl
; APPLICANT: Doi, Masayuki
; APPLICANT: Thyboll, Jill
; TITLE OF INVENTION: Recombinant Laminin 10
; FILE REFERENCE: 99-274-F
; CURRENT APPLICATION NUMBER: US/10/037,182
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,449
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/279,282
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1725
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-037-182-12

Query Match		91.0%;	Score 8873;	DB 14;	Length 1725;
Best Local Similarity		92.9%;	Pred. No. 0;		
Matches 1602;		Conservative 71;	Mismatches 52;	Indels 0;	Gaps 0;
QY	62	EPYCIIVSHLQEDKCFICNSQDPYHETLNPDSHLIENVVTFAPNRLKIWWQSENGVENV	121		
Db	1	EPYCIIVSHLQEDKCFICDSRDPYHETLNPDSHLIENVVTFAPNRLKIWWQSENGVENV	60		
QY	122	TIQLDLEAEFHFTHLIMTFKTERPAAMLIERSSDFGKTGWVYRYPAYDCEASFPGISTGP	181		
Db	61	TIQLDLEAEFHFTHLIMTFKTERPAAMLIERSSDFGKTGWVYRYPAYDCEASFPGISTGP	120		
QY	182	MKKVDDIIICDSRYSDIEPSTEGEVIFRALDPAPKIEDPYPSPRIQNLLKITNLRKIFVKLH	241		
Db	121	MKKVDDIIICDSRYSDIEPSTEGEVIFRALDPAPKIEDPYPSPRIQNLLKITNLRKIFVKLH	180		
QY	242	TLGDNLLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGHCRCR	301		
Db	181	TLGDNLLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGVNBEVEGMVHGHCRCR	240		
QY	302	HNTKGLNCELMDFYHDLPRWPAEGRNSNACKKNCNEHSISCHPDMVAVYLATGNVSGGV	361		
Db	241	HNTKGLNCELMDFYHDLPRWPAEGRNSNACKKNCNEHSSSCHFDMVAVFLATGNVSGGV	300		
QY	362	CDDCQHTMGRNCEQCKPFYQHPERDIRDNFCERCTCDPAGSQNEGICDSYTFSTGL	421		
Db	301	CDNCQHTMGRNCEQCKPFYQHPERDIRDNFCERCTCDPAGSENGGICDGYTDFSVGL	360		
QY	422	IAGQCRKLNVEGEHCDVCKEGFYDLSSDPFGCKSCACNPLGTIPGPNPCDSETGHCYC	481		
Db	361	IAGQCRKLNVEGERCDVCKEGFYDLSSDPFGCKSCACNPLGTIPGPNPCDSETGHCYC	420		
QY	482	KRLVTGQHCDCQLPEHNGLSNDLDGCRPCDCLGALNNSCFAESGQSCSRPHMIGRQCN	541		
Db	421	KRLVTGQRCDCQLPQHNGLSNDLDGCRPCDCLGALNNSCSEDSGQSCSLPHMIGRQCN	480		
QY	542	EVEPGYFATLDHYLYEAEANLPGVSIYERQYIQDRIPSWTGAGFVRVPEGAYLEFFI	601		
Db	481	EVEPGYFTTLDHYLYEAEANLPGVSVVVERQYIQDRIPSWTGAGFVRVPEGAYLEFFI	540		
QY	602	DNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPTSRCNGTIPDDNQWVSLSPGS	661		
Db	541	DNIPYSMEYEILIRYEPQLPDHWEKAVITVQRPGRIPASSRCNGTVPDDNQWVSLSPGS	600		
QY	662	RYVVLPRPVCFEKGTNYTVLELPOYTSSDSVESPFTLIDSLVLMPCYKSLDIFTVGS	721		
Db	601	RYVVLPRPVCFEKGMNYTVLELPOYTASGDSVESYTFIDSLVLMPCYKSLDIFTVGS	660		
QY	722	GDGVVNSAWETFORYRCLENSRSVVKTPMTDVCNRIIFSISALLHQTGLACECDPQGS	781		
Db	661	GDGEVNSAWETFORYRCLENSRSVVKTPMTDVCNRIIFSISALIHQTGLACECDPQGS	720		
QY	782	SSVCDPNGGQCQCRPNVGRICNRCAPGTFGFGPSGCKPCCECHLQGSVNAFCNPVTGQCH	841		
Db	721	SSVCDPNGGQCQCRPNVGRICNRCAPGTFGFGPNCGKPCDCHLQGSASAFCDAITGQCH	780		
QY	842	CFQGVYARQCDRCLPGHWGFPSCQPCQCNGHADDCTPVTGECLNCQDYTMHNCERCLAG	901		
Db	781	CFQGIYARQCDRCLPGYWGFPSPCQPCQCNGHALDCDVTYGECLSCQDYTTGHNCERCLAG	840		
QY	902	YFGDPIIGSGDHCRPCPCPDGSDGRQFARSCYQDPVTQLACVCDPGYIGSRCDCCASG	961		
Db	841	YFGDPIIGSGDHCRPCPCPDGSDGRQFARSCYQDPVTQLACVCDPGYIGSRCDCCASG	900		
QY	962	YFGNPSVGGSCQPCQCHNIDTTPDPEACDKETGRCLKLYHTEGEHCQFCFGYGDAL	1021		
Db	901	FFGNPSDFGSCQPCQCHNIDTTPDPEACDKTGRCLKLYHTEGDHQCQLCQYGYGDAL	960		
QY	1022	RQDCRKVCVNYLGTVOEHGNSGDCQCDKATGQCLCLPNVIGQNCDCRCPNTWQLASGTGC	1081		
Db	961	RQDCRKVCVNYLGTVKEHNSGSDCHDKATGQCSCLPNVIGQNCDCRCPNTWQLASGTGC	1020		

QY	1082	DPCNCNAAHSFGPSCNEFTGQCQCMPGFGGRTCECQELFWGDDVECRACDCDPRGIET	1141
Db	1021	GPCNCNAAHSFGPSCNEFTGQCQCMPGFGGRTCECQELFWGDDVECRACDCDPRGIET	1080
QY	1142	PQCDQSTGQCVCVEGVGPRCDKCTRGYSGVFPDCTPCHQCFCALWDVIIAELTNRTHREL	1201
Db	1081	PQCDQSTGQCVCVEGVGPRCDKCTRGYSGVFPDCTPCHQCFCALWDIIIGELTNRTHKFL	1140
QY	1202	EKAKALKISGVIGPYRETVDVSVERKVSEIKDILAQSPAAEPLKNIGNLFEEAEKLIKQVT	1261
Db	1141	EKAKALKISGVIGPYRETVDVSVEKKVNEIKDILAQSPAAEPLKNIGILFEEAEKLIKQVT	1200
QY	1262	EMVAQVEVKLSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSI	1321
Db	1201	EMVAQVEVKLTDTSQSNSTAGELGALQAEASLDKTVKELAEQLEFIKNSDIQGALDSI	1260
QY	1322	TKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVMMERESQFKKQEEQARLLDEL	1381
Db	1261	TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLESPPFKEQEEQARLLDEL	1320
QY	1382	AGKLOSLDLSAAAEMTCGTPPGASCSETECGPNCRCTDEGERKCGGPGGGLVTVAHNAW	1441
Db	1321	AGKLOSLDLSAAAQMTGTPPGADCSESECGPNCRCTDEGEKKCGGPGGGLVTVAHSAW	1380
QY	1442	QKAMDLDDVLSALAEVQLSKMVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNEELR	1501
Db	1381	QKAMDFDRDVLALAEVQLSKMVSEAKVRADEAKQNAQOVLLKTNATKEKVDKSNEDLR	1440
QY	1502	NLIKQIRNFLTQDSADLDSIEAVANEVLKMEPSTPQOLQNLTEDIRERVESLSQVEVIL	1561
Db	1441	NLIKQIRNFLTQDSADLDSIEAVANEVLKSGNASTPQOLQNLTEDIRERVETLSQVEVIL	1500
QY	1562	QHSAAADIARAEMLLEAKRASKSATDVKTADVMVKEALEEAEKAQVAAEKAIKQADEDIQ	1621
Db	1501	QQSAADIARAEMLLEAKRASKSATDVKTADVMVKEALEEAEKAQVAAEKAIKQADEDIQ	1560
QY	1622	GTQNLTSIESETAASETLFNASQRISELRNVVEELKRKAAQNSGEAEVIEKVYTVKQ	1681
Db	1561	GTQNLTSIESETAASETLTNASQRISELRNVVEELKRKAAQNSGEAEVIEKVYTVKQ	1620
QY	1682	SAEDVKKTLDGELDEKYKKVENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLLK	1741
Db	1621	NADDVKKTLDGELDEKYKKVESLIAQKTESADARRKAELLQNEAKTLLAQANSKLQLE	1680
QY	1742	DIERKVEDNQRYLEDKAQELARLEGEVRSLLKDISQKVAVYSTCL	1786
Db	1681	DIERKVEDNQRYLEDKAQELVRLEGEVRSLLKDISQKVAVYSTCL	1725

RESULT 8
US-10-443-349-4
; Sequence 4, Application US/10443349
; Publication No. US20040023856A1
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert E.
; APPLICANT: Wagman, David W.
; TITLE OF INVENTION: BLK CHAIN OF LAMININ AND METHODS OF USE
; FILE REFERENCE: 10287/021003
; CURRENT APPLICATION NUMBER: US/10/443,349
; CURRENT FILING DATE: 2003-05-22
; PRIOR APPLICATION NUMBER: US/09/161,872
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: US 08/735,893
; PRIOR FILING DATE: 1996-10-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1196
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(250)

OTHER INFORMATION: Human B1 chain									
FEATURE:									
NAME/KEY: DOMAIN									
LOCATION: (251)...(437)									
OTHER INFORMATION: Human B1 chain									
FEATURE:									
NAME/KEY: DOMAIN									
LOCATION: (438)...(807)									
OTHER INFORMATION: Human B1 chain									
FEATURE:									
NAME/KEY: DOMAIN									
LOCATION: (808)...(840)									
OTHER INFORMATION: Human B1 chain									
FEATURE:									
NAME/KEY: DOMAIN									
LOCATION: (841)...(1196)									
OTHER INFORMATION: Human B1 chain									
US-10-443-349-4									
Query Match 62.0%; Score 6044.5; DB 16; Length 1196;									
Best Local Similarity 67.6%; Pred. No. 0;									
Matches 1194; Conservative 0; Mismatches 1; Indels 571; Gaps 2;									
QY	22	QEFESYGAEGSCYPATGDLIGRAQKLSVTS-TCGLHKPEPYCIVSHLQEDKKCFICN	80						
Db	1	QEFESYGAEGSCYPATGDLIGRAQKLSVTSITTCGLHKPEPYCIVSHLQEDKKCFICN	60						
QY	81	SQDPYHETLNPDShLIENVTTFAPNRLKIWQSENGVENVTIQLDLEAEFTHLIMTF	140						
Db	61	SQDPYHETLNPDShLIENVTTFAPNRLKIWQSENGVENVTIQLDLEAEFTHLIMTF	120						
QY	141	KTFRAAMLIERSSDFGKTGWYRYFAYDCEASFPGISTGPMKKVDDIICDSRYSDIEPS	200						
Db	121	KTFRAAMLIERSSDFGKTGWYRYFAYDCEASFPGISTGPMKKVDDIICDSRYSDIEPS	180						
QY	201	TEGEVIFRALDPAFKIEDPYSPIQNLLKITNLRKIFVKLHTLIGDNLDSRMEIREKYYY	260						
Db	181	TEGEVIFRALDPAFKIEDPYSPIQNLLKITNLRKIFVKLHTLIGDNLDSRMEIREKYYY	240						
QY	261	AVYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGHCMCRHNTKGLNCELMDPYHDLPL	320						
Db	241	AVYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGHCMCRHNTKGLNCELMDPYHDLPL	300						
QY	321	WRPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGVCDDCOHNTMGRNCEQCKPF	380						
Db	301	WRPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGVCDDCOHNTMGRNCEQCKPF	360						
QY	381	YYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSLGIAGQCRCLNVEGEHCDVC	440						
Db	361	YYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSLGIAGQCRCLNVEGEHCDVC	420						
QY	441	KEGFYDLSSDDPFCKSKCACNPLGTIPGGNPCDSETHCYCKRLVTGQHCDQCLPEHWGL	500						
Db	421	KEGFYDLSSDDPFCKSKS-----	437						
QY	501	SNDLDGCRPCDDLGALNNSCFABSGQCSRPHMIGRQCNEVEPPGYFFATLDHYLYEAE	560						
Db	438	-----	437						
QY	561	EANLPGVSVIERQYIQDRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQL	620						
Db	438	-----	437						
QY	621	PDHWEKAVITVQRPGRIPPTSSRCGNTIPDDDNQVWSLSPGSRVYVLP RPVCFEKGTNYTV	680						
Db	438	-----	437						
QY	681	RLELPQYTSDDSDVESPYTLIDSLVLMPYCKSLDIFTVGGSGDWVWNSAWETFORYRCL	740						
Db	438	-----	437						
QY	741	ENSRSVVKTMTDVCRNIIIFSISALLHQTGLACECDPQGSLSVCDPNGGQCQCRPNVVG	800						

Db	438	-----	437
QY	801	RTCNRCAPGTFGFGPSGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDRCLPGHWG	860
Db	438	-----	437
QY	861	FPSCQPCQCNHADDCDPVTGECNLCQDYTMGHNCERCLAGYYGDPPIIGSDHCRPCPCP	920
Db	438	-----	437
QY	921	DGPDSGRQFARSCYQDPVTLQLACVCDPGYIGSRCDDCASGYFGNPSEVGSGCQPCQCHN	980
Db	438	-----	437
QY	981	NIDTTPACDKETGRCLKCLYHTEGEHCQCFRFGYYGDALRQDCRKVCNVLGTVOEHC	1040
Db	438	-----CVCNVLGTVOEHC	450
QY	1041	NGSDCQCDKATGQCLCLPNVIGQNCDCRCAPNTWQLASGTGCDPCNCAAHSPGSCNEFT	1100
Db	451	NGSDCQCDKATGQCLCLPNVIGQNCDCRCAPNTWQLASGTGCDPCNCAAHSPGSCNEFT	510
QY	1101	GQCQMPGFGGRTCECQELFWGDPDVECRACDCDPRGIETPQCDQSTGQCVCVEGVEGP	1160
Db	511	GQCQMPGFGGRTCECQELFWGDPDVECRACDCDPRGIETPQCDQSTGQCVCVEGVEGP	570
QY	1161	RCDKCTRGSYSGVFPDCTPCHQCFALWDVIAELTNRTHRFLEKAKALKISGVIGPYRET	1220
Db	571	RCDKCTRGSYSGVFPDCTPCHQCFALWDVIAELTNRTHRFLEKAKALKISGVIGPYRET	630
QY	1221	DSVERKVSEIKDILAQSPAAPLKNIGNLFEEAEKLIKDVTEMAQVEVKLSDTTSQSNS	1280
Db	631	DSVERKVSEIKDILAQSPAAPLKNIGNLFEEAEKLIKDVTEMAQVEVKLSDTTSQSNS	690
QY	1281	TAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTT	1340
Db	691	TAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTT	750
QY	1341	EPNSTVEQSALMRDRVEDVMMERESQFKEKEQEEQARLLDELAKLQSLDLSAAEMTCGT	1400
Db	751	EPNSTVEQSALMRDRVEDVMMERESQFKEKEQEEQARLLDELAKLQSLDLSAAEMTCGT	810
QY	1401	PPGASCSETECGGPNCRCTDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLALAEVEQ	1460
Db	811	PPGASCSETECGGPNCRCTDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLALAEVEQ	870
QY	1461	LSKMVSEAKLRADAEAKQSAEDILLKTNATKEKMDKSNELRNLIKQIRNFLTQDSADLDS	1520
Db	871	LSKMVSEAKLRADAEAKQSAEDILLKTNATKEKMDKSNELRNLIKQIRNFLTQDSADLDS	930
QY	1521	IEAVANEVLKMEMPSTPQQLQNLTEDIRERVESLSQVEVILQHSAAADIARAEMLLEBAKR	1580
Db	931	IEAVANEVLKMEMPSTPQQLQNLTEDIRERVESLSQVEVILQHSAAADIARAEMLLEBAKR	990
QY	1581	ASKSATDVKVTADMVKEALEEAEKAAQVAAEKAKIKQADEDIQGTQNLTSISETAASEET	1640
Db	991	ASKSATDVKVTADMVKEALEEAEKAAQVAAEKAKIKQADEDIQGTQNLTSISETAASEET	1050
QY	1641	LFNASQRISSELRNVEELKRKAAQNSGEAEYIEKVAVYTVKQSAEDVKKTLDGELDEKYYK	1700
Db	1051	LFNASQRISSELRNVEELKRKAAQNSGEAEYIEKVAVYTVKQSAEDVKKTLDGELDEKYYK	1110
QY	1701	VENLIAKKTESADARRKAEMLQNEAKTLQAQNSKQLLKDLEKRYEDNQRYLEDKAQE	1760
Db	1111	VENLIAKKTESADARRKAEMLQNEAKTLQAQNSKQLLKDLEKRYEDNQRYLEDKAQE	1170
QY	1761	LARLEGEVRSLLKDISQKVAVYSTCL	1786
Db	1171	LARLEGEVRSLLKDISQKVAVYSTCL	1196

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; Sequence 8, Application US/09938275
; Patent No. US20020111309A1
; GENERAL INFORMATION:
; APPLICANT: Gerardo Castillo
; APPLICANT: Alan Snow
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications
; TITLE OF INVENTION: of Laminin and Laminin-Derived Protein Fragments
; FILE REFERENCE: PROTEO.P03
; CURRENT APPLICATION NUMBER: US/09/938,275
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1801
; TYPE: PRT
; ORGANISM: Rattus No. US20020111309Alvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Swissprot P15800
; DATABASE ENTRY DATE: 1990-04-01
US-09-938-275-8

Query Match          52.2%; Score 5088.5; DB 9; Length 1801;
Best Local Similarity 51.2%; Pred. No. 5e-281;
Matches 916; Conservative 303; Mismatches 550; Indels 21; Gaps 9;

QY 7 LAFSFLALCARVRAQEPEFSY-GCAEGSCYPATGDLIGRAQLSVTSTCGLHKPEPYC 65
Db 21 LRLGLLSVLAATLAQVPSLDVPGSGSCYPATGDLVGRADRLTASSTCGLHSPQPYC 80

QY 66 IVSHLQEDKKFCICNSQDPYHETLNPDLSHLIENVVTFAPNRLKIWQSENGVENVTIQL 125
Db 81 IVSHLQDEKKFCICNSQDPYHETLNPDLSHLIENVVTFAPNRLKIWQSENGVENVTIQL 140

QY 126 DLEAEFHFTHLMTFKTRPAAMLIERSDFGKTGWVYFYFAYDCEASFPGISTGPMKKV 185
Db 141 DLEAEFHFTHLMTFKTRPAAMLIERSDFGKTGWVYFYFAYDCEASFPGISTGPMKKV 200

QY 186 DDIIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSRIQNLKTIINLRIFVKLHTLGD 245
Db 201 DDVVCESRYSEIEPSTEGEVIVRVLDPAIPIDPYSRIQNLKTIINLRVNLTRLHTLGD 260

QY 246 NLLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGFNEEVEGVMVHGCMCRHNTK 305
Db 261 NLLDPRREIREKYYAYVDMVVRGNCFCYGHASECAPVDGFNEEVEGVMVHGCMCRHNTK 320

QY 306 GLNCELMDPYHDLWPRAEGRNSNACKKNCNEHSISCHFDMAVYLATGVSGVCDDC 365
Db 321 GLNCEQCQDFYQDLPHWPAEDGHTHACRKECNGHSHSCHFDMAYVYLATGVSGVCDGC 380

QY 366 QHNTMGRNCEQCKPFYQHPERDIRDPNFCERCTCDPAGSQNEGICDSTDFSTGLIAGQ 425
Db 381 QHNTAGRHCELCRPFYQHPERDIRDPNFCERCTCDPAGSQNEGICDSTDFSTGLIAGQ 440

QY 426 CRCKLVNVEGHCDCVKEGFYDLSSEDPFGCKSCACNPLGTIPGPNPCDSETHGHCYCKRLV 485
Db 441 CRCKEHVVVTRCQCCRDGFFGLSASNPGRQCRCQNSRGTVPGGTPCDSSSGTCFCCKRLV 500

QY 486 TGQHCDCQCLPEHWGLSNDLDCRCPDCLDGLGALNNSCFAESGQSCSRPHMIGRQCNEVEP 545
Db 501 TGDGCDRLCPGHWGLSHDLGCRPCDCLDVGGLDPPQDEATGQPCPRPHMIGRRCQVQP 560

QY 546 GYFATLDHLYEAEANLPGVSIIVERQYIQDRIPSWTGAGFVRVPEGAYLEFFIDNIP 605
Db 561 GYFRPFLDHLTWEAEGAH-GQVLEVVRLVTRNTPSWTGVFVRLREGQVEFLVTSLP 619

QY 606 YSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPTRSSRCGNTIPDDNQVVSLSPGSRVYV 665
Db 620 RAMDYDLLRWEPQVPEQWAELELVQRPVPSAHSPCGHVLPDRDRDRIQGLMHPNTRVLV 679

QY 666 LPRPVCREKGTNYTVRLELPQVTSDDSDVESPYT----LIDSLVMPYCKSLDIFTVGG 721
Db 680 FPRPVCLEPGLSYKLKLTG-TGGRAPHPETPYSGSGLIDSLVLQPHVLMLEMF-----S 734
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QY 722 GDGVVNTNSAWETTFORYRCLENSRSVVVKTPTMTDVCNRIIFSISALLHQTGLACECDPQGS 781
Db 735 GGDAAALERRTTFFERYRCHHEGLMPSKTPLEACVPLLSASSLVYNGALPCQCDPQGS 794

QY 782 SSVCDPNGGQCQCRPNVVGRTCNRCAPGTGFGPSGCKPCCEHLQGSVNAFCNVTGQCH 841
Db 795 SSECNPHGGQCRCKPVGVRRCDAACATGYGFGPAGCAQCQSPDGAISALCEGTSGOCL 854

QY 842 CFQGVYARQCDRLCPGHWGPPSCQPCQCNHADDCTPVTGECNQCQDYMTHNCERCLAG 901
Db 855 CRTGAFGLRCDHCQRGQWGFNCRPCVCNCRADCECAHTGACLCGRDITGGEHCERCIAG 914

QY 902 YGDPPIIGSDHCRPCPCPDGDSGRQFARSQYQDPVTLQLACVCDPPIGYSRCDDCASG 961
Db 915 FHGDPRLPYGGQCRPCPCPEGPSQRHFAATSHRDRGYSQQIVCHCRAGYTLGRCEACAPG 974

QY 962 YFGNPSEVGGSCQPCQCHNNIDTTPDPAEDKGTGRCLKCLVHTEGEHCQCFRFGYGDAL 1021
Db 975 HFGDPSKPGGRQCQCECSGNIDPTDPCACDPHTGQCLRLCHHTGPHCHGCKPGFHHGQA 1034

QY 1022 RQDCRCKVCNYLGTVQEHGNGSD-CQCDKATGQCLCLPNVGNCDRCAPNTWQLASGTG 1080
Db 1035 RQSCHRCTCNLLGTDPPQPCSTDLCHCDPSTGQPCPLPHVGLSCDRCAPNFWNFTSGRG 1094

QY 1081 CDPNCNAAHSPGSCNEFTGQCCQCMGFGGRTCTCEQELFWGDDVECRACDCDPRGIE 1140
Db 1095 CQPCACHPSRARGPTCNEFTGQCHCHAGFGGRTCTCEQELFWGDDVECRACDCDPRGID 1154

QY 1141 TPQCDQSTGQCVVEGVEGPRCDKCTRGYSVGFPPDCTPCHQCFALWDVIAELTNTRHF 1200
Db 1155 KPQCHRSTGHSCRFPGVGVRCDCQARGFSGVFPACHPCFACFGDWDVVDLAARTRL 1214

QY 1201 LEKAKALKISGIVGPRYRETVDSEVERKVEIKDILA--QSPAAEPLKNIGNLFEAEKL-- 1256
Db 1215 EQWAQELQOTGVLAGFESSFLNLQGLGMVQAIVAARNTSAASTAK---LVEATEGLRH 1270

QY 1257 -IKDVTEMMAQVEVKLSDDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIR 1315
Db 1271 EIGKTTERTLQLEAELTDVQDENFNANHALSGLERDGLALNLTQLRDLQHLDLKHSN 1330

QY 1316 GALDSITKYFQMSLEAEERVNASTTEPNSTVEQSALMRDVEDVMMERESQFKKQEEQA 1375
Db 1331 GAYDSIRHAHQSTEAERRANASTFAIPSPVSNASDTRRAEVLMGARQENFRQHLAQ 1390

QY 1376 RLLDELQGLQSLDLSAAEMTCGTPPGASCSETECGGNCRTDEGERKCGGPGCGGLVT 1435
Db 1391 QALGRLSTHTSLTSLTGVNELVCGAPDAPCATSPCGGACCRDEDEDQPRCGGLGCSGAA 1450

QY 1436 VAHNAWQKAMDLDQDVLALAEVEQLSKMVSEAKLRADBAKQSAEDILLKTNAKEMDK 1495
Db 1451 TADLALGRARHTQAEALQALVEGGGILSRVSETRRQAEAAQQAALDKANASRGQVEQ 1510

QY 1496 SNEELRNLIKQIRNFLTQDSADLDSIEAVANEVLKMEMPTPQOLNLTEDIRERVESLS 1555
Db 1511 ANQELRELIONVKDFLSQEGADPDSIEMVATRVLDISIPASPEIQRLASEIAERVSLA 1570

QY 1556 QVEVILQHSAAADIAEAEMLLLEAKKASKSATDVKVTDVMDVKEALEEAEKAAQVAAEK 1615
Db 1571 DVTILAHMTMGDVRRAEQQLQDAQPARSRAEGERQKAEVQAALEAAQQAQGAQGAIRG 1630

QY 1616 ADEDIQTQNLTSIESETAASETLFNASQRISELENNVEELKRAAQNNGSEAEVIEKV 1675
Db 1631 AVVDTKXTEQTLQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 1690

QY 1676 VYTVKQSAEDVKKTLDELDEKVKVKNVENLIAKTEESADARRKAEMLQNEAKTLLAQNS 1735
Db 1691 AGSAQSRAREAEKQLREQVQDQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 1750

QY 1736 KLQLLKDLERKVEDNQRYLEDKAEQELARLEGEVRSLLKDISQKVAVYSTC 1785
Db 1751 KLQRLQLEGTYEENERELEVKAAQDLGLGLEARMSRVLQAINLQVQIYNTC 1800
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RESULT 11

US-09-845-583-6
; Sequence 6, Application US/09845583
; Patent No. US20020142954A1
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Brunken, William Joseph
; APPLICANT: Champlaud, Marie-France
; APPLICANT: Hunter, Dale
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
; FILE REFERENCE: 10287-056001
; CURRENT APPLICATION NUMBER: US/09/845,583
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/200,863
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1799
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-845-583-6

Query Match 51.8%; Score 5051.5; DB 9; Length 1799;

Best Local Similarity 50.8%; Pred. No. 6.4e-279;

Matches 907; Conservative 304; Mismatches 560; Indels 15; Gaps 8;

QY	7	LAFSFLALCRARVRAQEPESY-GCAEGSCYPATGDLIGRAQKLSVTSCTGLHKPEPYC	65
Db	21	LRLGLLSVLAAATLAQAPSLDVPSCSRGSCYPATGDLVGRADRLTASSCTGLHSPQPYC	80
QY	66	IVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVTTFAPNRLKIWQSENVENVTIQL	125
Db	81	IVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVTTFAPNRLKIWQSENVENVTIQL	140
QY	126	DLEAEFFHFLIMTFTKTERPAAMLLERSDFGKTGWVYRYFAYDCEASFISTGPMKKV	185
Db	141	DLEAEFFHFLIMTFTKTERPAAMLLERSDFGKTGWVYRYFAYDCEASFISTGPMKKV	200
QY	186	DDIICDSRYSYDIEPSTEGEVIFRALDPFAFKIEDPYSPRIQNLKILNLEIKFVKLHTLGD	245
Db	201	DDVVCESRYSEIEPSTEGEVIVRDLPAIPIDPYSRIQNLKILNLEIKFVKLHTLGD	260
QY	246	NLLDSRMEIREKYYAVYDMVRGNCFCYGHASECAPVDGFEVEGEMVHCHCMCRHNTK	305
Db	261	NLLDPRREIREKYYALVELVIRGNCFCYGHASQCAPGAPAHAEVGHGACICKHNTK	320
QY	306	GLNCELQMDFYDLPWRPAEGRNSNACKKNCNEHISCHFDMAVILATGNVSGVCDCC	365
Db	321	GLNCEQCFYQDLPWHPAEDGHTHACRKECNCNGHSHCHFDMAVILASGNVSGVCDGC	380
QY	366	QHNTMGRNCEQCKPFYYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSTGLIAGQ	425
Db	381	QHNTAGRHCEFCRPFYRDPDKMDRPAVCRPCDPMGSDGGRCDSDHDDPVLGLVSGQ	440
QY	426	CRCKLNVGEHCDVCKEGFYDLSSEDPFGCKSCACNPLGTIPGPNPCDSETGHYCKKRLV	485
Db	441	CRCKEHHVTRCQCRDGFGLSASDPRGCRQCQNSRGTVPGSSPCDSSSGTCFCCKRLV	500
QY	486	TGQHCDCLPEHGWGLSNDLQCRPCDCLGGLNNSCFAESGQSCCRPHMIGRQCNEVEP	545
Db	501	TGHGCDCLPGHGWGLSNDLQCRPCDCLGGLNNSCFAESGQSCCRPHMIGRQCNEVEP	560
QY	546	GYFATLDHYLYEAEANLPGVSIIVERQYIQDRIPSWTGTAGFVRVPEGAYLEFFIDNIP	605
Db	561	GYFRPFDLHTWEAAQ-GQVLEVRVLTNRTPSWTGTAGFVRVPEGAYLEFFIDNIP	619
QY	606	YSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPTSRRCNTIPDDNQVVSLSPGSRVYV	665
Db	620	RAMDYDILLRWEQVPEQWAELELMVQRPVPSAHSFPGHVLPKDDRIQGMHPNTRVLV	679

QY	666	LPRPVCFEKGTNYVRLELPQYTSSSDSVESPYT--LIDSLVLMPYCKSLDIFTVGGSGD	723
Db	680	FPRPVCLEPGISYKLLKLG-TGGRAPQETSYSGLLIDSLVLPQHVIVLEMF---SGG	734
QY	724	GVVNSAWETFORVRCLENSRSVVKTPMTDVCNIIIFSISALLHQTGLACECDPQGSLS	783
Db	735	DAALERRTTFRVRCHEGLMPSKAPLSETCAPLLISVSALIYNGALPCQCDPQGSLS	794
QY	784	VCDPNGQCQCRPNVVGRTNRCAPGTFGFGPSGCKPCBCHLOGSVNAFCNPVTGOCHCF	843
Db	795	ECSPHGGQCRKPGVVGRRCDVCATGYGFGPAGCQACQCSPDGALSALCEGTSGQCPCR	854
QY	844	QGVYARQCDRCLPGHGWFPSCQPCQCNHADDCCDPVTGECNCCDYTMGHNCERCLAGY	903
Db	855	PGAFGLRCDHCQCGWGFNCRPCVNCNGRADECDDTHGACLGCRDYGTCGHCERCIAHGF	914
QY	904	GDPIIGSDHCRPCPCPDGPDGSRQFARSCYQDPVTLQACVCDPGYIGSRCDDCASGVF	963
Db	915	GDPRLPYGGQCRPCPCPEGPGSRQHFATSCHRDGYSQIIVCHCRAGYTLRCEACAPGPF	974
QY	964	GNPSEVGGSCQPCQCHNNIDTTDPEACDKETGRCLKLYHTEGHCQFCRFGYGGDALRQ	1023
Db	975	GDPSKPGRCQLCECSGNIDPMDPDADCPHTGQCLRHNTGPHGCHGCKPGFHHGQAARQ	1034
QY	1024	DCRKCVCNVLGTVEHCNGSD-CQCDKATGQCLCLPNVIGNCDRCAPNTWQLASGTGCD	1082
Db	1035	SCHRCTCNLLGTDPRRCPTDLCHCDPSTGQCPCLPHVQGLNCHDCAPNFWNFTSGRGQ	1094
QY	1083	PCNCAAHSGFSPSCNEFTGQCCQCMFGGRTCTSECQELFWGDPDVECRACDCDPRGIETP	1142
Db	1095	PCACHPSRARGTCTNEFTGQCHCHAGFGGRTCTSECQELFWGDPDVECRACDCDPRGIDKP	1154
QY	1143	QCDQSTGQCVCEGVEGPRCDKCTRGYSGVFPDCTPCHQCFALWDVIAELTNRTHRFLE	1202
Db	1155	QCHRSTGHCSCRPVSGVRCDCQCARGSGVFPACHPCFACGWDVQDLAARTLRLEQ	1214
QY	1203	KAKALKISGVIGPYRETVDSEVERKVSEIKDILAQSPAAEPLKNIIGNLFEEAEKL---	1259
Db	1215	WAQELQQTGVLGAFESSFLNMQGLGMVQAISARNAS--AASAKLVEATEGLSHEIGK	1272
QY	1260	VTEMAQVEVKLSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALD	1319
Db	1273	TTERLTQLEAELTAVQDENFNANHALSGLERDGFALNLTQLDQHLKHSNLFGLAYD	1332
QY	1320	SITKYFQMSLEAEERNVASTTEPNSTVEQSALMRDRVEDVMMERESQFKEQEEQARLLD	1379
Db	1333	SIRHAHSQSTEAEARRANASTFAVSPVSNADTTRRTTEVLMAQKFNFRQLANQAALG	1392
QY	1380	ELAGKQLSLDLSAAAEEMTCGTPGASCSETGCGPNCRDTEGERKCGGPGCGGLVTVAHN	1439
Db	1393	RLSAHAHTLSLTGINELVCGAPGADPACATSPCGGAGCDEDEDGPRCGGLGCSGAAAPDL	1452
QY	1440	AWQKAMDLDQDVLALAEVEQLSKMVSEAKLRADAEAKQSAEDILLKTNAKEMDKSNEE	1499
Db	1453	ALGRARHSQAEQLRALVEGGGILSRVSETRRQAEAAQQAALDKANASRGQVEQANQE	1512
QY	1500	LRNLIKQIRNFLTQDSADLDSIEAVANEVLKMEPSTPQQLQNLTEDIRERVELSQVEV	1559
Db	1513	LRELIONVKDFLSQEGADPPSIEMVATRVLDISIPASPEIQRLASEIAERVSRLADVD	1572
QY	1560	ILQHSADIAAEMLLEAKRASKSATDVKVTADMVKEALEEAEAKQVAAEKAQKQADE	1619
Db	1573	ILAHTMGDVRRAEQLLQDAHRARSRAEGERQKAEVQAALAEAAQQAQGAIRGAVVD	1632
QY	1620	IQGTQNLTSIESETAASEETLNFNASQRISELRNVEELKRKAQNSGEAEYIEKVYTV	1679
Db	1633	TQNTQTLQVQERMAGAEKSNASAGERARQLDALLEALKLKRAGNSLAASAEETAGSA	1692
QY	1680	KQSAEDVKTKLDGELDEKYYKVENLIAKTEESADARRKAEMLQNEAKTLQAQNSKLQ	1739
Db	1693	QSRAREAKQLREQVQDQYQTVRALAEKAEGLAAQARAQAEQLRDEARDLLQAAQDKLQ	1752
QY	1740	LKOLERYEDNQRYLEDKAEELARLEGEVRSLLKDISQKAVYSTC	1785

RESULT 15
US-09-925-298-703
; Sequence 703, Application US/09925298
; Publication No. US20020039764A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103
; CURRENT APPLICATION NUMBER: US/09/925,298
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12

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; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 703
; LENGTH: 527
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (243)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (257)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (259)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (471)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (477)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (480)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (484)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (511)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (519)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;
US-09-925-298-703

Query Match      24.1%; Score 2348; DB 12; Length 527;
Best Local Similarity 87.8%; Pred. No. 1.4e-125;
Matches 481; Conservative 7; Mismatches 24; Indels 36; Gaps 3;

Qy 1151 CVCVEGVEGPRCDKCTRGYSGVFPDCTPCHQCFCALWDVIAELTNRTHRPLEKAKALKIS 1210
Db 1 CVCVEGVEGPRCDKCTRGYSGVFPDCTPCHQCFCALWDVIAELTNRTHRPLEKAKALKIS 60

Qy 1211 GVIGPYRETVDSEVERKVSSEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDVTEMMQAQVEVK 1270
Db 61 GVIGPYRETVDSEVERKVSSEIKDILAQSPAAEPLKNIGNLFEEAEKLIKDVTEMMQAQVEVK 120

Qy 1271 LSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFINKSDIRGALDSITKYFQMSLE 1330
Db 121 LSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFINKSDIRGALDSITKYFQMSLE 180

Qy 1331 AEERNASTTEPNSTVEQSALNRDRVEDVMMERESQFKEKEQEEQARLLDELAKLQSLDL 1390
Db 181 AEERNASTTEPNSTVEQSALNRDRVEDVMMERESQFKEKEQEEQARLLDELAKLQSLDL 240

Qy 1391 SAAEMTCGTPPGASCSETGCGPNCRTDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQD 1450
Db 241 SAXAEMTCGTPPGASCSEXECGPGNCRTDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQD 300

Qy 1451 VLSALAEVEQLSKMVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNEELNLIKQIRNF 1510
Db 301 VLSALAEVEQLSKMVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNEELNLIKQIRNF 360

Qy 1511 LTQDSADLDSIEAVANEVLKMPSTPQQLNLTERVESLSQVEVILQHSAAADIAR 1570
Db 361 LTQDSADLDSIEAVANEVLKMPSTPQQLNLTERVESLSQVEVILQHSAAADIAR 420

Qy 1571 AEMLLEEAKRASKSATDVKVTDVMVKEALEEAEKAQVAEAKAIKQADEDIQGTQNLLTSI 1630
Db 421 AEMLLEEAKRASKSATDVKVTDVMVKEALEEAEKAQVAEAKAIKQADEDI----- 470

Qy 1631 ESETAASEETLNFNASQRISSELRNVE----ELKRKAQNSGEAEYIEKVVTYVKQSAEDV 1686
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Db 471 -----XRNPEPXNFXLEFXKQQLSG-GNLVQRPVPRASSEFREDV 508
Qy 1687 KKTLDGEL 1694
Db 509 GRXLGKL 516

Search completed: May 18, 2004, 15:42:21
Job time : 53.4374 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:49:23 ; Search time 10.1546 Seconds
(without alignments)
6313.134 Million cell updates/sec

Title: US-10-037-182-6
Perfect score: 9754
Sequence: 1 MGLQLLAFSLALCRARV.....EVRSLKDISQKAVYSTCL 1786

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 240604 seqs, 35894274 residues

Total number of hits satisfying chosen parameters: 240604

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents AA New:
1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	9750	100.0	1786	6	US-10-796-280-770
2	6044.5	62.0	1196	6	US-10-841-139-4
3	5060.5	51.9	1798	6	US-10-796-307-899
4	5060.5	51.9	1798	6	US-10-796-307-900
5	3625.5	37.2	1670	1	PCT-US02-39555A-917
6	1675	17.2	1573	6	US-10-796-280-1353
7	1675	17.2	1573	6	US-10-796-280-1354
8	1645.5	16.9	3712	6	US-10-108-605A-103
9	1581	16.2	885	1	PCT-US02-39555A-2483
10	1574.5	16.1	3690	7	US-10-796-280-1384
11	1574.5	16.1	3690	7	US-60-568-219-509
12	1568.5	16.1	3690	1	PCT-US02-22858A-347
13	1568.5	16.1	3717	6	US-10-821-234-1076
14	1566	16.1	2107	6	US-10-796-280-1108
15	1566	16.1	2107	6	US-10-796-307-671
16	1566	16.1	2107	7	US-60-568-219-409
17	1566	16.1	2480	6	US-10-796-280-1106
18	1566	16.1	2480	7	US-10-796-307-669
19	1566	16.1	2480	7	US-60-568-219-407
20	1566	16.1	3116	6	US-10-796-280-1107
21	1566	16.1	3116	6	US-10-796-307-670
22	1566	16.1	3116	7	US-60-568-219-408
23	1525.5	15.6	3714	6	US-10-796-280-1383
24	1525.5	15.6	3714	7	US-60-568-219-508
25	1489	15.3	3332	1	PCT-US02-39555A-1160
26	1463	15.0	1165	6	US-10-841-139-2

27	1451.5	14.9	1147	6	US-10-841-139-3	Sequence 3, Appli
28	1342	13.8	249	6	US-10-841-139-6	Sequence 6, Appli
29	1077	11.0	1486	1	PCT-US02-39555A-2658	Sequence 2658, Ap
30	1003	10.3	250	6	US-10-841-139-7	Sequence 7, Appli
31	1001	10.3	628	6	US-10-831-979-5	Sequence 5, Appli
32	993	10.2	628	6	US-10-831-979-2	Sequence 2, Appli
33	991	10.2	628	6	US-10-100-683-8634	Sequence 8634, Ap
34	671.5	6.9	1547	6	US-10-453-372-886	Sequence 886, App
35	671.5	6.9	1577	6	US-10-453-372-882	Sequence 882, App
36	671.5	6.9	1577	6	US-10-453-372-884	Sequence 884, App
37	671.5	6.9	1620	6	US-10-453-372-868	Sequence 868, App
38	671.5	6.9	1653	6	US-10-453-372-866	Sequence 866, App
39	667	6.8	1594	6	US-10-453-372-860	Sequence 860, App
40	662	6.8	1418	6	US-10-453-372-864	Sequence 864, App
41	657.5	6.7	1450	6	US-10-453-372-874	Sequence 874, App
42	657	6.7	4265	7	US-60-563-440-1664	Sequence 1664, Ap
43	657	6.7	4346	7	US-60-548-091-384	Sequence 384, App
44	657	6.7	4346	7	US-60-568-219-343	Sequence 343, App
45	657	6.7	4347	7	US-60-548-091-383	Sequence 383, App

ALIGNMENTS

RESULT 1
US-10-796-280-770
; Sequence 770, Application US/10796280
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001510
; CURRENT APPLICATION NUMBER: US/10/796,280
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 68533
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 770
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-796-280-770

Query Match 100.0%; Score 9750; DB 6; Length 1786;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1785; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGLQLLAFSLALCRARVRAQEPESYCGAEGSCYPATGDLIGRAQKLSVTGGLHK	60
Db	1	MGLQLLAFSLALCRARVRAQEPESYCGAEGSCYPATGDLIGRAQKLSVTGGLHK	60
QY	61	PEPYCIIVSHLQEDKKCFICNSODPYHETLNPDLSHLIENVVTFAPNRLKIWQSENGVEN	120
Db	61	PEPYCIIVSHLQEDKKCFICNSODPYHETLNPDLSHLIENVVTFAPNRLKIWQSENGVEN	120
QY	121	VTIQLDLAEAFHFTLIMTFTKTPRPAAMLIERSDDFGKTGWVYRYFAYDCEASFPGISTG	180
Db	121	VTIQLDLAEAFHFTLIMTFTKTPRPAAMLIERSDDFGKTGWVYRYFAYDCEASFPGISTG	180
QY	181	PMKKVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPIQNLLKITNLRIKFKVL	240
Db	181	PMKKVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPIQNLLKITNLRIKFKVL	240
QY	241	HTLGDNLDSRMEIREKYYIYAVDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGCMC	300
Db	241	HTLGDNLDSRMEIREKYYIYAVDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGCMC	300
QY	301	RHNTKGLNCELMDYFHDLPWRPAEGRNSNACKKNCNHSISCHFDMAVYLATGNVSGG	360
Db	301	RHNTKGLNCELMDYFHDLPWRPAEGRNSNACKKNCNHSISCHFDMAVYLATGNVSGG	360
QY	361	VCDDCQHNTMGRNCEQCKPFYYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSTG	420
Db	361	VCDDCQHNTMGRNCEQCKPFYYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSTG	420

QY 421 LIAGQCRKLNVEGEHCDVCKEGFYDLSSSEDPFGCKSCACNPLGTIPGGNPCDSETHCY 480
DB 421 LIAGQCRKLNVEGEHCDVCKEGFYDLSSSEDPFGCKSCACNPLGTIPGGNPCDSETHCY 480
QY 481 CKRLVTGHCDCQLPEHWGLSNDLDGCRPCDCDLGGALNNSCFAESGCCSCRPIMIGRQC 540
DB 481 CKRLVTGHCDCQLPEHWGLSNDLDGCRPCDCDLGGALNNSCFAESGCCSCRPIMIGRQC 540
QY 541 NEVEPGYFATLDHYLYEAEEANLPGVSIIVERQYIQDRIPSWTGAGFVRVPEGAYLEFF 600
DB 541 NEVEPGYFATLDHYLYEAEEANLPGVSIIVERQYIQDRIPSWTGAGFVRVPEGAYLEFF 600
QY 601 IDNIPYSMEYDILIRYEPOLPDHWEKAVITVQRPGRIPRTSSRCGNTIPDDDNQVVSLSPG 660
DB 601 IDNIPYSMEYDILIRYEPOLPDHWEKAVITVQRPGRIPRTSSRCGNTIPDDDNQVVSLSPG 660
QY 661 SRYVVLPRPVCFEKGTNYTVRLELPQYTSDDSDVESPYTLIDSLVLMYPYCKSLDIFTVGG 720
DB 661 SRYVVLPRPVCFEKGTNYTVRLELPQYTSDDSDVESPYTLIDSLVLMYPYCKSLDIFTVGG 720
QY 721 SGDGVTNSAWETFORYRCLENSRSVVKTPMTDVCRNIIIFSISALLHQTGLACECDPQGS 780
DB 721 SGDGVTNSAWETFORYRCLENSRSVVKTPMTDVCRNIIIFSISALLHQTGLACECDPQGS 780
QY 781 LSSVCDPNGGQOCQCRPNVVGRTCNRCAPGTGFGSPGCKPCECHLQGSVNAFCNPVTGQC 840
DB 781 LSSVCDPNGGQOCQCRPNVVGRTCNRCAPGTGFGSPGCKPCECHLQGSVNAFCNPVTGQC 840
QY 841 HCFQGVYARQCDRLPGHWGFPSCQPCQCNCGHADDCTPVTGECINQDQYTMGHNCERCLA 900
DB 841 HCFQGVYARQCDRLPGHWGFPSCQPCQCNCGHADDCTPVTGECINQDQYTMGHNCERCLA 900
QY 901 GYGDPPIIGSGDHCRPCPCPDGPDGSRQFARSCYQDPVTIQLACVCDPGYIGSRCCDDCAS 960
DB 901 GYGDPPIIGSGDHCRPCPCPDGPDGSRQFARSCYQDPVTIQLACVCDPGYIGSRCCDDCAS 960
QY 961 GYFGNPFSEVGSCQPCQCHNNIDTTDPEACDKETGRCLKCLYHTEGEHCQFCRFGYIGDA 1020
DB 961 GYFGNPFSEVGSCQPCQCHNNIDTTDPEACDKETGRCLKCLYHTEGEHCQFCRFGYIGDA 1020
QY 1021 LRQDCRKVCNYLGTVOEHCHNGSDCQCDKATGQCLCLPNVIGNQCDRCAPNTWQLASGTG 1080
DB 1021 LQQDCRKVCNYLGTVOEHCHNGSDCQCDKATGQCLCLPNVIGNQCDRCAPNTWQLASGTG 1080
QY 1081 CDPNCNAAHSFGPSCNEFTGQCQCMFGGRTCECQELFWGDDPVECRACDCDPRGIE 1140
DB 1081 CDPNCNAAHSFGPSCNEFTGQCQCMFGGRTCECQELFWGDDPVECRACDCDPRGIE 1140
QY 1141 TPQCDQSTGQCVCEGVGPRCDKCTRGYSGVFPDCTPCHQCFALWDVIIAELTNRTHRF 1200
DB 1141 TPQCDQSTGQCVCEGVGPRCDKCTRGYSGVFPDCTPCHQCFALWDVIIAELTNRTHRF 1200
QY 1201 LEKAKALKISGVIGPYRETVDVSVERKVSEIKDILAQSPAAPLKNIGNLFEEAEKLIKDV 1260
DB 1201 LEKAKALKISGVIGPYRETVDVSVERKVSEIKDILAQSPAAPLKNIGNLFEEAEKLIKDV 1260
QY 1261 TEMMAQVEVKLSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDS 1320
DB 1261 TEMMAQVEVKLSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDS 1320
QY 1321 ITKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVMMERESQPKKEQEARLLDE 1380
DB 1321 ITKYFQMSLEAEERVNASTTEPNSTVEQSALMRDRVEDVMMERESQPKKEQEARLLDE 1380
QY 1381 LACKLQSLDLSAAAEWTCGTPPGASCSETGCGPNCRDTEGERKCGGPGCGGLVTVAHNA 1440
DB 1381 LACKLQSLDLSAAAEWTCGTPPGASCSETGCGPNCRDTEGERKCGGPGCGGLVTVAHNA 1440
QY 1441 WQKAMDLDQDVL SALAEVEQLSKMWSEAKLRADBAKQSAEDILLKTNATKEMDKSNEEL 1500
DB 1441 WQKAMDLDQDVL SALAEVEQLSKMWSEAKLRADBAKQSAEDILLKTNATKEMDKSNEEL 1500

QY 1501 RNLIKQIRNFELTQDSADLDSIEAVANEVLKMPSTPOOLQNLTEDIRERVESLSQVEVI 1560
DB 1501 RNLIKQIRNFELTQDSADLDSIEAVANEVLKMPSTPOOLQNLTEDIRERVESLSQVEVI 1560
QY 1561 LQHSAAADIARAEMLLLEEAKRASKSATDVKVTADMVKEALEEAEKAQVAAEKAIKQADEDI 1620
DB 1561 LQHSAAADIARAEMLLLEEAKRASKSATDVKVTADMVKEALEEAEKAQVAAEKAIKQADEDI 1620
QY 1621 QGTQNLTSIESETAASEETLFNASQRISELERNVVEELKRKAQNSGEAEYIEKVVTYTVK 1680
DB 1621 QGTQNLTSIESETAASEETLFNASQRISELERNVVEELKRKAQNSGEAEYIEKVVTYTVK 1680
QY 1681 QSAEDVKKTLDGELDEKYKKVENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLL 1740
DB 1681 QSAEDVKKTLDGELDEKYKKVENLIAKKTESADARRKAEMLQNEAKTLLAQANSKLQLL 1740
QY 1741 KDLERKYEDNQRYLEDKAQELARLEGEVRSLLKDISQKAVYSTCL 1786
DB 1741 KDLERKYEDNQRYLEDKAQELARLEGEVRSLLKDISQKAVYSTCL 1786

RESULT 2

US-10-841-139-4
; Sequence 4, Application US/10841139
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert E.
; APPLICANT: Wagman, David W.
; TITLE OF INVENTION: BLK CHAIN OF LAMININ AND METHODS OF USE
; FILE REFERENCE: 10287/021003
; CURRENT APPLICATION NUMBER: US/10/841,139
; CURRENT FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US/10/443,349
; PRIOR FILING DATE: 2003-05-22
; PRIOR APPLICATION NUMBER: US/09/161,872
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: US 08/735,893
; PRIOR FILING DATE: 1996-10-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1196
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(250)
; OTHER INFORMATION: Human B1 chain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (251)...(437)
; OTHER INFORMATION: Human B1 chain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (438)...(807)
; OTHER INFORMATION: Human B1 chain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (808)...(840)
; OTHER INFORMATION: Human B1 chain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (841)...(1196)
; OTHER INFORMATION: Human B1 chain
US-10-841-139-4

Query Match 62.0%; Score 6044.5; DB 6; Length 1196;
Best Local Similarity 67.6%; Pred. No. 1.3e-249;
Matches 1194; Conservative 0; Mismatches 1; Indels 571; Gaps 2;

QY 22 QPEFSGYCAEGSCYPATGDLILIGRAQKLSVTS-TCGLHKPEPYCIVSHLQEDKKCFICN 80
DB 1 QPEFSGYCAEGSCYPATGDLILIGRAQKLSVTS-TCGLHKPEPYCIVSHLQEDKKCFICN 60

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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:26:08 ; Search time 20.6673 Seconds
(without alignments)
9158.169 Million cell updates/sec

Title: US-10-037-182-4
Perfect score: 19876
Sequence: 1 DLYCKLVGGPVAGGDPNQT.....QGKALTQRHAKPSVSPLLWH 3635

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19876	100.0	3718	1 LMA5_MOUSE	Q61001 mus musculu
2	15847	79.7	3695	1 LMA5_HUMAN	Q15230 homo sapien
3	6403.5	32.2	3333	1 LMA3_MOUSE	Q61789 mus musculu
4	5018.5	25.2	3712	1 LMA_DROME	Q00174 drosophila
5	4831.5	24.3	3672	1 LML2_CAEEL	Q21313 caenorhabdi
6	3096	15.6	3106	1 LMA2_MOUSE	Q60675 mus musculu
7	3005	15.1	3110	1 LMA2_HUMAN	P24043 homo sapien
8	2792	14.0	3084	1 LMA1_MOUSE	P19137 mus musculu
9	2729.5	13.7	3075	1 LMA1_HUMAN	P25391 homo sapien
10	2182.5	11.0	1816	1 LMA4_HUMAN	Q16363 homo sapien
11	2149.5	10.8	1713	1 LMA3_HUMAN	Q16787 homo sapien
12	2132.5	10.7	1816	1 LMA4_MOUSE	P97927 mus musculu
13	1675	8.4	1798	1 LMB2_HUMAN	P55268 homo sapien
14	1672.5	8.4	1801	1 LMB2_RAT	P15800 rattus norv
15	1668.5	8.4	1799	1 LMB2_MOUSE	Q61292 mus musculu
16	1605	8.1	1786	1 LMB1_HUMAN	P07942 homo sapien
17	1584	8.0	1786	1 LMB1_MOUSE	P02469 mus musculu
18	1552	7.8	1790	1 LMB1_DROME	P11046 drosophila
19	1462.5	7.4	1587	1 LMG3_HUMAN	Q9Y6N6 homo sapien
20	1367	6.9	1581	1 LMG3_MOUSE	Q9F0B6 mus musculu
21	1344.5	6.8	1607	1 LMG1_MOUSE	P02468 mus musculu
22	1323.5	6.7	1609	1 LMG1_HUMAN	P11047 homo sapien
23	1312	6.6	1639	1 LMG1_DROME	P15215 drosophila
24	1221	6.1	1535	1 LML1_CAEEL	Q18823 caenorhabdi
25	1204	6.1	3707	1 PGEM_MOUSE	Q05793 mus musculu
26	1104	5.6	4391	1 PGEM_HUMAN	P98160 homo sapien
27	947	4.8	1191	1 LMG2_MOUSE	Q61092 mus musculu
28	946	4.8	1193	1 LMG2_HUMAN	Q13753 homo sapien
29	839	4.2	1172	1 LMB3_HUMAN	Q13751 homo sapien
30	799.5	4.0	1168	1 LMB3_MOUSE	Q61087 mus musculu
31	799	4.0	3375	1 UN52_CAEEL	Q06561 caenorhabdi
32	754	3.8	2321	1 NTC3_HUMAN	Q9UM47 homo sapien
33	699	3.5	2319	1 NTC3_RAT	Q9R172 rattus norv

34	698.5	3.5	2437	1 NTC1_BRARE	P46530 brachydanio
35	694.5	3.5	2556	1 NTC1_HUMAN	P46531 homo sapien
36	689.5	3.5	2318	1 NTC3_MOUSE	Q61982 mus musculu
37	677	3.4	606	1 NET1_CHICK	Q90922 gallus gall
38	675.5	3.4	2471	1 NTC2_HUMAN	Q04721 homo sapien
39	675.5	3.4	2703	1 NOTC_DROME	P07207 drosophila
40	670	3.4	604	1 NET1_MOUSE	O09118 mus musculu
41	666	3.4	604	1 NET1_HUMAN	O95631 homo sapien
42	665	3.3	2471	1 NTC2_RAT	Q9GW30 rattus norv
43	654	3.3	612	1 UNC6_CAEEL	P34710 caenorhabdi
44	651	3.3	2524	1 NOTC_XENLA	P21783 xenopus lae
45	649.5	3.3	2470	1 NTC2_MOUSE	O35516 mus musculu

ALIGNMENTS

RESULT 1
LMA5_MOUSE STANDARD; PRT; 3718 AA.
AC Q61001; Q9JHQ6;
DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Laminin alpha-5 chain precursor.
GN LAMA5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-92 FROM N.A., AND SEQUENCE OF 41-46.
RX MEDLINE=21818471; PubMed=11829758;
RA Garbe J.H., Gohring W., Mann K., Timpl R., Sasaki T.;
RT "Complete sequence, recombinant analysis and binding to laminins and
sulphated ligands of the N-terminal domains of laminin alpha3B and
alpha5 chains.";
RL Biochem. J. 362:213-221(2002).
RN [2]
RP SEQUENCE OF 84-3718 FROM N.A.
RX STRAIN=C57BL/6 X CBA; TISSUE=Lung;
MEDLINE=96081906; PubMed=7499364;
RA Miner J.H., Lewis R.M., Sanes J.R.;
RT "Molecular cloning of a novel laminin chain, alpha 5, and widespread
expression in adult mouse tissues.";
RL J. Biol. Chem. 270:28523-28526(1995).
RN [3]
RP REVISIONS.
RA Miner J.H., Lewis R.M., Sanes J.R.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
is thought to mediate the attachment, migration and organization
of cells into tissues during embryonic development by interacting
with other extracellular matrix components.
CC -!- FUNCTION: ALPHA-5 CHAIN MAY BE THE MAJOR LAMININ ALPHA CHAIN OF
ADULT EPITHELIAL AND/OR ENDOTHELIAL BASAL LAMINAE.
CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
different polypeptide chains (alpha, beta, gamma), which are bound
to each other by disulfide bonds into a cross-shaped molecule
comprising one long and three short arms with globules at each
end.
CC -!- SUBCELLULAR LOCATION: Extracellular; found in the basement
membranes (major component).
CC -!- TISSUE SPECIFICITY: In adult, high levels in heart, lung, and
kidney; lower in brain, muscle and testis; very low in liver, gut
and skin. Expressed in many tissues in embryonic day 11.
CC -!- DOMAIN: The alpha-helical domains I and II are thought to interact
with other laminin chains to form a coiled coil structure.
CC -!- DOMAIN: Domains VI, IV and G are globular.
CC -!- SIMILARITY: Contains 1 laminin N-terminal domain.
CC -!- SIMILARITY: Contains 22 laminin EGF-like domains.
CC -!- SIMILARITY: Contains 2 laminin IV domains.
CC -!- SIMILARITY: Contains 5 laminin G-like domains.

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or send an email to license@isb-sib.ch).

CC EMBL; AJ293593; CAB99255.1; -.
CC EMBL; U37501; AAC53430.1; -.
CC PIR; T10053; T10053.
CC HSSP; P02468; 1TLE.
CC MGD; MGI:105382; Lama5.
CC GO; GO:0005604; C:basement membrane; IDA.
CC GO; GO:0005178; F:integrin binding; IDA.
CC GO; GO:0030324; P:lung development; IMP.
CC InterPro; IPR008985; ConA like lec_gl.
CC InterPro; IPR006209; EGF_like.
CC InterPro; IPR008212; Lam_N2.
CC InterPro; IPR000034; Laminin_B.
CC InterPro; IPR002049; Laminin_EGF.
CC InterPro; IPR001791; Laminin_G.
CC InterPro; IPR008211; LamNT.
CC Pfam; PF00052; laminin_B; 1.
CC Pfam; PF00053; laminin_EGF; 17.
CC Pfam; PF00054; laminin_G; 2.
CC Pfam; PF00055; laminin_Nterm; 1.
CC PRINTS; PR00011; EGF_LAMININ.
CC ProDom; PD002082; Lam_N2; 1.
CC ProDom; PD003031; Laminin_B; 1.
CC SMART; SM00180; EGF_Lam; 20.
CC SMART; SM00281; LamB; 1.
CC SMART; SM00282; LamG; 5.
CC SMART; SM00136; LamNT; 1.
CC PROSITE; PS00022; EGF_1; 19.
CC PROSITE; PS01186; EGF_2; 3.
CC PROSITE; PS01248; LAMININ_TYPE_EGF; 19.
CC PROSITE; PS00025; LAM_G_DOMAIN; 5.
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
FT SIGNAL 1 40
FT CHAIN 41 3718 LAMININ ALPHA-5 CHAIN.
FT DOMAIN 41 304 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 305 363 LAMININ EGF-LIKE 1.
FT DOMAIN 364 433 LAMININ EGF-LIKE 2.
FT DOMAIN 434 479 LAMININ EGF-LIKE 3.
FT DOMAIN 500 546 LAMININ EGF-LIKE 4.
FT DOMAIN 547 592 LAMININ EGF-LIKE 5.
FT DOMAIN 593 637 LAMININ EGF-LIKE 6.
FT DOMAIN 638 682 LAMININ EGF-LIKE 7.
FT DOMAIN 683 728 LAMININ EGF-LIKE 8.
FT DOMAIN 729 781 LAMININ EGF-LIKE 9.
FT DOMAIN 782 833 LAMININ EGF-LIKE 10.
FT DOMAIN 834 855 LAMININ EGF-LIKE 11 (INCOMPLETE).
FT DOMAIN 856 1442 LAMININ DOMAIN IV 1 (DOMAIN IV B).
FT DOMAIN 1443 1488 LAMININ EGF-LIKE 12.
FT DOMAIN 1489 1532 LAMININ EGF-LIKE 13.
FT DOMAIN 1533 1581 LAMININ EGF-LIKE 14.
FT DOMAIN 1582 1632 LAMININ EGF-LIKE 15.
FT DOMAIN 1633 1642 LAMININ EGF-LIKE 16 (N-TERMINAL).
FT DOMAIN 1643 1831 LAMININ DOMAIN IV 2 (DOMAIN IV A).
FT DOMAIN 1832 1864 LAMININ EGF-LIKE 17.
FT DOMAIN 1865 1914 LAMININ EGF-LIKE 18.
FT DOMAIN 1915 1970 LAMININ EGF-LIKE 19.
FT DOMAIN 1971 2024 LAMININ EGF-LIKE 20.
FT DOMAIN 2025 2071 LAMININ EGF-LIKE 21.
FT DOMAIN 2072 2118 LAMININ EGF-LIKE 22.
FT DOMAIN 2119 2168 LAMININ EGF-LIKE 23.
FT DOMAIN 2169 2735 DOMAIN II AND I.
FT DOMAIN 2736 2947 LAMININ G-LIKE 1.
FT DOMAIN 2947 3119 LAMININ G-LIKE 2.
FT DOMAIN 3128 3296 LAMININ G-LIKE 3.

FT DOMAIN 3337 3511 LAMININ G-LIKE 4.
FT DOMAIN 3518 3689 LAMININ G-LIKE 5.
FT DOMAIN 2257 2464 COILED COIL (POTENTIAL).
FT DOMAIN 2330 2464 COILED COIL (POTENTIAL).
FT DOMAIN 2604 2621 COILED COIL (POTENTIAL).
FT DOMAIN 2639 2705 COILED COIL (POTENTIAL).
FT SITE 1723 1725 CELL ATTACHMENT SITE (POTENTIAL).
FT SITE 1839 1841 CELL ATTACHMENT SITE (POTENTIAL).
FT DISULFID 305 314 BY SIMILARITY.
FT DISULFID 307 327 BY SIMILARITY.
FT DISULFID 329 338 BY SIMILARITY.
FT DISULFID 341 361 BY SIMILARITY.
FT DISULFID 364 373 BY SIMILARITY.
FT DISULFID 366 398 BY SIMILARITY.
FT DISULFID 401 410 BY SIMILARITY.
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FT DISULFID 500 512 BY SIMILARITY.
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FT DISULFID 523 532 BY SIMILARITY.
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FT DISULFID 547 559 BY SIMILARITY.
FT DISULFID 549 566 BY SIMILARITY.
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FT DISULFID 593 605 BY SIMILARITY.
FT DISULFID 595 611 BY SIMILARITY.
FT DISULFID 613 622 BY SIMILARITY.
FT DISULFID 625 635 BY SIMILARITY.
FT DISULFID 638 650 BY SIMILARITY.
FT DISULFID 640 656 BY SIMILARITY.
FT DISULFID 658 667 BY SIMILARITY.
FT DISULFID 670 680 BY SIMILARITY.
FT DISULFID 683 695 BY SIMILARITY.
FT DISULFID 685 702 BY SIMILARITY.
FT DISULFID 704 713 BY SIMILARITY.
FT DISULFID 716 726 BY SIMILARITY.
FT DISULFID 1443 1455 BY SIMILARITY.
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FT DISULFID 1569 1579 BY SIMILARITY.
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FT DISULFID 1584 1601 BY SIMILARITY.
FT DISULFID 1603 1612 BY SIMILARITY.
FT DISULFID 1615 1630 BY SIMILARITY.
FT DISULFID 1665 1674 BY SIMILARITY.
FT DISULFID 1867 1881 BY SIMILARITY.
FT DISULFID 1884 1893 BY SIMILARITY.
FT DISULFID 1896 1912 BY SIMILARITY.
FT DISULFID 1915 1930 BY SIMILARITY.
FT DISULFID 1917 1939 BY SIMILARITY.
FT DISULFID 1941 1950 BY SIMILARITY.
FT DISULFID 1953 1968 BY SIMILARITY.
FT DISULFID 1971 1986 BY SIMILARITY.
FT DISULFID 1973 1993 BY SIMILARITY.
FT DISULFID 1996 2005 BY SIMILARITY.
FT DISULFID 2008 2022 BY SIMILARITY.
FT DISULFID 2072 2083 BY SIMILARITY.
FT DISULFID 2074 2090 BY SIMILARITY.
FT DISULFID 2092 2101 BY SIMILARITY.
FT DISULFID 2104 2116 BY SIMILARITY.
FT DISULFID 2119 2126 BY SIMILARITY.
FT DISULFID 2121 2133 BY SIMILARITY.
FT DISULFID 2135 2144 BY SIMILARITY.
FT DISULFID 2147 2166 BY SIMILARITY.
FT DISULFID 2169 INTERCHAIN (PROBABLE).

Query Match				100.0%; Score 19876; DB 1; Length 3718;			
Best Local Similarity				100.0%; Pred. No. 0;			
Matches 3635; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
QY	1	DLYCKLVGGPVAGGDPNQTIGQYCDICTAANSNKAHPVSN	60	1	DLYCKLVGGPVAGGDPNQTIGQYCDICTAANSNKAHPVSN	60	
Db	84	DLYCKLVGGPVAGGDPNQTIGQYCDICTAANSNKAHPVSN	143	84	DLYCKLVGGPVAGGDPNQTIGQYCDICTAANSNKAHPVSN	143	
QY	61	YNEVNVTLDLGQVHFVAYVLIKFANSRPPDLWLVERSTDFGHTYQPMQFFASSKRDCLER	120	61	YNEVNVTLDLGQVHFVAYVLIKFANSRPPDLWLVERSTDFGHTYQPMQFFASSKRDCLER	120	
Db	144	YNEVNVTLDLGQVHFVAYVLIKFANSRPPDLWLVERSTDFGHTYQPMQFFASSKRDCLER	203	144	YNEVNVTLDLGQVHFVAYVLIKFANSRPPDLWLVERSTDFGHTYQPMQFFASSKRDCLER	203	
QY	121	FGPRTLERTITODDDVICTEYSRIVPLENGEIVVSLVNGRPGALNFSYLLRDFTKATN	180	121	FGPRTLERTITODDDVICTEYSRIVPLENGEIVVSLVNGRPGALNFSYLLRDFTKATN	180	
Db	204	FGPRTLERTITODDDVICTEYSRIVPLENGEIVVSLVNGRPGALNFSYLLRDFTKATN	263	204	FGPRTLERTITODDDVICTEYSRIVPLENGEIVVSLVNGRPGALNFSYLLRDFTKATN	263	
QY	181	IRLRFRLRTNTLLGHLMGKALRDPVTTRRRYYYYSIKDISIGGRVCVCHGHADYCDADPLDPF	240	181	IRLRFRLRTNTLLGHLMGKALRDPVTTRRRYYYYSIKDISIGGRVCVCHGHADYCDADPLDPF	240	
Db	264	IRLRFRLRTNTLLGHLMGKALRDPVTTRRRYYYYSIKDISIGGRVCVCHGHADYCDADPLDPF	323	264	IRLRFRLRTNTLLGHLMGKALRDPVTTRRRYYYYSIKDISIGGRVCVCHGHADYCDADPLDPF	323	
QY	241	RLQACQHNTCGGSCDRCCPGFNQPKPATTDSANECQSCNCHGHAYDCYDPEVDRRN	300	241	RLQACQHNTCGGSCDRCCPGFNQPKPATTDSANECQSCNCHGHAYDCYDPEVDRRN	300	
Db	324	RLQACQHNTCGGSCDRCCPGFNQPKPATTDSANECQSCNCHGHAYDCYDPEVDRRN	383	324	RLQACQHNTCGGSCDRCCPGFNQPKPATTDSANECQSCNCHGHAYDCYDPEVDRRN	383	
QY	301	ASQNDNVYQGGVCLDCQHHTTGINCERCLPGFFRAPDQLDSPHVCRPCDCESDFTDG	360	301	ASQNDNVYQGGVCLDCQHHTTGINCERCLPGFFRAPDQLDSPHVCRPCDCESDFTDG	360	
Db	384	ASQNDNVYQGGVCLDCQHHTTGINCERCLPGFFRAPDQLDSPHVCRPCDCESDFTDG	443	384	ASQNDNVYQGGVCLDCQHHTTGINCERCLPGFFRAPDQLDSPHVCRPCDCESDFTDG	443	
QY	361	TCEDLTGRICYCRPNFTGELCAACABGYTDFPHCYPLPSFPFHNDTREQVLPAGIIVNCDN	420	361	TCEDLTGRICYCRPNFTGELCAACABGYTDFPHCYPLPSFPFHNDTREQVLPAGIIVNCDN	420	
Db	444	TCEDLTGRICYCRPNFTGELCAACABGYTDFPHCYPLPSFPFHNDTREQVLPAGIIVNCDN	503	444	TCEDLTGRICYCRPNFTGELCAACABGYTDFPHCYPLPSFPFHNDTREQVLPAGIIVNCDN	503	
QY	421	AAGTQGNACRKDPRLGRVCVKPNFRGAHCELCAPEGFHGPSCHPCQCQSSPGVANSLCDPES	480	421	AAGTQGNACRKDPRLGRVCVKPNFRGAHCELCAPEGFHGPSCHPCQCQSSPGVANSLCDPES	480	
Db	504	AAGTQGNACRKDPRLGRVCVKPNFRGAHCELCAPEGFHGPSCHPCQCQSSPGVANSLCDPES	563	504	AAGTQGNACRKDPRLGRVCVKPNFRGAHCELCAPEGFHGPSCHPCQCQSSPGVANSLCDPES	563	
QY	481	GQCMRTGFEGDRCDHICALGYFHFPLCQLCGCSPAGTLPPEGDEAGRCQCRCRPFDPGPHCD	540	481	GQCMRTGFEGDRCDHICALGYFHFPLCQLCGCSPAGTLPPEGDEAGRCQCRCRPFDPGPHCD	540	
Db	564	GQCMRTGFEGDRCDHICALGYFHFPLCQLCGCSPAGTLPPEGDEAGRCQCRCRPFDPGPHCD	623	564	GQCMRTGFEGDRCDHICALGYFHFPLCQLCGCSPAGTLPPEGDEAGRCQCRCRPFDPGPHCD	623	
QY	541	RCLPGYHGYPDCHACACDPRGALDQOCGVGGLCHCRPONTGATCOECSPGFYFPSPCIPC	600	541	RCLPGYHGYPDCHACACDPRGALDQOCGVGGLCHCRPONTGATCOECSPGFYFPSPCIPC	600	
Db	624	RCLPGYHGYPDCHACACDPRGALDQOCGVGGLCHCRPONTGATCOECSPGFYFPSPCIPC	683	624	RCLPGYHGYPDCHACACDPRGALDQOCGVGGLCHCRPONTGATCOECSPGFYFPSPCIPC	683	
QY	601	HCSADGSLHTTCDPTTGQCRPRVTGLHCDMCPVPGAYNFPYCEAGSCHPAGLAPANPAL	660	601	HCSADGSLHTTCDPTTGQCRPRVTGLHCDMCPVPGAYNFPYCEAGSCHPAGLAPANPAL	660	
Db	684	HCSADGSLHTTCDPTTGQCRPRVTGLHCDMCPVPGAYNFPYCEAGSCHPAGLAPANPAL	743	684	HCSADGSLHTTCDPTTGQCRPRVTGLHCDMCPVPGAYNFPYCEAGSCHPAGLAPANPAL	743	
QY	661	PETQAPCMCRAHVEGPSDCRCKPGYWGLSASNPEGCTRCSDPRGTLGGVTECQNGQCF	720	661	PETQAPCMCRAHVEGPSDCRCKPGYWGLSASNPEGCTRCSDPRGTLGGVTECQNGQCF	720	
Db	744	PETQAPCMCRAHVEGPSDCRCKPGYWGLSASNPEGCTRCSDPRGTLGGVTECQNGQCF	803	744	PETQAPCMCRAHVEGPSDCRCKPGYWGLSASNPEGCTRCSDPRGTLGGVTECQNGQCF	803	
QY	721	CKAHVCGKTCACAKDGFGLDYADYFGCRSCRCDVGGALGQGCCEPKTGACRCRPNTOGPT	780	721	CKAHVCGKTCACAKDGFGLDYADYFGCRSCRCDVGGALGQGCCEPKTGACRCRPNTOGPT	780	
Db	804	CKAHVCGKTCACAKDGFGLDYADYFGCRSCRCDVGGALGQGCCEPKTGACRCRPNTOGPT	863	804	CKAHVCGKTCACAKDGFGLDYADYFGCRSCRCDVGGALGQGCCEPKTGACRCRPNTOGPT	863	
QY	781	CSEPAKDHYLPDLHMRLELEBAATPEGHVRFGFNPLEFENFSWRGYAHMMAIQPRIVA	840	781	CSEPAKDHYLPDLHMRLELEBAATPEGHVRFGFNPLEFENFSWRGYAHMMAIQPRIVA	840	
Db	864	CSEPAKDHYLPDLHMRLELEBAATPEGHVRFGFNPLEFENFSWRGYAHMMAIQPRIVA	923	864	CSEPAKDHYLPDLHMRLELEBAATPEGHVRFGFNPLEFENFSWRGYAHMMAIQPRIVA	923	
QY	841	RLNVTSPDLFRLVFRYVNRGSTSVNGQISVREEGKLSSCTNCTEQSQPVAFPPSTEPAFV	900	841	RLNVTSPDLFRLVFRYVNRGSTSVNGQISVREEGKLSSCTNCTEQSQPVAFPPSTEPAFV	900	
Db	924	RLNVTSPDLFRLVFRYVNRGSTSVNGQISVREEGKLSSCTNCTEQSQPVAFPPSTEPAFV	983	924	RLNVTSPDLFRLVFRYVNRGSTSVNGQISVREEGKLSSCTNCTEQSQPVAFPPSTEPAFV	983	
QY	901	TVPQSGFGEPPFVLPNGIIMWVLAEGVLLDYVLLPSTYEAALLQHRVTEACTYRPSAL	960	901	TVPQSGFGEPPFVLPNGIIMWVLAEGVLLDYVLLPSTYEAALLQHRVTEACTYRPSAL	960	
Db	984	TVPQSGFGEPPFVLPNGIIMWVLAEGVLLDYVLLPSTYEAALLQHRVTEACTYRPSAL	1043	984	TVPQSGFGEPPFVLPNGIIMWVLAEGVLLDYVLLPSTYEAALLQHRVTEACTYRPSAL	1043	
QY	961	HSTENCLVYAHLPDLGFPSPAAGTEALCRHDNSLRPCPTTEQLSPSHPLATCFGSDVDIQ	1020	961	HSTENCLVYAHLPDLGFPSPAAGTEALCRHDNSLRPCPTTEQLSPSHPLATCFGSDVDIQ	1020	
Db	1044	HSTENCLVYAHLPDLGFPSPAAGTEALCRHDNSLRPCPTTEQLSPSHPLATCFGSDVDIQ	1103	1044	HSTENCLVYAHLPDLGFPSPAAGTEALCRHDNSLRPCPTTEQLSPSHPLATCFGSDVDIQ	1103	

QY	1021	LEMAVFPQGGYVLVVEYVGEDSHQEMGVAVHTPQAPQQGVNLNHPCPYSSSLCRSPARDT	1080	1021	LEMAVFPQGGYVLVVEYVGEDSHQEMGVAVHTPQAPQQGVNLNHPCPYSSSLCRSPARDT	1080	
Db	1104	LEMAVFPQGGYVLVVEYVGEDSHQEMGVAVHTPQAPQQGVNLNHPCPYSSSLCRSPARDT	1163	1104	LEMAVFPQGGYVLVVEYVGEDSHQEMGVAVHTPQAPQQGVNLNHPCPYSSSLCRSPARDT	1163	
QY	1081	QHHLAIFHLDSIASIRLTAEQAFFLHSHVTLVPVEEFSTEFVEPRVFCVSSHGTENPSSA	1140	1081	QHHLAIFHLDSIASIRLTAEQAFFLHSHVTLVPVEEFSTEFVEPRVFCVSSHGTENPSSA	1140	
Db	1164	QHHLAIFHLDSIASIRLTAEQAFFLHSHVTLVPVEEFSTEFVEPRVFCVSSHGTENPSSA	1223	1164	QHHLAIFHLDSIASIRLTAEQAFFLHSHVTLVPVEEFSTEFVEPRVFCVSSHGTENPSSA	1223	
QY	1141	ACLASRFPKPPQPIILKDCQVLPPLPDLPLTQSQELSPGAPPEGPQRPPTAVDPNAEPT	1200	1141	ACLASRFPKPPQPIILKDCQVLPPLPDLPLTQSQELSPGAPPEGPQRPPTAVDPNAEPT	1200	
Db	1224	ACLASRFPKPPQPIILKDCQVLPPLPDLPLTQSQELSPGAPPEGPQRPPTAVDPNAEPT	1283	1224	ACLASRFPKPPQPIILKDCQVLPPLPDLPLTQSQELSPGAPPEGPQRPPTAVDPNAEPT	1283	
QY	1201	LLRHPQGTWFTTQVPTLGRYAFLLHGYQPVHPSPFVVEVLINGGRIWQGHANASFCPHGY	1260	1201	LLRHPQGTWFTTQVPTLGRYAFLLHGYQPVHPSPFVVEVLINGGRIWQGHANASFCPHGY	1260	
Db	1284	LLRHPQGTWFTTQVPTLGRYAFLLHGYQPVHPSPFVVEVLINGGRIWQGHANASFCPHGY	1343	1284	LLRHPQGTWFTTQVPTLGRYAFLLHGYQPVHPSPFVVEVLINGGRIWQGHANASFCPHGY	1343	
QY	1261	GCRTLVLCEGQTMLDVTDNELTIVTVRVEGRWLWLDYVLIIVPEDAYSSSYLQEEPLDKSY	1320	1261	GCRTLVLCEGQTMLDVTDNELTIVTVRVEGRWLWLDYVLIIVPEDAYSSSYLQEEPLDKSY	1320	
Db	1344	GCRTLVLCEGQTMLDVTDNELTIVTVRVEGRWLWLDYVLIIVPEDAYSSSYLQEEPLDKSY	1403	1344	GCRTLVLCEGQTMLDVTDNELTIVTVRVEGRWLWLDYVLIIVPEDAYSSSYLQEEPLDKSY	1403	
QY	1321	DFISHCATQGYHISPSSSSPFCRNAATSLSLFYNNGALPCGCHEVGAVSPTCEPFGGQCP	1380	1321	DFISHCATQGYHISPSSSSPFCRNAATSLSLFYNNGALPCGCHEVGAVSPTCEPFGGQCP	1380	
Db	1404	DFISHCATQGYHISPSSSSPFCRNAATSLSLFYNNGALPCGCHEVGAVSPTCEPFGGQCP	1463	1404	DFISHCATQGYHISPSSSSPFCRNAATSLSLFYNNGALPCGCHEVGAVSPTCEPFGGQCP	1463	
QY	1381	CRGHVIGRDCSRCATGYWGFNCRPCDCGARLCELTGQCICPPRTVPPDCLVCQPSFG	1440	1381	CRGHVIGRDCSRCATGYWGFNCRPCDCGARLCELTGQCICPPRTVPPDCLVCQPSFG	1440	
Db	1464	CRGHVIGRDCSRCATGYWGFNCRPCDCGARLCELTGQCICPPRTVPPDCLVCQPSFG	1523	1464	CRGHVIGRDCSRCATGYWGFNCRPCDCGARLCELTGQCICPPRTVPPDCLVCQPSFG	1523	
QY	1441	CHPLVGCCECNCSPGVQELTDPTCDMDSGQCRCPNVAGRRCDTCAFGFYGYPSCRPCD	1500	1441	CHPLVGCCECNCSPGVQELTDPTCDMDSGQCRCPNVAGRRCDTCAFGFYGYPSCRPCD	1500	
Db	1524	CHPLVGCCECNCSPGVQELTDPTCDMDSGQCRCPNVAGRRCDTCAFGFYGYPSCRPCD	1583	1524	CHPLVGCCECNCSPGVQELTDPTCDMDSGQCRCPNVAGRRCDTCAFGFYGYPSCRPCD	1583	
QY	1501	CHEAGTNASVCDPLTGQCHCKENVQGSRCDCQVRGTFSLDAANPKGCTRCFCFGATERCG	1560	1501	CHEAGTNASVCDPLTGQCHCKENVQGSRCDCQVRGTFSLDAANPKGCTRCFCFGATERCG	1560	
Db	1584	CHEAGTNASVCDPLTGQCHCKENVQGSRCDCQVRGTFSLDAANPKGCTRCFCFGATERCG	1643	1584	CHEAGTNASVCDPLTGQCHCKENVQGSRCDCQVRGTFSLDAANPKGCTRCFCFGATERCG	1643	
QY	1561	NSNLARHEFVDMEGWLLSSDRQVVPHEHRPEIELLHADLRSVADTFSELYWQAPPSYLG	1620	1561	NSNLARHEFVDMEGWLLSSDRQVVPHEHRPEIELLHADLRSVADTFSELYWQAPPSYLG	1620	
Db	1644	NSNLARHEFVDMEGWLLSSDRQVVPHEHRPEIELLHADLRSVADTFSELYWQAPPSYLG	1703	1644	NSNLARHEFVDMEGWLLSSDRQVVPHEHRPEIELLHADLRSVADTFSELYWQAPPSYLG	1703	
QY	1621	DRVSSYCGTLHYELHSETQRGDIPIPIYESRDPDVVLQGNQMSIAFLELAYPPPGQVHRGQL	1680	1621	DRVSSYCGTLHYELHSETQRGDIPIPIYESRDPDVVLQGNQMSIAFLELAYPPPGQVHRGQL	1680	
Db	1704	DRVSSYCGTLHYELHSETQRGDIPIPIYESRDPDVVLQGNQMSIAFLELAYPPPGQVHRGQL	1763	1704	DRVSSYCGTLHYELHSETQRGDIPIPIYESRDPDVVLQGNQMSIAFLELAYPPPGQVHRGQL	1763	
QY	1681	QVVEGNFRHLETHNPVSREELMMVLAGEQLQIRALFSQTSSSVSLRRVVLEVAASEARG	1740	1681	QVVEGNFRHLETHNPVSREELMMVLAGEQLQIRALFSQTSSSVSLRRVVLEVAASEARG	1740	
Db	1764	QVVEGNFRHLETHNPVSREELMMVLAGEQLQIRALFSQTSSSVSLRRVVLEVAASEARG	1823	1764	QVVEGNFRHLETHNPVSREELMMVLAGEQLQIRALFSQTSSSVSLRRVVLEVAASEARG	1823	
QY	1741	PPASNVELCMCPANYRGDSCQECAPGYRDTKGLFLGRCPVQCCHGSHSDRCLPSSGICVVG	1800	1741	PPASNVELCMCPANYRGDSCQECAPGYRDTKGLFLGRCPVQCCHGSHSDRCLPSSGICVVG	1800	
Db	1824	PPASNVELCMCPANYRGDSCQECAPGYRDTKGLFLGRCPVQCCHGSHSDRCLPSSGICVVG	1883	1824	PPASNVELCMCPANYRGDSCQECAPGYRDTKGLFLGRCPVQCCHGSHSDRCLPSSGICVVG	1883	
QY	1801	CQHNTEGDQECRCRPGFVSSDPSPNPASPCVSCPCPLAVPSNNFADGCVLRNGRTQCLCRP	1860	1801	CQHNTEGDQECRCRPGFVSSDPSPNPASPCVSCPCPLAVPSNNFADGCVLRNGRTQCLCRP	1860	
Db	1884	CQHNTEGDQECRCRPGFVSSDPSPNPASPCVSCPCPLAVPSNNFADGCVLRNGRTQCLCRP	1943	1884	CQHNTEGDQECRCRPGFVSSDPSPNPASPCVSCPCPLAVPSNNFADGCVLRNGRTQCLCRP	1943	
QY	1861	GYAGASCERCAPGFFGNPLVLGSSCQPCDCSGNGDPNMI FSDCDPLTGACRGCLRHTTGP	1920	1861	GYAGASCERCAPGFFGNPLVLGSSCQPCDCSGNGDPNMI FSDCDPLTGACRGCLRHTTGP	1920	
Db	1944	GYAGASCERCAPGFFGNPLVLGSSCQPCDCSGNGDPNMI FSDCDPLTGACRGCLRHTTGP	2003	1944	GYAGASCERCAPGFFGNPLVLGSSCQPCDCSGNGDPNMI FSDCDPLTGACRGCLRHTTGP	2003	
QY	1921	HCERCAPGYGNALLPGNCTRCDCSPCGTETCDPQSGRCCLCKAGVTGQRCDCRCLEGYFGF	1980	1921	HCERCAPGYGNALLPGNCTRCDCSPCGTETCDPQSGRCCLCKAGVTGQRCDCRCLEGYFGF	1980	
Db	2004	HCERCAPGYGNALLPGNCTRCDCSPCGTETCDPQSGRCCLCKAGVTGQRCDCRCLEGYFGF	2063	2004	HCERCAPGYGNALLPGNCTRCDCSPCGTETCDPQSGRCCLCKAGVTGQRCDCRCLEGYFGF	2063	
QY	1981	EQCQGCRCPCACGPAAGKSECHPOSQCHCQPGTGTGPOCLCECAPGYWGLPEKGCRRCCQCP	2040	1981	EQCQGCRCPCACGPAAGKSECHPOSQCHCQPGTGTGPOCLCECAPGYWGLPEKGCRRCCQCP	2040	
Db	2064	EQCQGCRCPCACGPAAGKSECHPOSQCHCQPGTGTGPOCLCECAPGYWGLPEKGCRRCCQCP	2123	2064	EQCQGCRCPCACGPAAGKSECHPOSQCHCQPGTGTGPOCLCECAPGYWGLPEKGCRRCCQCP	2123	
QY	2041	GHCDEHTGHCTCPPGLSGERCDTCSQQHQVVPVPGKPGGHGHCHEVCDHCWVLLDLDLERA	2100	2041	GHCDEHTGHCTCPPGLSGERCDTCSQQHQVVPVPGKPGGHGHCHEVCDHCWVLLDLDLERA	2100	
Db	2124	GHCDEHTGHCTCPPGLSGERCDTCSQQHQVVPVPGKPGGHGHCHEVCDHCWVLLDLDLERA	2183	2124	GHCDEHTGHCTCPPGLSGERCDTCSQQHQVVPVPGKPGGHGHCHEVCDHCWVLLDLDLERA	2183	
QY	2101	GALLPAIREQLQGINASSAAWALHRLNASIADLQSLRRPPGPRYQAAQQLQTLEQSI	2160	2101	GALLPAIREQLQGINASSAAWALHRLNASIADLQSLRRPPGPRYQAAQQLQTLEQSI	2160	

Db 2184 GALLPAIREQLOGINASSAAWALHRLNINASIADLQSKLRPPGPRYQAAQQLQLEQOSI 2243
QY 2161 SLQODTERLGSOATGVQAGQQLDTESTLGRAQKLLSVRAVGRALNELASRMQGGSP 2220
Db 2244 SLQODTERLGSOATGVQAGQQLDTESTLGRAQKLLSVRAVGRALNELASRMQGGSP 2303
QY 2221 GDALVPSGEQLRWALAEVERLLWDMRTRDLGAQGAFAEAEALAEQRLMARVQEOITSFWE 2280
Db 2304 GDALVPSGEQLRWALAEVERLLWDMRTRDLGAQGAFAEAEALAEQRLMARVQEOITSFWE 2363
QY 2281 ENQSLATHIRDOLAQYESGLMDLREALNQAVNTTREAEEELNSRNQERVKEALQWKQELSQ 2340
Db 2364 ENQSLATHIRDOLAQYESGLMDLREALNQAVNTTREAEEELNSRNQERVKEALQWKQELSQ 2423
QY 2341 DNATLKATLOASLILGHVSELLOGIDQAKEDLEHLAASLDGAWTPLLKRMQAFSPASSK 2400
Db 2424 DNATLKATLOASLILGHVSELLOGIDQAKEDLEHLAASLDGAWTPLLKRMQAFSPASSK 2483
QY 2401 VDLVEAAEAHAQKLNQALAINLSGIIILGINQDRFIQRAVEASNAYSSILQAVQAAEDAAGQ 2460
Db 2484 VDLVEAAEAHAQKLNQALAINLSGIIILGINQDRFIQRAVEASNAYSSILQAVQAAEDAAGQ 2543
QY 2461 ALRQASRTWVQVQGLAAGARQLLANSSALEETILGHQGRGLGAQRLQAGIQLHNVM 2520
Db 2544 ALRQASRTWVQVQGLAAGARQLLANSSALEETILGHQGRGLGAQRLQAGIQLHNVM 2603
QY 2521 ARKNQLAQIQBAQAMLAMDTSETSEKIAHAKAVAAEALSTATHVOSQLOGMKNVERWQ 2580
Db 2604 ARKNQLAQIQBAQAMLAMDTSETSEKIAHAKAVAAEALSTATHVOSQLOGMKNVERWQ 2663
QY 2581 SQLGGLOGQDLSOVERDASSSVSTLEKTLPLQLLAKLSRLNKGVHNASLALSANIGRVRK 2640
Db 2664 SQLGGLOGQDLSOVERDASSSVSTLEKTLPLQLLAKLSRLNKGVHNASLALSANIGRVRK 2723
QY 2641 LIAQARSAASKVKVSMKFNRSRGVRLRPPRDADLAAYTALKFHIQSPVPAPEPGKNTGD 2700
Db 2724 LIAQARSAASKVKVSMKFNRSRGVRLRPPRDADLAAYTALKFHIQSPVPAPEPGKNTGD 2783
QY 2701 HFVLYMGSRQATGDMGVSLRNQKVHWYRLGKAGPTTILSIDENIGEQAFAVSDRTLOF 2760
Db 2784 HFVLYMGSRQATGDMGVSLRNQKVHWYRLGKAGPTTILSIDENIGEQAFAVSDRTLOF 2843
QY 2761 GHMSVTVEKQWVHEIKGDTVAPGSEGLNLNHPDDDFVYVGGYPSNFTPPPELRFPGYLGC 2820
Db 2844 GHMSVTVEKQWVHEIKGDTVAPGSEGLNLNHPDDDFVYVGGYPSNFTPPPELRFPGYLGC 2903
QY 2821 IEMETLNEEVSYLYNFEQTFMLDTAVDKPCARSKATGDPWLTDGSLYDGSFARISFEKQ 2880
Db 2904 IEMETLNEEVSYLYNFEQTFMLDTAVDKPCARSKATGDPWLTDGSLYDGSFARISFEKQ 2963
QY 2881 FSNTKRFQDQBLRLVSYNGIIFFLKQESQFLCLAVQEGTLVLFYDFGSLGKADPLQPPQA 2940
Db 2964 FSNTKRFQDQBLRLVSYNGIIFFLKQESQFLCLAVQEGTLVLFYDFGSLGKADPLQPPQA 3023
QY 2941 LTAASKAIQVFLLAGNRKRVLRVERATVFSVDQDNMLEMADAYYLGVPPEQLPLSLRQ 3000
Db 3024 LTAASKAIQVFLLAGNRKRVLRVERATVFSVDQDNMLEMADAYYLGVPPEQLPLSLRQ 3083
QY 3001 LFPSSGGSVRCIKGKIKALGVYVDLKRNLNTTGISFGCTADLLVGRMTWTFHGHGFLPLALPD 3060
Db 3084 LFPSSGGSVRCIKGKIKALGVYVDLKRNLNTTGISFGCTADLLVGRMTWTFHGHGFLPLALPD 3143
QY 3061 VAPITEVYSGFGFRGTQDNNLLYRTSPDGPYQVSLRGHVTTLRFMNQEVETQRFVADG 3120
Db 3144 VAPITEVYSGFGFRGTQDNNLLYRTSPDGPYQVSLRGHVTTLRFMNQEVETQRFVADG 3203
QY 3121 APHYVAFYSNVTGVWLYVDDQLQVKSHERTTTMLQLOPEEPSRLLGLGFLPVSGTFHNFS 3180
Db 3204 APHYVAFYSNVTGVWLYVDDQLQVKSHERTTTMLQLOPEEPSRLLGLGFLPVSGTFHNFS 3263
QY 3181 GCISNVFQRLRGPRVFDLHQNMGSVNVSVGCTPAQLIETSRATAQKVSRRSRQPSQDL 3240

Db 3264 GCISNVFQRLRGPRVFDLHQNMGSVNVSVGCTPAQLIETSRATAQKVSRRSRQPSQDL 3323
QY 3241 ACTTLPWLPGTIQDAYQFGGGLPSYLFQVIGISPSHRNRLHLSMLVRPHAAASQGLLLSTAPM 3300
Db 3324 ACTTLPWLPGTIQDAYQFGGGLPSYLFQVIGISPSHRNRLHLSMLVRPHAAASQGLLLSTAPM 3383
QY 3301 SGRSPSLVFLNHHGFVAQTEGPPRLQVQSRQHSRAGQWHRVSVRWGMQQIQLVVDGSQ 3360
Db 3384 SGRSPSLVFLNHHGFVAQTEGPPRLQVQSRQHSRAGQWHRVSVRWGMQQIQLVVDGSQ 3443
QY 3361 TWSQKALHHRVPRABRPQPYTTLVSGGLPASSYSSKLPVSVGFSGCLKKLQLDKQPLRTP 3420
Db 3444 TWSQKALHHRVPRABRPQPYTTLVSGGLPASSYSSKLPVSVGFSGCLKKLQLDKQPLRTP 3503
QY 3421 QMVGVTPCVSGPLEDGLFFPGSEGVVTTLELPKAKMPYVSLELEMRPLAAAGLIFHLGQAL 3480
Db 3504 QMVGVTPCVSGPLEDGLFFPGSEGVVTTLELPKAKMPYVSLELEMRPLAAAGLIFHLGQAL 3563
QY 3481 ATPYMQLVKLTQEVLLQANDGAGEFSTWVTYPKLCGRWHRVAVIMGRDRTLRLVDTQSN 3540
Db 3564 ATPYMQLVKLTQEVLLQANDGAGEFSTWVTYPKLCGRWHRVAVIMGRDRTLRLVDTQSN 3623
QY 3541 HTTGRLPESLAGSPALLHLGSLPKSSTARPELPAYRGCLRKLLINGAPVNVTSVQIQGA 3600
Db 3624 HTTGRLPESLAGSPALLHLGSLPKSSTARPELPAYRGCLRKLLINGAPVNVTSVQIQGA 3683
QY 3601 VGMRGCPSPGTLALSQKQKALTQORHAKPSVSPLLWH 3635
Db 3684 VGMRGCPSPGTLALSQKQKALTQORHAKPSVSPLLWH 3718

RESULT 2
LMA5_HUMAN
ID LMA5_HUMAN STANDARD; PRT; 3695 AA.
AC O15230; Q8WZA7; Q9H1P1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Laminin alpha-5 chain precursor.
GN LMA5 OR KIAA0533 OR KIAA1907.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehaeslaih M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McMay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Williams S.A.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";

RL Nature 414:865-871(2001).
RN [2]
RP SEQUENCE OF 197-1934 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=21456161; PubMed=11572484;
RA Nagase T., Kikuno R., Ohara O.;
RT "prediction of the coding sequences of unidentified human genes. XXI.
RT The complete sequences of 60 new cDNA clones from brain which code for
RT large proteins.";
RL DNA Res. 8:179-187(2001).
RN [3]
RP SEQUENCE OF 2051-3695 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98290545; PubMed=9628581;
RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
RA Nomura N., Ohara O.;
RT "prediction of the coding sequences of unidentified human genes. IX.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.";
RL DNA Res. 5:31-39(1998).
RN [4]
RP SEQUENCE OF 2743-3695 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=97415425; PubMed=9271224;
RA Durkin M.E., Loechel F., Mattei M.-G., Gilpin B.J., Albrechtsen R.,
RA Wewer U.M.;
RT "Tissue-specific expression of the human laminin alpha5-chain, and
RT mapping of the gene to human chromosome 20q13.2-13.3 and to distal
RT mouse chromosome 2 near the locus for the ragged (Ra) mutation.";
RL FEBS Lett. 411:296-300(1997).
RN [5]
RP EXPRESSION IN RETINA.
RX MEDLINE=20422761; PubMed=10964957;
RA Libby R.T., Champilaud M.-F., Claudepierre T., Xu Y., Gibbons E.P.,
RA Koch M., Burgess R.E., Hunter D.D., Brunken W.J.;
RT "Laminin expression in adult and developing retinae: evidence of two
RT novel CNS laminins.";
RL J. Neurosci. 20:6517-6528(2000).
RN [6]
RP -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
RP is thought to mediate the attachment, migration and organization
RP of cells into tissues during embryonic development by interacting
RP with other extracellular matrix components.
RN [7]
RP -!- SUBUNIT: Laminin-15 complex is an heterotrimer composed of three
RP chains (alpha-5/beta-2/gamma-3) which are bound to each other by
RP disulfide bonds into a cross-shaped molecule comprising one long
RP and three short arms with globules at each end.
RN [8]
RP -!- SUBCELLULAR LOCATION: Extracellular; found in the basement
RP membranes (major component).
RN [9]
RP -!- TISSUE SPECIFICITY: Expressed in heart, lung, kidney, skeletal
RP muscle, pancreas, retina and placenta. Little or no expression in
RP brain and liver.
RN [10]
RP -!- DOMAIN: Domain G is globular and is part of the major cell-binding
RP site located in the long arm of the laminin heterotrimer.
RN [11]
RP -!- SIMILARITY: Contains 1 laminin N-terminal domain.
RN [12]
RP -!- SIMILARITY: Contains 22 laminin EGF-like domains.
RN [13]
RP -!- SIMILARITY: Contains 2 laminin IV domains.
RN [14]
RP -!- SIMILARITY: Contains 5 laminin G-like domains.
RN [15]
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RN [16]
RP -----
RP EMBL; AL354836; CAC22309.1; ALT_SEQ.
RP EMBL; AL354836; CAC22310.1; -.
RP EMBL; AB067494; BAB67800.1; -.
RP EMBL; AB011105; BAA25459.1; -.
RP EMBL; Z95636; CAB09137.1; -.
RP HSSP; P02468; 1KLO.
RP Genew; HGNC:6485; LAMA5.

DR MIM; 601033; -.
DR InterPro; IPR008985; ConA like_lec_gl.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR008212; Lam_N2.
DR InterPro; IPR000034; Laminin_B.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR008211; LamNT.
DR Pfam; PF00052; laminin_B; 1.
DR Pfam; PF00053; laminin_EGF; 18.
DR Pfam; PF00054; laminin_G; 2.
DR Pfam; PF00055; laminin_Nterm; 1.
DR PRINTS; PR00011; EGF_LAMININ.
DR PRODom; PD002082; Lam_N2; 1.
DR PRODom; PD003031; Laminin_B; 1.
DR SMART; SM00180; EGF_Lam; 20.
DR SMART; SM00281; LamB; 1.
DR SMART; SM00282; LamG; 5.
DR SMART; SM00136; LamNT; 1.
DR PROSITE; PS00022; EGF_1; 19.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 19.
DR PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
FT SIGNAL 1 35 POTENTIAL.
FT CHAIN 36 3695 LAMININ ALPHA-5 CHAIN.
FT DOMAIN 36 299 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 300 358 LAMININ EGF-LIKE 1.
FT DOMAIN 359 428 LAMININ EGF-LIKE 2.
FT DOMAIN 429 474 LAMININ EGF-LIKE 3.
FT DOMAIN 494 540 LAMININ EGF-LIKE 4.
FT DOMAIN 541 586 LAMININ EGF-LIKE 5.
FT DOMAIN 587 631 LAMININ EGF-LIKE 6.
FT DOMAIN 632 676 LAMININ EGF-LIKE 7.
FT DOMAIN 677 722 LAMININ EGF-LIKE 8.
FT DOMAIN 723 775 LAMININ EGF-LIKE 9.
FT DOMAIN 776 828 LAMININ EGF-LIKE 10. (INCOMPLETE).
FT DOMAIN 829 850 LAMININ EGF-LIKE 11 (DOMAIN IV B).
FT DOMAIN 851 1437 LAMININ DOMAIN IV 1 (DOMAIN IV B).
FT DOMAIN 1438 1483 LAMININ EGF-LIKE 12.
FT DOMAIN 1484 1527 LAMININ EGF-LIKE 13.
FT DOMAIN 1528 1576 LAMININ EGF-LIKE 14.
FT DOMAIN 1577 1627 LAMININ EGF-LIKE 15.
FT DOMAIN 1628 1637 LAMININ EGF-LIKE 16 (N-TERMINAL).
FT DOMAIN 1638 1830 LAMININ DOMAIN IV 2 (DOMAIN IV A).
FT DOMAIN 1831 1864 LAMININ EGF-LIKE 16 (C-TERMINAL).
FT DOMAIN 1864 1912 LAMININ EGF-LIKE 17.
FT DOMAIN 1913 1968 LAMININ EGF-LIKE 18.
FT DOMAIN 1969 2022 LAMININ EGF-LIKE 19.
FT DOMAIN 2023 2069 LAMININ EGF-LIKE 20.
FT DOMAIN 2070 2116 LAMININ EGF-LIKE 21.
FT DOMAIN 2117 2166 LAMININ EGF-LIKE 22.
FT DOMAIN 2167 2735 DOMAIN II AND I.
FT DOMAIN 2736 2929 LAMININ G-LIKE 1.
FT DOMAIN 2941 3115 LAMININ G-LIKE 2.
FT DOMAIN 3124 3292 LAMININ G-LIKE 3.
FT DOMAIN 3340 3513 LAMININ G-LIKE 4.
FT DOMAIN 3520 3692 LAMININ G-LIKE 5.
FT DOMAIN 2203 2221 COILED COIL (POTENTIAL).
FT DOMAIN 2335 2466 COILED COIL (POTENTIAL).
FT DOMAIN 2510 2670 COILED COIL (POTENTIAL).
FT SITE 1722 1724 CELL ATTACHMENT SITE (POTENTIAL).
FT SITE 1838 1840 CELL ATTACHMENT SITE (POTENTIAL).
FT DISULFID 300 309 BY SIMILARITY.
FT DISULFID 302 322 BY SIMILARITY.
FT DISULFID 324 333 BY SIMILARITY.
FT DISULFID 336 356 BY SIMILARITY.
FT DISULFID 359 368 BY SIMILARITY.
FT DISULFID 361 393 BY SIMILARITY.
FT DISULFID 396 405 BY SIMILARITY.
FT DISULFID 408 426 BY SIMILARITY.
FT DISULFID 429 440 BY SIMILARITY.

FT	DISULFID	431	447	BY SIMILARITY.
FT	DISULFID	449	458	BY SIMILARITY.
FT	DISULFID	461	471	BY SIMILARITY.
FT	DISULFID	494	506	BY SIMILARITY.
FT	DISULFID	496	515	BY SIMILARITY.
FT	DISULFID	517	526	BY SIMILARITY.
FT	DISULFID	529	538	BY SIMILARITY.
FT	DISULFID	541	553	BY SIMILARITY.
FT	DISULFID	543	560	BY SIMILARITY.
FT	DISULFID	562	571	BY SIMILARITY.
FT	DISULFID	574	584	BY SIMILARITY.
FT	DISULFID	587	599	BY SIMILARITY.
FT	DISULFID	589	605	BY SIMILARITY.
FT	DISULFID	607	616	BY SIMILARITY.
Query Match 79.7%; Score 15847; DB 1; Length 3695;				
Best Local Similarity 79.4%; Pred. No. 0;				
Matches 2876; Conservative 276; Mismatches 451; Indels 18; Gaps 8;				
QY	1	DLYCKLVGGPVAGGDPNQTIQGYCDICTAANSNKAHPVSNNAIDGTERWQSPPLSRGLE	60	
DB	79	DLYCKLVGGPVAGGDPNQTIQGYCDICTAANSNKAHPASNAIDGTERWQSPPLSRGLE	138	
QY	61	YNEVNTLDLQGVFHVAYVLIKFAANSRPRDLWVLERSTDFGTYQPWFASFRRDCLER	120	
DB	139	YNEVNTLDLQGVFHVAYVLIKFAANSRPRDLWVLESMDFRTYQPWFASFRRDCLER	198	
QY	121	FGPRTLERITQDDVICTTEYSRIVPLENGEIVVSLVNGRPGALNFYSPLLRDFTKATN	180	
DB	199	FGPQTLERITRDAACITTEYSRIVPLENGEIVVSLVNGRPGAMNFYSPLLRFTKATN	258	
QY	181	IRLRLRINTLLGLMKGALRDPVTTRRYYSIKDISIGRCVCHGHADVCDKADPLDPF	240	
DB	259	VRLRLRINTLLGLMKGALRDPVTTRRYYSIKDISIGRCVCHGHADACADKADPLDPF	318	
QY	241	RLQACQHNTOGSCDRCCPGFNQOPWKPATDTSANECSCNCHGHAYDCCYDPEVDRRN	300	
DB	319	RLQCTQHNTCGTCDRCPCPGFNQOPWKPATANSANECSCNCHGHATDCYDPEVDRR	378	
QY	301	ASQNDNVYQGGVCLDCQHHTTGINCERCLPGFFRAPDQPLDSEPHVCRPCDESDFTDG	360	
DB	379	ASQSLDGTQGGVCLDCQHHTTGINCERCLPGFYRSPNHLPLDSEPHVCRRCNCESTFDG	438	
QY	361	TCEDLTGRCYCRPNFTGELCAACAEVYTDFFHCYPLSPFPHNDTREQLVPAQIVNCDN	420	
DB	439	TCEDLTGRCYCRPNFSGERCDCVCAEGFTGFPSCYPTPS-SSNDTREQLVPAQIVNCDN	497	
QY	421	AAGTQGNACKRDPRLGRVCVKNPFRGAHCELCAPGFHGPSCHPCQCSSPGVANSLCDPES	480	
DB	498	AAGTQGNACKRDPRLVGRCLCKPNFQTHCELCAPGFHGPSCHPCQCSSPGVANSLCDPES	557	
QY	481	GQCMRTGEGDRCDHCHALGYTHFPLCQCGSPAGTLPEGCEAGRCQCRPGFDGPHCD	540	
DB	558	GQCRVRVPEGATCDRCAPGYTHFPLCQCGSPAGTLPEGCEAGRCQCRPGFDGPHCD	617	
QY	541	RCLPGYHGYPDCHACACDPRGALDQCGVGLCHCRPGNTGATCQECSPGFYGFPSICPC	600	
DB	618	RCRPGYHGFPCNCACTCDPRGALDQCGVGLCHCRPGNTGATCQECSPGFYGFPSICPC	677	
QY	601	HCSADGSLHTTCDPTTGQCRCPRTVGLHCDMCPGAYNFPYCEAGSCHPAGLAPANPAL	660	
DB	678	HCSAEGSLHAAACDPRSGQCSRCPRTVGLRCDTCVPGAYNFPYCEAGSCHPAGLAPDPA	737	
QY	661	PETQAPCMCAHVEGPSCDRCXKPGYWLGSANPEGCTRCSCDPRGLGGVTECQ-GNGQC	719	
DB	738	PEAQVPCMAHVEGPSCDRCXKPGYWLGSANPEGCTRCSCDPRGLGGVTECQ-GNGQC	797	
QY	720	FKAHVCGKTAACKDGFGLDYADYFGCRSCRCVGGALGQCEPKTGACRCRPNTOGP	779	
DB	798	FKBHVCGQACASCKDGFGLDYADYFGCRSCRCVGGALGQCEPKTGACRCRPNTOGP	857	
QY	780	TCSEPAKHLYLPDLHMLRLEEEAATPEGHAVRFGFNPLEFENFWSRGYAHMMAIQPRIV	839	

DB	858	TCSEPAKHLYLPDLHMLRLEEEAATPEGHAVRFGFNPLEFENFWSRGYAHMMAIQPRIV	917	
QY	840	ARLNVTSPLDLRLVRYVNRGSTVNGQISVREBGLSSCTNCTEQSQVAFPPSTEPAF	899	
DB	918	ARLNVTSPLDLRLVRYVNRGAMSVGRVSVREBGRSATCANCTAQSQVAFPPSTEPAF	977	
QY	900	VTVPQGFGEFVLPNGIWAALLVEAEGVLLDYVLLPSTYYEAAALQHRVTEACTYRPSA	959	
DB	978	ITVPQGFGEFVLPNGIWAALLVEAEGVLLDYVLLPSTYYEAAALQHRVTEACTYRPSA	1037	
QY	960	LHSTENCLVYAHLPDGFPSAAGTEALCRHNSLPRPCPTQLSPSHPLATCFGSDVDI	1019	
DB	1038	QOSGDNCLLYTHLPDGFPSAAGLEALCRQNSLPRPCPTQLSPSHPLITCTGSDVDV	1097	
QY	1020	QLEMAVPPQGYVLLVVEYVGEDSHQEMGVAVHTPQAPQQGVLLNHPYSSSLCRSPARD	1079	
DB	1098	QLQVAVPPQGYVLLVVEYANEDARQEVGVAVHTPQAPQQGLSLHPLCLYSLTLCRGRTARD	1157	
QY	1080	TQHHLAIFHLDSIASIRLTAEQAHHFLHSVTLVPVEEFSTEFVEPRVFCVSSHGTENPSS	1139	
DB	1158	TQHLAVFHLDSIASIRLTAEQAHHFLHSVTLVPVEEFSTEFVEPRVFCVSSHGTENPSS	1217	
QY	1140	AACLASRFPKPPQPIILKDCQVLPPLPDLPLTQSQELSPGAPPEGPQPRPPTAVDPNAEP	1199	
DB	1218	AACLPSPFPKPPQPIILRDCQVLPPLPDLPLTQSQELSPGAPPEGPQPRPPTAVDPNAEP	1277	
QY	1200	TLRHPQGTVFTTQVPTLGRYAFLLHGYQVHPSPFVEVLINGRIWQHANASFCPHG	1259	
DB	1278	TLRHPQGTVFTTQVPTLGRYAFLLHGYQVHPSPFVEVLINGRIWQHANASFCPHG	1337	
QY	1260	YGCRTLVLCGQTMLDVTDNELTVTVRVEGRWLMDYLVIVBEDAYSSSYLQEEPLDKS	1319	
DB	1338	YGCRTLVLCGQTMLDVTDNELTVTVRVEGRWLMDYLVIVBEDAYSSSYLQEEPLDKS	1397	
QY	1320	YDFISHCATQGYHISPSSSSPFCRNAATSLSLFYNNALPCGCGHEVAVSPTCEPFGGQC	1379	
DB	1398	YDFISHCATQGYHISPSSSSPFCRNAATSLSLFYNNALPCGCGHEVAVSPTCEPFGGQC	1457	
QY	1380	PCRGHVIGRDCSRCATGYWGFPCNCRPCDCCGALCDELGTQCICPPRTVPPDCLVCQPSF	1439	
DB	1458	PCRGHVIGRDCSRCATGYWGFPCNCRPCDCCGALCDELGTQCICPPRTVPPDCLVCQPSF	1517	
QY	1440	GCHPLVGCBCNCSGPGVQELTDTPTCDMDSGQCRPNVAGRCRDTCAPGYGYPSRCPC	1499	
DB	1518	GCHPLVGCBCNCSGPGVQELTDTPTCDMDSGQCRPNVAGRCRDTCAPGYGYPSRCPC	1577	
QY	1500	DCHEAGTMASVCDPLTGQCHCKENVOGSRCDQCRVGTFSLDAAANPKGCTRCFCFGATERC	1559	
DB	1578	DCHEAGTMASVCDPLTGQCHCKENVOGSRCDQCRVGTFSLDAAANPKGCTRCFCFGATERC	1637	
QY	1560	GNSNLARHEFVDMEGWVLLSSDRQVVPHEHRPEIELLHADLR---SVADTFSELYWQAP	1615	
DB	1638	RSSSYTRQEFVDMEGWVLLSSDRQVVPHEHRPEIELLHADLR---SVADTFSELYWQAP	1697	
QY	1616	PSYLGDRVSSYGGTLRYELHSETORGDIFIPYERRPDVVLQGNQMSIAFLELAYPPPGV	1675	
DB	1698	PSYLGDRVSSYGGTLRYELHSETORGDIFIPYERRPDVVLQGNQMSIAFLELAYPPPGV	1757	
QY	1676	HRGQLQVLEGNFRHLETHNPVSRBELMMVLAGLEQLQIRALFSQTSSSVSLRRVLEVAS	1735	
DB	1758	HRGQLQVLEGNFRHLETHNPVSRBELMMVLAGLEQLQIRALFSQTSSSVSLRRVLEVAS	1817	
QY	1736	EAGRPPASNVLCMCPANYRGDSQCECAPGYRDTKGLFGRVCVPCQCHGHSRCLPGS	1795	
DB	1818	PAGQALASNVLCMCPANYRGDSQCECAPGYRDTKGLFGRVCVPCQCHGHSRCLPGS	1877	
QY	1796	GICVGCQHNTEGDCQCRCPGFVSSDPSNPASPCVSCPLAVPSNNFADGCVLRNGRTQ	1855	
DB	1878	GVCVDCQHNTEGDCQCRCPGFVSSDPSNPASPCVSCPLAVPSNNFADGCVLRNGRTQ	1936	
QY	1856	CLCRPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSNGNDPNMIFSDCDPLTGACRGCLR	1915	
DB	1937	CLCRPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSNGNDPNMIFSDCDPLTGACRGCLR	1996	

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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:26:08 ; Search time 21.0085 Seconds
(without alignments)
9158.169 Million cell updates/sec

Title: US-10-037-182-2
Perfect score: 20118
Sequence: 1 MAKRLCAGSALCVGRPRGPA.....AMTRSVEVHGAVGASGCPAA 3695

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20093	99.9	3695	1 LMA5_HUMAN	O15230 homo sapien
2	16101.5	80.0	3718	1 LMA5_MOUSE	Q61001 mus musculus
3	6689.5	33.3	3333	1 LMA3_MOUSE	Q61789 mus musculus
4	5097	25.3	3712	1 LMA_DROME	Q00174 drosophila
5	4974	24.7	3672	1 LML2_CAEL	Q21313 caenorhabdi
6	3141.5	15.6	3106	1 LMA2_MOUSE	Q60675 mus musculus
7	3103.5	15.4	3110	1 LMA2_HUMAN	P24043 homo sapien
8	2933	14.6	3084	1 LMA1_MOUSE	P19137 mus musculus
9	2854	14.2	3075	1 LMA1_HUMAN	P25391 homo sapien
10	2260.5	11.2	1713	1 LMA3_HUMAN	Q16787 homo sapien
11	2147.5	10.7	1816	1 LMA4_HUMAN	Q16363 homo sapien
12	2128.5	10.6	1816	1 LMA4_MOUSE	P97927 mus musculus
13	1613.5	8.0	1801	1 LMB2_RAT	P15800 rattus norv
14	1604	8.0	1799	1 LMB2_MOUSE	Q61292 mus musculus
15	1600.5	8.0	1798	1 LMB2_HUMAN	P55268 homo sapien
16	1573.5	7.8	1786	1 LMB1_HUMAN	P07942 homo sapien
17	1572.5	7.8	1786	1 LMB1_MOUSE	P02469 mus musculus
18	1525.5	7.6	1790	1 LMB1_DROME	P11046 drosophila
19	1460	7.3	1587	1 LMG3_HUMAN	Q9Y6N6 homo sapien
20	1403.5	7.0	1581	1 LMG3_MOUSE	Q9R0B6 mus musculus
21	1348.5	6.7	1607	1 LMG1_MOUSE	P02468 mus musculus
22	1338	6.7	1639	1 LMG1_DROME	P15215 drosophila
23	1313	6.5	1609	1 LMG1_HUMAN	P11047 homo sapien
24	1296	6.4	3707	1 PGBM_MOUSE	Q05793 mus musculus
25	1234	6.1	1535	1 LML1_CAEL	Q18823 caenorhabdi
26	1140	5.7	4391	1 PGBM_HUMAN	P98160 homo sapien
27	956.5	4.8	1193	1 LMG2_HUMAN	Q13753 homo sapien
28	923.5	4.6	1191	1 LMG2_MOUSE	Q61092 mus musculus
29	916.5	4.6	1172	1 LMB3_HUMAN	Q13751 homo sapien
30	870	4.3	1168	1 LMB3_MOUSE	Q61087 mus musculus
31	814	4.0	3375	1 UN52_CAEL	Q06561 caenorhabdi
32	799	4.0	2321	1 NTC3_HUMAN	Q9um47 homo sapien
33	781	3.9	2318	1 NTC3_MOUSE	Q61982 mus musculus

34	777	3.9	2319	1 NTC3_RAT	Q9rl72 rattus norv
35	739.5	3.7	606	1 NET1_CHICK	Q90922 gallus gall
36	724	3.6	604	1 NET1_MOUSE	Q09118 mus musculus
37	720	3.6	604	1 NET1_HUMAN	O95631 homo sapien
38	710.5	3.5	2471	1 NTC2_HUMAN	Q04721 homo sapien
39	707.5	3.5	2470	1 NTC2_MOUSE	O35516 mus musculus
40	707	3.5	612	1 UNC6_CAEL	P34710 caenorhabdi
41	706.5	3.5	2003	1 NTC4_HUMAN	Q99466 homo sapien
42	699	3.5	2556	1 NTC1_HUMAN	P46531 homo sapien
43	693	3.4	2531	1 NTC1_RAT	Q07008 rattus norv
44	692.5	3.4	2471	1 NTC2_RAT	Q9qw30 rattus norv
45	691.5	3.4	2437	1 NTC1_BRARE	P46530 brachydanio

ALIGNMENTS

RESULT 1
LMA5_HUMAN
ID LMA5_HUMAN STANDARD; PRT; 3695 AA.
AC O15230; Q8WZA7; Q9H1P1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Laminin alpha-5 chain precursor.
GN LAMA5 OR KIAA0533 OR KIAA1907.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Leivaeslahti M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie I.J., McIay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN [2]
RP SEQUENCE OF 197-1934 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=21456161; PubMed=11572484;
RA Nagase T., Kikuno R., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XXI.
RT The complete sequences of 60 new cDNA clones from brain which code for
RT large proteins.";
RL DNA Res. 8:179-187(2001).
RN [3]
RP SEQUENCE OF 2051-3695 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98290545; PubMed=9628581;

RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
RA Nomura N., Ohara O.,
RT "Prediction of the coding sequences of unidentified human genes. IX.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.";
RL DNA Res. 5:31-39(1998).
RN [4]
RP SEQUENCE OF 2743-3695 FROM N.A.
RX TISSUE=Placenta;
RA MEDLINE=97415425; PubMed=9271224;
RA Durkin M.E., Loechele F., Mattei M.-G., Gilpin B.J., Albrechtsen R.,
RA Wewer U.M.;
RT "Tissue-specific expression of the human laminin alpha5-chain, and
RT mapping of the gene to human chromosome 20q13.2-13.3 and to distal
RT mouse chromosome 2 near the locus for the ragged (Ra) mutation.";
RL FEBS Lett. 411:296-300(1997).
RN [5]
RP EXPRESSION IN RETINA.
RX MEDLINE=20422761; PubMed=10964957;
RA Libby R.T., Champiaud M.-F., Claudepierre T., Xu Y., Gibbons E.P.,
RA Koch M., Burgess R.E., Hunter D.D., Brunken W.J.;
RT "Laminin expression in adult and developing retinae: evidence of two
RT novel CNS laminins.";
RL J. Neurosci. 20:6517-6528(2000).
CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components.
CC -!- SUBUNIT: Laminin-15 complex is an heterotrimer composed of three
CC chains (alpha-5/beta-2/gamma-3) which are bound to each other by
CC disulfide bonds into a cross-shaped molecule comprising one long
CC and three short arms with globules at each end.
CC -!- SUBCELLULAR LOCATION: Extracellular; found in the basement
CC membranes (major component).
CC -!- TISSUE SPECIFICITY: Expressed in heart, lung, kidney, skeletal
CC muscle, pancreas, retina and placenta. Little or no expression in
CC brain and liver.
CC -!- DOMAIN: Domain G is globular and is part of the major cell-binding
CC site located in the long arm of the laminin heterotrimer.
CC -!- SIMILARITY: Contains 1 laminin N-terminal domain.
CC -!- SIMILARITY: Contains 22 laminin EGF-like domains.
CC -!- SIMILARITY: Contains 2 laminin IV domains.
CC -!- SIMILARITY: Contains 5 laminin G-like domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AL354836; CAC22309.1; ALT_SEQ.
DR EMBL; AL354836; CAC22310.1; -.
DR EMBL; AB067494; BAB67800.1; -.
DR EMBL; AB011105; BAA25459.1; -.
DR EMBL; Z95636; CAB09137.1; -.
DR HSSP; P02468; 1KLO.
DR Genew; HGNC:6485; LAMAS.
DR MIM; 601033; -.
DR InterPro; IPR008985; ConA like lec_g1.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR008212; Lam_N2.
DR InterPro; IPR000034; Laminin_B.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR008211; LamNT.
DR Pfam; PF00052; laminin_B; 1.
DR Pfam; PF00053; laminin_EGF; 18.
DR Pfam; PF00054; laminin_G; 2.
DR Pfam; PF00055; laminin_Nterm; 1.
DR PRINTS; PR00011; EGFLAMININ.
DR ProDom; PD002082; Lam_N2; 1.

DR ProDom; PD003031; Laminin_B; 1.
DR SMART; SM00180; EGF_Lam; 20.
DR SMART; SM00281; LamB; 1.
DR SMART; SM00282; LamG; 5.
DR SMART; SM00136; LamNT; 1.
DR PROSITE; PS00022; EGF_1; 19.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS01248; LAMININ TYPE EGF; 19.
DR PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
FT SIGNAL 1 35
FT CHAIN 36 3695 LAMININ ALPHA-5 CHAIN.
FT DOMAIN 36 299 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 300 358 LAMININ EGF-LIKE 1.
FT DOMAIN 359 428 LAMININ EGF-LIKE 2.
FT DOMAIN 429 474 LAMININ EGF-LIKE 3.
FT DOMAIN 494 540 LAMININ EGF-LIKE 4.
FT DOMAIN 541 586 LAMININ EGF-LIKE 5.
FT DOMAIN 587 631 LAMININ EGF-LIKE 6.
FT DOMAIN 632 676 LAMININ EGF-LIKE 7.
FT DOMAIN 677 722 LAMININ EGF-LIKE 8.
FT DOMAIN 723 775 LAMININ EGF-LIKE 9.
FT DOMAIN 776 828 LAMININ EGF-LIKE 10.
FT DOMAIN 829 850 LAMININ EGF-LIKE 11 (INCOMPLETE).
FT DOMAIN 851 1437 LAMININ DOMAIN IV 1 (DOMAIN IV B).
FT DOMAIN 1438 1483 LAMININ EGF-LIKE 12.
FT DOMAIN 1484 1527 LAMININ EGF-LIKE 13.
FT DOMAIN 1528 1576 LAMININ EGF-LIKE 14.
FT DOMAIN 1577 1627 LAMININ EGF-LIKE 15.
FT DOMAIN 1628 1637 LAMININ EGF-LIKE 16 (N-TERMINAL).
FT DOMAIN 1638 1830 LAMININ DOMAIN IV 2 (DOMAIN IV A).
FT DOMAIN 1831 1863 LAMININ EGF-LIKE 16 (C-TERMINAL).
FT DOMAIN 1864 1912 LAMININ EGF-LIKE 17.
FT DOMAIN 1913 1968 LAMININ EGF-LIKE 18.
FT DOMAIN 1969 2022 LAMININ EGF-LIKE 19.
FT DOMAIN 2023 2069 LAMININ EGF-LIKE 20.
FT DOMAIN 2070 2116 LAMININ EGF-LIKE 21.
FT DOMAIN 2117 2166 LAMININ EGF-LIKE 22.
FT DOMAIN 2167 2735 DOMAIN II AND I.
FT DOMAIN 2736 2929 LAMININ G-LIKE 1.
FT DOMAIN 2941 3115 LAMININ G-LIKE 2.
FT DOMAIN 3124 3292 LAMININ G-LIKE 3.
FT DOMAIN 3340 3513 LAMININ G-LIKE 4.
FT DOMAIN 3520 3692 LAMININ G-LIKE 5.
FT DOMAIN 2203 2221 COILED COIL (POTENTIAL).
FT DOMAIN 2335 2466 COILED COIL (POTENTIAL).
FT DOMAIN 2510 2670 COILED COIL (POTENTIAL).
FT SITE 1722 1724 CELL ATTACHMENT SITE (POTENTIAL).
FT SITE 1838 1840 CELL ATTACHMENT SITE (POTENTIAL).
FT DISULFID 300 309 BY SIMILARITY.
FT DISULFID 302 322 BY SIMILARITY.
FT DISULFID 324 333 BY SIMILARITY.
FT DISULFID 336 356 BY SIMILARITY.
FT DISULFID 359 368 BY SIMILARITY.
FT DISULFID 361 393 BY SIMILARITY.
FT DISULFID 396 405 BY SIMILARITY.
FT DISULFID 408 426 BY SIMILARITY.
FT DISULFID 429 440 BY SIMILARITY.
FT DISULFID 431 447 BY SIMILARITY.
FT DISULFID 449 458 BY SIMILARITY.
FT DISULFID 461 471 BY SIMILARITY.
FT DISULFID 494 506 BY SIMILARITY.
FT DISULFID 496 515 BY SIMILARITY.
FT DISULFID 517 526 BY SIMILARITY.
FT DISULFID 529 538 BY SIMILARITY.
FT DISULFID 541 553 BY SIMILARITY.
FT DISULFID 543 560 BY SIMILARITY.
FT DISULFID 562 571 BY SIMILARITY.
FT DISULFID 574 584 BY SIMILARITY.
FT DISULFID 587 599 BY SIMILARITY.
FT DISULFID 589 605 BY SIMILARITY.
FT DISULFID 607 616 BY SIMILARITY.

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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:58 ; Search time 33.4531 Seconds
(without alignments)
10452.141 Million cell updates/sec

Title: US-10-037-182-4
Perfect score: 19876
Sequence: 1 DLYCKLVGGPVAGGDPNQTI.....QGRKALTQRHAKPSVSPLLWH 3635

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19876	100.0	3635	2 T10053	laminin alpha 5 ch
2	5018.5	25.2	3712	2 S18253	laminin alpha-1 ch
3	4831.5	24.3	3672	2 T23433	hypothetical prote
4	4820.5	24.3	3704	2 T37316	probable laminin a
5	3096	15.6	3106	1 S53868	laminin alpha-2 ch
6	2792	14.0	3084	1 NMM5A	laminin alpha-1 ch
7	2729.5	13.7	3075	2 S14458	laminin alpha-1 ch
8	2530	12.7	3102	2 T43291	laminin alpha chai
9	2460	12.4	2823	2 T23064	hypothetical prote
10	2460	12.4	2823	2 F87908	protein T22A3.8 li
11	2182.5	11.0	1816	1 S68960	laminin alpha-4 ch
12	2149.5	10.8	1713	2 A55347	adhesive ligand ep
13	1675	8.4	1798	2 S53869	laminin beta-2 cha
14	1672.5	8.4	1801	1 NMR5	laminin beta-2 cha
15	1605	8.1	1786	1 NMMHUB1	laminin beta-1 cha
16	1584	8.0	1786	1 NMM5B1	laminin beta-1 cha
17	1582.5	8.0	1797	2 A55677	laminin beta-2 cha
18	1549	7.8	1790	1 NMMFEB1	laminin beta-1 cha
19	1486	7.5	1808	2 T15039	hypothetical prote
20	1344.5	6.8	1607	1 NMM5B2	laminin gamma-1 ch
21	1323.5	6.7	1609	1 NMMHUB2	laminin gamma-1 ch
22	1311	6.6	1639	1 NMMFEB2	laminin gamma-1 ch
23	1221	6.1	1557	2 T28811	hypothetical prote
24	1212.5	6.1	1751	1 NMMHUBH	laminin alpha-2 ch
25	1204	6.1	3707	2 S18252	heparan sulfate pr
26	1104	5.6	4391	2 A38096	perlecan precursor
27	1033	5.2	1574	2 T13954	MEGF6 protein - ra
28	949	4.8	1193	2 A44018	laminin B2t chain
29	908.5	4.6	1192	2 S69000	laminin gamma 2 ch

30	900	4.5	1620	2 T27283	hypothetical prote
31	844	4.2	1170	2 A53612	laminin B1k chain
32	799.5	4.0	1168	2 I56985	kalinin B1 - mouse
33	799	4.0	3375	2 T19821	hypothetical prote
34	785.5	4.0	2295	2 C88369	protein unc-52 [im
35	781	3.9	1160	2 F88369	protein unc-52 [im
36	754	3.8	2321	2 S78549	notch3 protein - h
37	698.5	3.5	2437	2 S42612	transmembrane prot
38	697	3.5	2555	2 A40043	notch protein homo
39	689.5	3.5	2318	2 S45306	notch 3 protein -
40	677	3.4	606	2 A54665	netrin-1 precursor
41	675.5	3.4	1111	2 T26972	hypothetical prote
42	674.5	3.4	2703	1 A24420	notch protein - fr
43	665	3.3	2471	2 A49128	cell-fate determin
44	654	3.3	612	2 JH0799	laminin-related pr
45	653	3.3	1964	2 T09059	notch4 - mouse

ALIGNMENTS

RESULT 1

T10053

laminin alpha 5 chain - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2003

C;Accession: T10053

R;Miner, J.H.; Lewis, R.M.; Sanes, J.R.

submitted to the EMBL Data Library, November 1997

A;Reference number: Z16923

A;Accession: T10053

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-3635 <MIN>

A;Cross-references: EMBL:U37501; NID:g2599231; PID:g2599232

C;Genetics:

A;Gene: Lama5

C;Keywords: basement membrane; cell binding; extracellular matrix

F;1888-1939/Domain: laminin-type EGF-like homology <LEG>

F;1942-1970/Domain: EGF homology <EGF>

Query Match 100.0%; Score 19876; DB 2; Length 3635;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3635; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	DLYCKLVGGPVAGGDPNQTIQGYCDICTAANSNKAHPVSNADIGTERWWQSPPLSRGLE	60
DB	1	DLYCKLVGGPVAGGDPNQTIQGYCDICTAANSNKAHPVSNADIGTERWWQSPPLSRGLE	60
QY	61	YNEVNTLDLGQVHFVAYVLIKFANSRPPDLWLVERSTDFGHTYQPWQFFASSKRDCLER	120
DB	61	YNEVNTLDLGQVHFVAYVLIKFANSRPPDLWLVERSTDFGHTYQPWQFFASSKRDCLER	120
QY	121	FGPRTLERTQDDDVICTTEYSRIVPLENGEIVVSLVNGRPGALNFSYSPLLRDFTKATN	180
DB	121	FGPRTLERTQDDDVICTTEYSRIVPLENGEIVVSLVNGRPGALNFSYSPLLRDFTKATN	180
QY	181	IRLRLRNTLLGLHLMGKALRDPVTTRRYYSIKDISIGRCVCHGHADVCDKQPLDPF	240
DB	181	IRLRLRNTLLGLHLMGKALRDPVTTRRYYSIKDISIGRCVCHGHADVCDKQPLDPF	240
QY	241	RLQACQHNTCGGSCDRCCPGFNQWPWKPAATTDSANECQCNCHGHAYDCYYDPEVDRRN	300
DB	241	RLQACQHNTCGGSCDRCCPGFNQWPWKPAATTDSANECQCNCHGHAYDCYYDPEVDRRN	300
QY	301	ASQNDNVYGGGVCLDCQHHTTGINCERCLPGFFRAPDQPLDSPHVCRPCDCESDFTDG	360
DB	301	ASQNDNVYGGGVCLDCQHHTTGINCERCLPGFFRAPDQPLDSPHVCRPCDCESDFTDG	360
QY	361	TCEDLTGRCYCRPNFTGELCAACAEGYTDFPHCYPLPSFPHNDTREQVLPAGQIVNCDN	420
DB	361	TCEDLTGRCYCRPNFTGELCAACAEGYTDFPHCYPLPSFPHNDTREQVLPAGQIVNCDN	420

QY	421	AAGTOGNACRDXPRLGRCVCKPNFRGAHCELCAPGFHGPSCHPCQCSSPGVANSLCDPES	480
Db	421	AAGTOGNACRDXPRLGRCVCKPNFRGAHCELCAPGFHGPSCHPCQCSSPGVANSLCDPES	480
QY	481	GQCMCRTGFEGDRCDHICALGYHFHPLCQLCGCSPAGTLPPEGCEAGRCQCRPGDFGPHCD	540
Db	481	GQCMCRTGFEGDRCDHICALGYHFHPLCQLCGCSPAGTLPPEGCEAGRCQCRPGDFGPHCD	540
QY	541	RCLPGYHGYPDCHACACDPRGALDQCGVGGLCHCRPGNTGATCEBCSPGFYGFPPSCIPC	600
Db	541	RCLPGYHGYPDCHACACDPRGALDQCGVGGLCHCRPGNTGATCEBCSPGFYGFPPSCIPC	600
QY	601	HCSADGSLHTTCDPTTGQCRCPRTVGLHCDMCPVGAYNFPYCEAGSCHPAGLAPANPAL	660
Db	601	HCSADGSLHTTCDPTTGQCRCPRTVGLHCDMCPVGAYNFPYCEAGSCHPAGLAPANPAL	660
QY	661	PETQAPCMCRAHVEGPSDCRCKPGYWGLSASNPEGCTRCSCDPRGTLGGVTECOQNGQCF	720
Db	661	PETQAPCMCRAHVEGPSDCRCKPGYWGLSASNPEGCTRCSCDPRGTLGGVTECOQNGQCF	720
QY	721	CAHAVCGKTCACAKDGFGLDYADYFGCRSCRCDDVGGALGQGCCEPKTGACRCRPNTOGPT	780
Db	721	CAHAVCGKTCACAKDGFGLDYADYFGCRSCRCDDVGGALGQGCCEPKTGACRCRPNTOGPT	780
QY	781	CSEPAKDHLYLPLDHHMRLELEBAATPEGHAVRFGFNPLEFFENFWSRGYAHMMAIQPRIVA	840
Db	781	CSEPAKDHLYLPLDHHMRLELEBAATPEGHAVRFGFNPLEFFENFWSRGYAHMMAIQPRIVA	840
QY	841	RLNVTSPDLFRLVFRVYVNRGSTSVNGQISVREBEGLSSCTNCTEQSQPVAFPPSTEPAFV	900
Db	841	RLNVTSPDLFRLVFRVYVNRGSTSVNGQISVREBEGLSSCTNCTEQSQPVAFPPSTEPAFV	900
QY	901	TVPQRGFGEFVLPNGIOWALLVEAEGVLLDYVLLPSTYYEALLQHRVTEACTYRPSAL	960
Db	901	TVPQRGFGEFVLPNGIOWALLVEAEGVLLDYVLLPSTYYEALLQHRVTEACTYRPSAL	960
QY	961	HSTENCLVYAHLPDGFPPSAAGTEALCRHDNSLPRPCPTEQLSPSHPPLATCFGSDVDIQ	1020
Db	961	HSTENCLVYAHLPDGFPPSAAGTEALCRHDNSLPRPCPTEQLSPSHPPLATCFGSDVDIQ	1020
QY	1021	LEMVAVPQGGYVLLVVEYVGEDSHQEMGVAVHTPQRAQQGVNLNHPCPYSSLCRSPARDT	1080
Db	1021	LEMVAVPQGGYVLLVVEYVGEDSHQEMGVAVHTPQRAQQGVNLNHPCPYSSLCRSPARDT	1080
QY	1081	QHHLAIFHLDSEASIRLTAEQAHHFLHSVTLVPVEEFSTEFVEPRVFCVSSHGTFPSSA	1140
Db	1081	QHHLAIFHLDSEASIRLTAEQAHHFLHSVTLVPVEEFSTEFVEPRVFCVSSHGTFPSSA	1140
QY	1141	ACLASRFKPPQPIILKDCQVLPPLPDLPLTQSQELSPGAPPEGPQPRPPTAVDPNAEPT	1200
Db	1141	ACLASRFKPPQPIILKDCQVLPPLPDLPLTQSQELSPGAPPEGPQPRPPTAVDPNAEPT	1200
QY	1201	LLRHPQGTVFTTQVPTLGRYAFLLHGYQPVHPSFPVEVLINGGRIWGHANASFCPHGY	1260
Db	1201	LLRHPQGTVFTTQVPTLGRYAFLLHGYQPVHPSFPVEVLINGGRIWGHANASFCPHGY	1260
QY	1261	GCRTLVLCEGOTMLDVTDNELTVTVRVPEGRWLWLDYVLIVPEDAYSSSYLQEEPLDKSY	1320
Db	1261	GCRTLVLCEGOTMLDVTDNELTVTVRVPEGRWLWLDYVLIVPEDAYSSSYLQEEPLDKSY	1320
QY	1321	DFISHCATQGYHISPSSSPFCRNAATSLSLFYNNGALPCGCHEVGAVSPTCEPFGGQCP	1380
Db	1321	DFISHCATQGYHISPSSSPFCRNAATSLSLFYNNGALPCGCHEVGAVSPTCEPFGGQCP	1380
QY	1381	CRGHVIGRDCSRCATGYWGFPPNCRPCDCGARLCELTGQCICPPRTVPPDCLVCQPQSF	1440
Db	1381	CRGHVIGRDCSRCATGYWGFPPNCRPCDCGARLCELTGQCICPPRTVPPDCLVCQPQSF	1440
QY	1441	CHPLVGCEECNCSGPGVQELTDPTCDMDSGQCRCPNVAGRRCDTCAPGFYGYPSCRPCD	1500
Db	1441	CHPLVGCEECNCSGPGVQELTDPTCDMDSGQCRCPNVAGRRCDTCAPGFYGYPSCRPCD	1500
QY	1501	CHEAGTMASVCDPLTGQCHCKENVQGSRCDCQCRVGTFSLDAANPKGCTRCFCFGATERCG	1560

Db	1501	CHEAGTMASVCDPLTGQCHCKENVQGSRCDCQCRVGTFSLDAANPKGCTRCFCFGATERCG	1560
QY	1561	NSNLARHEFVDMEGWVLLSSDRQVVPHEHRPEIELLHADLRSVADTFSELYWQAPPSYLG	1620
Db	1561	NSNLARHEFVDMEGWVLLSSDRQVVPHEHRPEIELLHADLRSVADTFSELYWQAPPSYLG	1620
QY	1621	DRVSSYGGTTLHYELHSETQRGDIPIPYESRPPDVVLQGNQMSIAFLFLAYPPPGQVHRGQL	1680
Db	1621	DRVSSYGGTTLHYELHSETQRGDIPIPYESRPPDVVLQGNQMSIAFLFLAYPPPGQVHRGQL	1680
QY	1681	OLVEGNFRHLETHNPVSREELMMVLAGLEQLQIRALFSQTSSSSVSLRRVVLVASEAGRG	1740
Db	1681	OLVEGNFRHLETHNPVSREELMMVLAGLEQLQIRALFSQTSSSSVSLRRVVLVASEAGRG	1740
QY	1741	PPASNVELCMCPANYRGDSQCECAPGYRDTKGLFLGRCPVCQCHGHSRCLPGSGICVCG	1800
Db	1741	PPASNVELCMCPANYRGDSQCECAPGYRDTKGLFLGRCPVCQCHGHSRCLPGSGICVCG	1800
QY	1801	COHNTEGDQCERCPRPGFVSSDPSNPASPCVSCPCPLAVPSNNFADGCVLRNGRTOCLCRP	1860
Db	1801	COHNTEGDQCERCPRPGFVSSDPSNPASPCVSCPCPLAVPSNNFADGCVLRNGRTOCLCRP	1860
QY	1861	GYAGASCERCAPGFNGNPLVLGSSCQPCDCSGNGDPNMIFSDCDPLTGACRGLRHTTGP	1920
Db	1861	GYAGASCERCAPGFNGNPLVLGSSCQPCDCSGNGDPNMIFSDCDPLTGACRGLRHTTGP	1920
QY	1921	HCERCAPGFYGNALLPGNCTRCDCSPCGTETCDPQSGRCLCKAGVTGQRCDRCLEGYFGF	1980
Db	1921	HCERCAPGFYGNALLPGNCTRCDCSPCGTETCDPQSGRCLCKAGVTGQRCDRCLEGYFGF	1980
QY	1981	EQCQGCRCPCACGPAKGSCHPQSGQCHQCPGTTGPQCLECAPGYWGLPEKGCRRCCQCP	2040
Db	1981	EQCQGCRCPCACGPAKGSCHPQSGQCHQCPGTTGPQCLECAPGYWGLPEKGCRRCCQCP	2040
QY	2041	GHCDPHTGHTCTCPPGLSGERCDCQSQHQVVPFGKPGGHIHCEVCDHCVVLLDDDLERA	2100
Db	2041	GHCDPHTGHTCTCPPGLSGERCDCQSQHQVVPFGKPGGHIHCEVCDHCVVLLDDDLERA	2100
QY	2101	GALLPAIREQLQGINASSAAWARLHRLNASIADLQSKLRRPPGPRYQAAQQLQTLQOQSI	2160
Db	2101	GALLPAIREQLQGINASSAAWARLHRLNASIADLQSKLRRPPGPRYQAAQQLQTLQOQSI	2160
QY	2161	SIQODTERLGSQATGVQAGQQLDPTTESITLGRAQKLLESVRAVGRALNELASRMGQSP	2220
Db	2161	SIQODTERLGSQATGVQAGQQLDPTTESITLGRAQKLLESVRAVGRALNELASRMGQSP	2220
QY	2221	GDALVPSGEQLRWALAEVERLLWDMRTRDLGAQGAVAEAEALAEARLMARVQEQLTSFWE	2280
Db	2221	GDALVPSGEQLRWALAEVERLLWDMRTRDLGAQGAVAEAEALAEARLMARVQEQLTSFWE	2280
QY	2281	ENQSLATHIRDQLAQYESGLMDLREALNQAVNTTREAEEELNSRNQERVKELQWKQELSQ	2340
Db	2281	ENQSLATHIRDQLAQYESGLMDLREALNQAVNTTREAEEELNSRNQERVKELQWKQELSQ	2340
QY	2341	DNATLKATLQAASLIILGHVSELLQGIQAKEDIEHLAASLDGAWTPLLKRMQAFSPASSK	2400
Db	2341	DNATLKATLQAASLIILGHVSELLQGIQAKEDIEHLAASLDGAWTPLLKRMQAFSPASSK	2400
QY	2401	VDLVEAAEAHAQKLNQLAINLSGIIILGINQDRFIQRAVEASNAYSSILOAVQAEDAAGQ	2460
Db	2401	VDLVEAAEAHAQKLNQLAINLSGIIILGINQDRFIQRAVEASNAYSSILOAVQAEDAAGQ	2460
QY	2461	ALRQASRTWEMVQVQGLAAGARQLLANSSALLETILGHQGRGLAQGRLOAAGIQLHNW	2520
Db	2461	ALRQASRTWEMVQVQGLAAGARQLLANSSALLETILGHQGRGLAQGRLOAAGIQLHNW	2520
QY	2521	ARKNQIAAQIOEAQAMLAMDTSETSEKIAHAKAVAAEALSTATHVQSLOQGMKNVERWQ	2580
Db	2521	ARKNQIAAQIOEAQAMLAMDTSETSEKIAHAKAVAAEALSTATHVQSLOQGMKNVERWQ	2580
QY	2581	SQLGGLQGDLSOVERDASSVSTLEKTLPLQALLAKLSRLNRRGVHNASIALSANIGRVRK	2640

Db 2581 SQLGLQGDLSQVERDASSVSTLEKTLPLLAKLSRLNRGVHNASLALSANIGVRK 2640
Qy LIAQARSAASKVKVSMKFNRSRGVRLRPPRDLADLAAYTALKFHIQSPVPAPEPKNTGD 2700
Db LIAQARSAASKVKVSMKFNRSRGVRLRPPRDLADLAAYTALKFHIQSPVPAPEPKNTGD 2700
Qy HFVLYMGSRQATGDMGVSLRNQKVHVYRLGKAGPTTLSIDENIGEFAAASIDRTLOF 2760
Db HFVLYMGSRQATGDMGVSLRNQKVHVYRLGKAGPTTLSIDENIGEFAAASIDRTLOF 2760
Qy GHMSVTVEKQMVHEIKGDTVAPGSEGLLNHLHPDDFVFYVGGYPSNFTPEPLRFPYLG 2820
Db GHMSVTVEKQMVHEIKGDTVAPGSEGLLNHLHPDDFVFYVGGYPSNFTPEPLRFPYLG 2820
Qy IEMETLNEEVVSLYNEFEQTFMLDTAVDKPCARSKATGDPWLTDGSLDCSGFARISFEKQ 2880
Db IEMETLNEEVVSLYNEFEQTFMLDTAVDKPCARSKATGDPWLTDGSLDCSGFARISFEKQ 2880
Qy FSNTKRFQDELRLVSYNGIIFFLKQESQFLCLAVQEGTLVLFYDFGSLGKKADPLQPPQA 2940
Db FSNTKRFQDELRLVSYNGIIFFLKQESQFLCLAVQEGTLVLFYDFGSLGKKADPLQPPQA 2940
Qy LTAASKAIQVFLLAGNRKRVLRVERATVFSVDQNMNLEMADAYLGGVPEQLPLSLRQ 3000
Db LTAASKAIQVFLLAGNRKRVLRVERATVFSVDQNMNLEMADAYLGGVPEQLPLSLRQ 3000
Qy LPPSGSVRGCIKGIKALGKYVDLKRLLNTTGISGCTADLLVGRMTFHGHGFLPLALPD 3060
Db LPPSGSVRGCIKGIKALGKYVDLKRLLNTTGISGCTADLLVGRMTFHGHGFLPLALPD 3060
Qy VAPITEVYSGFGRGTQDNLLYYRTSPDPGYQVSLREGHVTLRFMNOBETQRVFADG 3120
Db VAPITEVYSGFGRGTQDNLLYYRTSPDPGYQVSLREGHVTLRFMNOBETQRVFADG 3120
Qy APHYVAFYSNVTGVWLVYDDQLQVKSHERTTLMQLQPEEPSRLLLGGLPVSGTFHNFS 3180
Db APHYVAFYSNVTGVWLVYDDQLQVKSHERTTLMQLQPEEPSRLLLGGLPVSGTFHNFS 3180
Qy GCISNVFVQRLRGPQRFVDFLQNMGSVNVSVGCTPAQLIETSRATAQKYSRRSRQPSQDL 3240
Db GCISNVFVQRLRGPQRFVDFLQNMGSVNVSVGCTPAQLIETSRATAQKYSRRSRQPSQDL 3240
Qy ACTTPWLPGTIQDAYQFGGFLPSYLQFVGISPSHNRHLHLSMLVRPHAAASQGLLSTAPM 3300
Db ACTTPWLPGTIQDAYQFGGFLPSYLQFVGISPSHNRHLHLSMLVRPHAAASQGLLSTAPM 3300
Qy SGRSPSLVFLNHHGFVAQTEGPGPRLOVQSRQHSRAGQWHRVSVRWGMQIQLVVDGSQ 3360
Db SGRSPSLVFLNHHGFVAQTEGPGPRLOVQSRQHSRAGQWHRVSVRWGMQIQLVVDGSQ 3360
Qy TWSQKALHHRVPRAERPQPYTLVSGGLPASSYSSKLPVSVGFSGCLKKLQLDKQPLRTP 3420
Db TWSQKALHHRVPRAERPQPYTLVSGGLPASSYSSKLPVSVGFSGCLKKLQLDKQPLRTP 3420
Qy QMVGVTPCVSGPLEDGLFPFGSEGVVTLPLPKAKMPYVSLELEMRPLAAAGLIFHLGQAL 3480
Db QMVGVTPCVSGPLEDGLFPFGSEGVVTLPLPKAKMPYVSLELEMRPLAAAGLIFHLGQAL 3480
Qy ATPYMQLKVLTEQVLLQANDGAGEFSTWVTYPKLCGRWHRVAVIMGRDTLRLEVDTSQN 3540
Db ATPYMQLKVLTEQVLLQANDGAGEFSTWVTYPKLCGRWHRVAVIMGRDTLRLEVDTSQN 3540
Qy HTTGRLPESLAGSPALLHLGSLPKSSTARPELPAVRCGLRKLKLLINGAPVNVITASVQIQGA 3600
Db HTTGRLPESLAGSPALLHLGSLPKSSTARPELPAVRCGLRKLKLLINGAPVNVITASVQIQGA 3600
Qy VGMRGCPSGTLLALSQKGKALTQRHAKPSVSPLLWH 3635
Db VGMRGCPSGTLLALSQKGKALTQRHAKPSVSPLLWH 3635

laminin alpha-1 chain precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 16-Sep-1992 #sequence_revision 24-Jul-1997 #text_change 10-Dec-1999
C:Accession: S28399; S18253
R:Kusche-Gullberg, M.; Garrison, K.; MacKrell, A.J.; Fessler, J.H.
EMBO J. 11, 4519-4527, 1992
A:Title: Laminin A chain: expression during Drosophila development and genomic sequence.
A:Reference number: S28399; MUID:93049203; PMID:1425586
A:Accession: S28399
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-3712 <KUS>
A:Cross-references: GB:M96388; NID:g157799; PIDN:AAA28662.1; PID:g157800
R:Garrison, K.; MacKrell, A.J.; Fessler, J.H.
J. Biol. Chem. 266, 22899-22904, 1991
A:Title: Drosophila laminin A chain sequence, interspecies comparison, and domain structure.
A:Reference number: S18253; MUID:92078147; PMID:1744083
A:Accession: S18253
A:Molecule type: mRNA
A:Residues: 1762-3712 <GAR>
A:Cross-references: EMBL:M75882; NID:g157797; PIDN:AAA28661.1; PID:g157798
C:Genetics:
A:Gene: FlyBase:Lana
A:Cross-references: FlyBase:FBgn0002526
C:Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like homology
C:Keywords: basement membrane; cell binding; coiled coil; disulfide bond; extracellular
F:273-330/Domain: laminin-type EGF-like homology <LEG>
F:333-400/Domain: laminin-type EGF-like homology <LE02>
F:541-584/Domain: laminin-type EGF-like homology <LE01>
F:1776-2115/Domain: III <DOM3>
F:1776-1806/Domain: laminin-type EGF-like homology #status atypical <LE1>
F:1809-1856/Domain: laminin-type EGF-like homology <LE2>
F:1859-1914/Domain: laminin-type EGF-like homology <LE3>
F:1917-1967/Domain: laminin-type EGF-like homology <LE4>
F:1970-2014/Domain: laminin-type EGF-like homology <LE5>
F:2017-2061/Domain: laminin-type EGF-like homology <LE6>
F:2064-2109/Domain: laminin-type EGF-like homology <LE7>
F:2116-2697/Domain: I/II, heptad repeats <DOM2>
F:2698-3712/Domain: G <DOMG>
F:2698-2863/Domain: repeat G1 <RG1>
F:2864-3048/Domain: repeat G2 <RG2>
F:3049-3223/Domain: repeat G3 <RG3>
F:3079-3200/Domain: laminin G repeat homology <LG3>
F:3334-3528/Domain: repeat G4 <RG4>
F:3529-3712/Domain: repeat G5 <RG5>
F:1847,1850,1943,2024,2196,2215,2267,2301,2323,2482,2524,2538,2569,2699,2720,2890,2938,31

Query Match 25.2%; Score 5018.5; DB 2; Length 3712;
Best Local Similarity 31.3%; Pred. No. 5.7e-222;
Matches 1227; Conservative 595; Mismatches 1527; Indels 569; Gaps 122;

Qy 1 DLYCKLVGGPVAGGDPN-QTIQGOYCDICTAANSNKAHPVSNADGTERWQSPPLSRGL 59
Db 51 ELYCKLVGANTTEHDHIDYSVIQGVQVCDYCDPTVPERNHPPENADGTEAWWQSPPLSRGM 110
Qy 60 EYNEVNTLDLQGVFHVAYVLIKFNANSPRPDLWVLERSTDFGHTYQWPQWFFASKKRDCLE 119
Db 111 KENEVNLTFINFEQEFHVAYLFIKMGNSPRPGLWTLKSTDYKKTWTWQHFSDTPADCE 170
Qy 120 RFGPRTLERITQDDDDVICTTEYSRIVPLENGEIVVSLVNGRPGALNFSYSPLLRDFTKAT 179
Db 171 YFGKDYKPIITRDDDDVICTTEYSKIVPLENGEIPVYMLNRPSTNYFNSTVLQEWTRAT 230
Qy 180 NTRLRLRNTLLGLHMGKALRDPVTVTRRYYSIKDISIGGRVCVCHGADVCADKDPDLP 239
Db 231 NVIRLLRLTKNLLGLHMSVARQDPTVTRRYFYSIKDISIGGRCMCNHGDTCVVKDPKSP 290
Qy 240 FR-LQACQHNTCGSCDRCCPGFNGQPKWPAITDTSANECQSCNCHGHAYDCYDPEVDR 298
Db 291 VRILACRCQHHTTCGIQCNCCPGFEQKKWRQNTNARPFNCEPCNCHGHSNECKYDEEVR 350
Qy 299 RNASQNDNVYQGGVCLDQHTTGINCERCLPGFFRAPDQPLDSPHVCPCDCESDFT 358

Db 351 KGLSLDIHGHVDDGGVCQNCQNTVGINCNCKKPKYRPRKXKHNWETDVCSPCQCDYFFS 410
QY 359 DGTCEDLTGRYCVRPNFTGELCAACAEYTDFFPHCYPLPSFPNDHTREQVLPAGQIVNCD 418
Db 411 TGHCEETGNCBCEAAAFQPPSCDSCAYGYGPNC-----RE-----CE 449
QY 419 CNAAGTQGNACRKDPRLGRVCVKNPFRGAHCELCAPGFHG-PSCHPCQCSSPGVANSLCD 477
Db 450 CNLNGTNGYHCEAESSG-QQCPCKINFAGAYCKQCAEGYGFPECKACECNKIGSITNDCN 508
QY 478 PESGQCMCRTPGEGDRCDHICALGYFHFPLCQLCGCSPAGTLPEGCD-EAGRCQCRPGFDG 536
Db 509 VTTGECKCLTNGGDNCEKXGIFNYPTCSYCDNQGTESEICNKQSGQCICREGFGG 568
QY 537 PHCDRCLPGYHGYDPDCHACADPRGALDOQCGVGGCHCRPGNCGATCQECSPGYGFPS 596
Db 569 PRCDQCLPGFYNPDPCKPCNCSSTGSSAITCDNTGKCNLNNFAGKQCTLCTAGYYSYPD 628
QY 597 CIPCHCSADGSLHTTCDPTTGQCRRCRPRVTGLHCDMCPGAYNFPYCEAGSCHPAGLAP- 655
Db 629 CLPCHCDSHSGQVSCN-SDGQCLCQPNFDRQCDCKEGFYNPFSCEDCNCDPAGVIDK 687
QY 656 -ANPALPETQAPCMCAHVEGPSDCRCKPGYWGLSASNPEGCTRCSCDPRGTLGGVTECQ 714
Db 688 FAGCGSVVPGELCKCKERTVTRICNECKPLYWNLNISNTEGCEICDQWTDGTISALDTC 747
QY 715 G-NGQCFKAHVCGKTAACKDGGFFGLDYADYFGCRSCRCDDVGALGQGCCEPXTGACRCR 773
Db 748 SKSGQCPCKPHTQGRRCQECRDTGTFDLDSASLFGCKDCSDVGSWQSVCDKISGQCKCH 807
QY 774 PNTQOPTCSEPAKDHVLPDLHMRLELEZAAPEGHAVRFGFNPLEFENFWSRGYAHMMA 833
Db 808 PRITGLACTQPLTTHFFFTLHQFYEDGSLPSGTQVRYDYDEAAPPFGSSKGYVVFNA 867
QY 834 IQPRIVARLNVTSPLRFLVFRYVNRGTSVNGQISVREEGKLSSTCNCTEQSQPVAFPP 893
Db 868 IQNDVRNEVNFVKSLLYRVLRYVNPNAENVATISVTSNPLE-----VDQHVKVLQP 922
QY 894 STEPAPVTV--PQGFGEFVLPNGIWAALLVER-EGVLLDYVLLPSTYYEAAALQHRVT 950
Db 923 TSEPQFVTVAGPLGVKPSAIVLDPGRYVFTTKANKVMULDYFVLLPAAAYEAGILTRHS 982
QY 951 EACTYRPSALHSTENCLVYAHPLDGFPSAAGTEALCRHNSLPRPCPTQLSPSH--- 1006
Db 983 NPC-----ELGNMELCRHYKYASVEVFPSPATPFVI--GENSKPTNPVETYTDPHLQIV 1035
QY 1007 -----PPLATCFGSDVDIQLEMAVPPQGOYVLVVEYGE-----DSHQENGVAHTPORA 1056
Db 1036 SHVGDIPVLS---GSQNELHYIVDVPRSGRYIFVDYISDRNFPDSYY---INLKLKDNP 1089
QY 1057 PQQGVNLHPCPYSSLCRSPARDTQHHLAIFHLDSB--ASIRLTA-----EQAHFFLHSVTL 1111
Db 1090 DSETSULLYPCLYSTICRTSVNEDGMEKS-FYINKEDLQPVIIADIEDGSRFPPIISVTA 1148
QY 1112 VPVEEFSTEFVEPRVFCVSSHGTNPSSAACLASRPKPPQPIILKDCQVLPPLPDLPLT 1171
Db 1149 IPVDQWSIDYINPSPCVI-----HDQQCATPKFRSVP-----DSKIEFETD---- 1191
QY 1172 QSQELSPGAPPEGPPRPTAVDPNAEPTLL-RHPQGTVVFTTQV-----PTLGRYAFLLH 1226
Db 1192 HEDRIATNKPPY-----ASLDERVKLVHLDSONEATIVIESKVDTAKENL--FVILVK 1242
QY 1227 GYQVHPSPFPVEVLINGGR-IWQGHANASFCPHGYGCRTLVLCGQTMLDVTDNELTVTV 1285
Db 1243 YYQPSHPKYQVYVYTLTAGKNQYDKGFDIQHCPSSSGCRGVRIRPAGEGSFEI-DDEFKFTI 1301
QY 1286 RVPEGRWLWDYVLIVPEDAYSSSYLQEEPLDKSYDFTSHCATQGYHISPSSSSPFCRNA 1345
Db 1302 TTDRSQSVWLDYLVVWPLKQYNDLLVEETFDQTKFQNCGHDFHIT-HNASDFCKKS 1360
QY 1346 ATSLSLFVNGALPCGCHEVGAVSPTCEPFGGQCPGCRGHVGRDCSRCATGYWGFPPNCRP 1405
Db 1361 VFSLTADYNSGALPCNCDYAGSTSFEPFGGQCCQCKPNVIERTCGRCSRRIYGFPPDCKP 1420

QY 1406 CDC-GARLCELTGQCICPPRTVPPDCLVCQPQSPFGCHPLVGCCECNCSGPGVQELTDPT 1464
Db 1421 CKCPNSAMCEPTTGECMCPNPNVIGDLCEKCAPNTYGFHFQVIGCEBACNPMGIAN-GNSQ 1479
QY 1465 CDMDSGQCRCPNVAGRRCDTCAFGFYGPSPCRPCDCHEAGTMASVCDPLTGQCHCKENV 1524
Db 1480 CDLFNGTCECRQNIETGRACDVCSNGYFNPFPHECEQCSCHKPGTELEVCCKIDGACFCCKNV 1539
QY 1525 QGSRCDQCRVGTFSLSDAANPKGCTRCFCFGATERCG-----NSNLARH-----EFVD 1571
Db 1540 VGRDCDQCVDTGYNLQESNPDGCTTCFCFGKTSRCD SAYLRVYNVSLKLVHSITTFEFHE 1599
QY 1572 MEGWVLLSSDRQVVPVHEHRPEIEL-----LHAD--LRSVADTFSELYWQAPPSYLG----- 1620
Db 1600 ES-----IKFDMMPVPAD-----EILLNETTLKADFTLREVND-----ERPAYFGVLDYL 1644
QY 1621 ----DRVSSYGGTLHYELHSETQRGDIFIPYESRPDVVLQGNQMSIAPLELAYPPPGQVH 1676
Db 1645 LNQNNHISAYGGDLAYTLHFTSGFDGKYI---VAPDVILFSEHNALVHTSYEQPSRNEPF 1701
QY 1677 RGQLQVVEGNFRHLETHNPVSREELMMVLAGLEQLQIRALFSQTSVSLRRRVLEVASE 1736
Db 1702 TNRVNIVESNFQTI-SGKPVSRADFMVLRDLKVFIFIRANYWEQTLVTHLSDDVYLTLADE 1760
QY 1737 AGRPPASN---VELCMCPANYRGSDCQECAPGYRDTKGLFLGRVCPQCHGSHDRCLP 1793
Db 1761 DADGTGEYQFLAVERCSCPPGYSGHSCEDCAPGYRDPSPGYGICYPCBCNGHSETCDC 1820
QY 1794 GSGICVGCQHNTEGQECRCRPGFVSSDPSNPASPCVPCPLAVPSNNFADGCVLNRGR 1853
Db 1821 ATGICSKCQHGTEGDHCERCVSYYGNATNGTPGDCMICACPLPFDNNFATSCEISEG 1880
QY 1854 TQ--CLCRPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSNGDPMIFSDCDPLTGACR 1911
Db 1881 DOIHCECKPGYTPRCESCANGFYGEPEISIGQVCKPCCECSGNINPEDQGS-CDTRTGECL 1939
QY 1912 GCLRHTTTPHCERCAPGFYGNALLPGNCTRCDCSPCGTETCDPQSGRCCLKAGVTGQRCD 1971
Db 1940 RCLNNTFGAACNLCAFGFYGDALIKNCQSCDCDGLGTQTCDFVGVCTCHENVIGDRCD 1999
QY 1972 RCLGYFGFEQCCQCRPCACGPAKSGSECHPQSCQCHCQPGTTPQCILECAPGYWGLPEK 2031
Db 2000 RCKPDHYGFESGVGCRACDCGAASNSTQCDPHTGHCAKSGVTGRQCRCRCAVDHWKYEKD 2059
QY 2032 GCRRCQCPRGH-----CDPHTGHCTCPPGLSGERCDCSCQHQHVVPKPGGHHIHCVC 2086
Db 2060 GCTPCNCNQYSRGFGCNPNTGKCQCLPGVIGDRCDACPNRW---VLIKDEG---CQEC 2112
QY 2087 DHCVVLLDDLERAGALLPAIREQLOGINASSAAWARLRLN-----ASIADLQSKLRRP 2141
Db 2113 NNCHHALLDVTDRLMYQIDSV--LEDFNSVTLLAFTSQKLYNDYDLADELPKVKLLDP 2169
QY 2142 PGPYQAAQQLQTLQEQSISLQDTERLGSQATVGQAGQLLDTTESTLGRAQKLLSV 2201
Db 2170 -----NSVDLSPSKKANSELESDAKSYAKQVQNQTLANAFDIRERSSTTLGNITVAY--- 2220
QY 2202 RAVGRALNELASRMGQSGPDALVPSGEQLRWALAEVERLLWDMRTRDLGAQGAVAEAEAL 2261
Db 2221 -----DEAVKSADQAKEALASVEALSKNLE---AAASTKIDAAL 2256
QY 2262 AEAQRLMARVQ-----EQLTSFWEENQSLATHIRDQ---LAQYESGLMDLRE 2305
Db 2257 EQAQHILGQINGTSIELTPNEQVLEKARKLYEEVNTLVLPKAKQNSLALKNNDIGEFSD 2316
QY 2306 ALNQAVENTTREAELNSRNOERVKEALQWKQELSQDNATLKATLOA-----A 2352
Db 2317 HLEDLFNWS-EASQAKSADVERNRVANQKAFDNSKEDTVSEQKLOAEKNIKDAGNFING 2375
QY 2353 SLILGHVSELQIGIDQAKEDLEHLAASLDGAWTPLLKRNQAFSPASSKVDLVEAAFAHAQ 2412
Db 2376 DLTLNQINQKLDNLRDALNELNSFNKNVD---EELPVREDQHKHEADALTDQAE-----Q 2426

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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:58 ; Search time 34.0053 Seconds
(without alignments)
10452.141 Million cell updates/sec

Title: US-10-037-182-2
Perfect score: 20118
Sequence: 1 MAKRLCAGSALCVRGPRGA.....AMTRSVVHGAVGASGCPAA 3695

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78.*
1: Pirl.*
2: Pirl.*
3: Pirl.*
4: Pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15839	78.7	3635	2 T10053	laminin alpha 5 ch
2	5097	25.3	3712	2 S18253	laminin alpha-1 ch
3	4974	24.7	3672	2 T23433	hypothetical prote
4	4964	24.7	3704	2 T37316	probable laminin a
5	3141.5	15.6	3106	1 S53868	laminin alpha-2 ch
6	2933	14.6	3084	1 MMSA	laminin alpha-1 ch
7	2854	14.2	3075	2 S14458	laminin alpha-1 ch
8	2601	12.9	3102	2 T43291	laminin alpha chai
9	2514	12.5	2823	2 T23064	hypothetical prote
10	2514	12.5	2823	2 F87908	protein T22A3.8 li
11	2260.5	11.2	1713	2 A55347	adhesive ligand ep
12	2147.5	10.7	1816	1 S68960	laminin alpha-4 ch
13	1613.5	8.0	1801	1 MMRTS	laminin beta-2 cha
14	1602.5	8.0	1798	2 S53869	laminin beta-2 cha
15	1573.5	7.8	1786	1 MMHUB1	laminin beta-1 cha
16	1572.5	7.8	1786	1 MMMSB1	laminin beta-1 cha
17	1532.5	7.6	1797	2 A55677	laminin beta-1 cha
18	1509.5	7.5	1797	2 T15099	laminin beta-2 cha
19	1498	7.4	1808	2 T15099	hypothetical prote
20	1348.5	6.7	1607	1 MMMSB2	laminin gamma-1 ch
21	1337	6.6	1639	1 MMFFB2	laminin gamma-1 ch
22	1313	6.5	1609	1 MMHUB2	laminin gamma-1 ch
23	1296	6.4	3707	2 S18252	heparan sulfate pr
24	1234	6.1	1557	2 T28811	hypothetical prote
25	1224.5	6.1	1751	1 MMHUMH	laminin alpha-2 ch
26	1146	5.7	4391	2 A38096	perlecan precursor
27	1004.5	5.0	1574	2 T13954	MEGF6 protein - ra
28	957.5	4.8	1193	2 A44018	laminin B2t chain
29	921	4.6	1620	2 T27283	hypothetical prote

30	917.5	4.6	1170	2 A53612	laminin Blk chain
31	887	4.4	1192	2 S69000	laminin gamma 2 ch
32	870	4.3	1168	2 I56985	kalinin B1 - mouse
33	814	4.0	3375	2 T19821	hypothetical prote
34	799	4.0	2295	2 C88369	protein unc-52 [im
35	799	4.0	2321	2 S78549	notch3 protein - h
36	794.5	3.9	1160	2 F88369	protein unc-52 [im
37	781	3.9	2318	2 S45306	notch 3 protein -
38	739.5	3.7	606	2 A54665	netrin-1 precursor
39	707	3.5	612	2 JH0799	laminin-related pr
40	695	3.5	2555	2 A40043	notch protein homo
41	692.5	3.4	2471	2 A49128	cell-fate determin
42	691.5	3.4	2437	2 S42612	transmembrane prot
43	690	3.4	2531	2 S18188	notch protein homo
44	684	3.4	581	2 B54665	netrin-2 precursor
45	676.5	3.4	2703	1 A24420	notch protein - fr

ALIGNMENTS

RESULT 1

T10053
laminin alpha 5 chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2003
C:Accession: T10053
R:Miner, J.H.; Lewis, R.M.; Sanes, J.R.
submitted to the EMBL Data Library, November 1997

A:Reference number: Z16923
A:Accession: T10053
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-3635 <MIN>
A:Cross-references: EMBL:U37501; NID:g2599231; PID:g2599232
C:Genetics:
A:Gene: Lama5
C:Keywords: basement membrane; cell binding; extracellular matrix
F:1888-1939/Domain: laminin-type EGF-like homology <LEG>
F:1942-1970/Domain: EGF homology <EGF>

Query Match 78.7%; Score 15839; DB 2; Length 3635;
Best Local Similarity 79.4%; Pred. No. 0;
Matches 2874; Conservative 277; Mismatches 452; Indels 18; Gaps 8;

QY	79	DLCKLVGGPVAGDPNQITIRGOYCDICTAANSNKAHPASNAIDGTERWQSPPLSRGLE	138
DB	1	DLCKLVGGPVAGDPNQITIRGOYCDICTAANSNKAHPASNAIDGTERWQSPPLSRGLE	60
QY	139	YNEVNVTLDLGVHVAVYLKFNAPRDLWVLSMDFGRTYQWQFPASSKRDCLER	198
DB	61	YNEVNVTLDLGVHVAVYLKFNAPRDLWVLSMDFGRTYQWQFPASSKRDCLER	120
QY	199	FGPOTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRPGAMNFSYSPLLREFTKATN	258
DB	121	FGPOTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRPGAMNFSYSPLLREFTKATN	180
QY	259	VRLRFLRTNTLLGHLMGKALRDPVTTRRYYSIKDISIGRCVCHGHADACDAKDPDPF	318
DB	181	IRLRLRNTNTLLGHLMGKALRDPVTTRRYYSIKDISIGRCVCHGHADACDAKDPDPF	240
QY	319	RLQCTQHNTCGGTCDRCPCGFNQWPKPATANSANECQSCNCHGHAYDCYDPEVDRRN	378
DB	241	RLQCTQHNTCGGTCDRCPCGFNQWPKPATANSANECQSCNCHGHAYDCYDPEVDRRN	300
QY	379	ASQSLDGTGYQGGVCLDQHHHTAGVNCERCLPGFYRSPNHPDLSPHVCRRCNCESDFTDG	438
DB	301	ASQSLDGTGYQGGVCLDQHHHTAGVNCERCLPGFYRSPNHPDLSPHVCRRCNCESDFTDG	360
QY	439	TCEDLTGRCYCRPNFSGERCDCVCAEGFTGFPSCYPTPS-SSNDTREQVLPAQIVNCDCS	497
DB	361	TCEDLTGRCYCRPNFSGERCDCVCAEGFTGFPSCYPTPS-SSNDTREQVLPAQIVNCDCS	420

QY 498 AAGTOGNACRKPVRVGRCLCKPNFQTHCELCAPGYFGPGQPCQCSSPGVADDRCDPDT 557
DDB 421 AAGTOGNACRKPRLGRVCCKPNFRGAHCELCAPGFHGPSCHPCQCSSPGVANSLCDPES 480
QY 558 GQCRVREGATCDRCAPGYFHFPLCQLCGCSPAGTLPPEGDEAGRCLCQPEFAGPHCD 617
DDB 481 GQCMCRTGEGDRCDHCALGYFHFPLCQLCGCSPAGTLPPEGDEAGRCCQCRPGFDFPHCD 540
QY 618 RCRPGYHGFPCNCACTCDPRGALDQLCGAGGLCRCPGYTGTACQECSPGFHGFPSVCVPC 677
DDB 541 RCLPGYHGYPDDCHACACDPRGALDQCCGVGGLCHCRPGNTGATCQECSPGFYGFPSICPC 600
QY 678 HCSAEGSLHAACDPRSGQCSRCRPRVTGLRCDTCVPGAYNFPYCEAGSCHPAGLAPVDPAL 737
DDB 601 HCSADGSLHTTCDPTTGQCRRCRPRVTGLHCDMCPVGAYNFPYCEAGSCHPAGLAPANPAL 660
QY 738 PEAVPCMCRAHVEGSPCDRCCKPGFWGLSPSNPEGCTRCSDLRGTGLGVAECQPGTGQC 797
DDB 661 PETQAPCMCRAHVEGSPCDRCCKPGYWLGSASNPEGCTRCSDPRGTGLGVTECQ-GNGQC 719
QY 798 FCKPHVCGOACASCKDGFGLDQADYFGCRSCRCIDIGGALGSCPEPRTGVCRCRPNTQGP 857
DDB 720 FCKAHVCGKTCACACKDGFGLDYADYFGCRSCRCIDVGALGQCEPKTGACRCRPNQGP 779
QY 858 TCSEPARDHVLPDLHHLRLELEEAATPEGHAVRFGFNPLEFENFESWRGYAQMAPPVQPRIV 917
DDB 780 TCSEPAKDHVLPDLHLMRLELEEAATPEGHAVRFGFNPLEFENFESWRGYAHMMAIQPRIV 839
QY 918 ARLNLTSPDLFWLVRYVNRGAMSVSGRVSVREEGRSAAACANTAQSPQVAFPPSTEPAP 977
DDB 840 ARLNVTSPDLFRLVRYVNRGSTSVNGOISVREEGKLSSTCNCTEQSPQVAFPPSTEPAP 899
QY 978 ITVPQRGFGEFVLPNGTAWLRVEAEGVLLDYVWLLPSAYYEAALLQLRVTEACTYRPSA 1037
DDB 900 VTPVQRGFGEFVLPNGIWALLVEAEGVLLDYVWLLPSTYYEAALLQHRVTEACTYRPSA 959
QY 1038 QQSGDNCLLYTHLPDGFPSAAGLEALCRQDNLSLPRPCPTEQLSPSHPPLITCTGSDVDV 1097
DDB 960 LHSTENCLVYAHLPDGFPSAAGTEALCRHDNSLPRPCPTEQLSPSHPPLATCFGSDVDI 1019
QY 1098 QLQVAVPQGRYALVVEYANEDARQEVGVAVHTPQAPQOGLLSLHPCLYSTLCRGTAARD 1157
DDB 1020 QLEMAVPPQGVYLVVEYGEDSHQEMGVAVHTPQAPQOGLVNLHPCPYSSLCRSPARD 1079
QY 1158 TQDHLAVFHLDBEASVRLTAEQARFFLHGVTLPVPIEEFSPFVEPRVSCISSHGAFGPNS 1217
DDB 1080 TQHHLAIFHLDBEASIRLTAEOAHFFLHSVTLVPVEEFSTEFVEPRVFCVSSHGTENPSS 1139
QY 1218 AACLPSRFPKPPQPIILRDCQVILPPLPGGLPLTHAQDLTPATSPAGERPRPPTAVDPDAEP 1277
DDB 1140 AACLASRFPKPPQPIILKDCQVLPPLPPLDTQSQELSPGAPPEGEQPRPPTAVDPDAEP 1199
QY 1278 TLLREPQATVFTTHVPTLGRYAFLLHGYPDAHPTFPVEVLINAGRVMQGHANASFCPHG 1337
DDB 1200 TLLRHPQGTVFTTQVPTLGRYAFLLHGYPVHPSPFVEVLINGRIWQGHANASFCPHG 1259
QY 1338 YGCRTLVCEGOALLDVTHSELTVTVRVPGRWLWLDYLVVVPENVYSFGYLREEPLDKS 1397
DDB 1260 YGCRTLVCEGTMLDVTDNELTVTVRVPGRWLWLDYLVIVPEDAYSSSYLQEEPLDKS 1319
QY 1398 YDFISHCAAQGYHISPSSSSLFCRNAASLSLFYNNGARPCGCHVEGATGPTCEPFGGQC 1457
DDB 1320 YDFISHCATQGYHISPSSSSPFCRNAATSLSLFYNNGALPCGCHVEGAVSPTCEPFGGQC 1379
QY 1458 PCHAHVIGRDCSRCATGYWGFPCNCRPCDCGARLDELGTQCICPPRTIPPDCCLLCQPQTF 1517
DDB 1380 PCRGHVIGRDCSRCATGYWGFPCNCRPCDCGARLDELGTQCICPPRTVPPDCLVCQPQSF 1439
QY 1518 GCHPLVGCCECNSGPGIQELTDPTCDTDSGQCKRCPNVTGRRCDTCSPGFHGYPRCRPC 1577
DDB 1440 GCHPLVGCCECNSGPGVQELTDPTCDMDSGQCRCPNVAGRRCDTCAFGYGYPSCRPC 1499
QY 1578 DCHEAGTAPGVCDPLTGQCYCKENVQGPCKDCQCSLGTFSLDAANPKGCTRCFCFGATERC 1637

DDB 1500 DCHEAGTMASVCDPLTGQCHCKENVQGSRCDCQCRVGTFSLDAANPKGCTRCFCFGATERC 1559
QY 1638 RSSSYTRQEFVDMEGWVLLSTDROVVPHERQPGTEMLRADLRHVPEAVPEAFPELYWQAP 1697
DDB 1560 GNSNLARHEFVDMEGWVLLSSDRQVVPHEHRPEIELLHADLR----SVADTFSELYWQAP 1615
QY 1698 PSYLGDRVSSYGGTLRYELHSETORGDVFPVPMESRPDVVLQGNQMSITFLEPAYPTPGHV 1757
DDB 1616 PSYLGDRVSSYGGTLHYELHSETORGDIFIPYESRPDVVLQGNQMSIAFLELAYPPPGQV 1675
QY 1758 HRGQLQVVEGNFRHTETRTNVSREELMMVLASLEQLQIRALFSQISSAVSLRRVALEVAS 1817
DDB 1676 HRGQLQVVEGNFRHLETHNPVSREELMMVLAGLEQLQIRALFSQISSAVSLRRVLEVAS 1735
QY 1818 PAGQGALASNVVELCLCPASRYGDSQCECAPGFYRDVKGLFGRVCPCQCHGSHDRCLPGS 1877
DDB 1736 EAGRGPASNVVELCMCPANYRGDSQCECAPGYRDTKGLFGRVCPCQCHGSHDRCLPGS 1795
QY 1878 GVCVDCQHNTGEGAHCCERCOAGFMSS-RDDPSAPCVSCPCPLSPVSNFAEGCVLRGGRTQ 1936
DDB 1796 GICVGCQHNTGEGDQCERCRCRPGFVSSDPSNPASPCVSCPCPLAVPSNNFADGCVLRNGRTQ 1855
QY 1937 CLCKPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSGNGDPNLLPSDDCDPLTGACRGCLR 1996
DDB 1856 CLCRPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSGNGDPNMIFFSDCDPLTGACRGCLR 1915
QY 1997 HTTGPRCEICAPGFYGNALLPGNCTRCDCCTPCGTEACDPHSGHCLCKAGVTGRRCDRCQE 2056
DDB 1916 HTTGPHCERCAPGFYGNALLPGNCTRCDCSPCGTETCDPQSGRCLCKAGVTGQRCDRCLE 1975
QY 2057 GHFGNGCGGCRPCACGPAEAGSECHPSQSGQCHCRPGTGMGPQCRECAPGYWGLPEQGCR 2116
DDB 1976 GYFGFEQCGCEPCACGPAKAGSECHPSQSGQCHCQPGTGTGPOCLECAPGYWGLPEKGCR 2035
QY 2117 CQCPGGRCDPHTGRNCNPPGLSGERCDCSCQHQVVPVPGPVGHSIHCEVCDHCVVLLLD 2176
DDB 2036 CQCPRGHCDPHTGHCTCPPGLSGERCDCSCQHQVVPVPGKPGHGHCEVCDHCVVLLLD 2095
QY 2177 DLERAGALLPAIHEQLRGINASSMAWARLHRLNASIADLQSQLRSPGLGPRHETAQQLLEV 2236
DDB 2096 DLERAGALLPAIREQLQGINASSAAWARLHRLNASIADLQSKLRPPGPRYQAAQLOTL 2155
QY 2237 EQQSTSLGQDARRLGGQAVGTRDQASQLLAGTEATLGHAKTLAAIRAVIDRTLSELMSQT 2296
DDB 2156 EQQISLQDDTERLGSQATGVQOQAGQLDTESTLGRAQKLLSVRAVGRALNELASRM 2215
QY 2297 GHLGLANASAPSGEQLLRTLAEVERLLWENRARDLGAPOAAAEAEALAAQRLARVQEQ 2356
DDB 2216 GQSGPDALVPSGEQLRWALAEVERLLWNRTRDLGAQGAVAEAEALAEARLMARVQEQ 2275
QY 2357 SSLWEENQALATQTRDRLAHEAGLMDLREALNRAVDATREAOELNSRNQERLEALQK 2416
DDB 2276 TSFWEENQSLATHIRDQLAQYESGLMDLREALNQAVENTTREAEELNSRNQERVKEALQWK 2335
QY 2417 QELSRDNATLQATLHAARDTLASVFRLLHSLDQAKEELERLAASLDGARTPLLQRMQTF 2476
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QY 2477 PAGSKRLRVEAAEAHAQQLGQALNLSSITLDVNQDRLTQRAIEASNAYSRILOAVQAAE 2536
DDB 2396 PASSKVDLVEAAEAHAQKLNQLAINLSGIILGINQDRFIQRAVEASNAYSRILOAVQAAE 2455
QY 2537 DAAGQALQOQADHTWATVVRQGLVDRAQQLLANSTALEEAMLOEQORQLVWAAALQARTQ 2596
DDB 2456 DAAGQALRQASRTWEMVVRGLAAGARQLLANSSALEETILGHQRLGLAQGRLOAAGIQ 2515
QY 2597 LRDVRAKQDQLEAHIQAAQAMLAMDTDETSKIAHAKAVAAEAQDTATRVQSLOQAMQEN 2656
DDB 2516 LHNVWARKNQLAQIQEAQAMLAMDTSETSEKIAHAKAVAAEALSTATHVQSLOQGMQKN 2575
QY 2657 VERWQGYEGLRGQDLQQAVALDAGHSVSTLEKTLPLQALLAKLSILENRGVHNASLALSASI 2716

Db 317 KWRQNTNARPPNCEPCNCHGHSNECKYDEEVNRKGLSLDIHGYDGGVCQNCQHNTVG 376

QY 403 VNCERCLPGFYRSPNHLPLDSPHVCRRCNCESDFTDGTCEDLTGRCYCPRNFSGERCDVCA 462

Db 377 INCNKCKPYRPGKHWNEDVCSPOCDYFFSTGHCHEETGNCECRAAFQPPSCDSCA 436

QY 463 EGFTGPPSCYPTPSSSNDTREQVLPAGQIVNCDCSAAGTOGNACRKDPVRVGRCLCKPNFQ 522

Db 437 YGYGYPCN-----RE-----CECNLNGTNGYHCEAESG-QQCPCKINFA 475

QY 523 GTHCELCAPIFYG-PGCQPCQCSSPGVADDRCDPDTGQCRVRGFEAGATCDRCAPGYFHF 581

Db 476 GAYCKQCAEGYGFPECKACECNKIGSITNDCNVTTGECCKLTNFGGDNCCERCKHGYFNY 535

QY 582 PLCQLCGCSPAGTLPBGCD-EAGRCLCQPEFAGPHCDRCRPGVHGFPNCOACTCDPRGAL 640

Db 536 PTCSYCDNDQGTSEIENKQSGQICREGGFGPRCDQCLPGFNYPCCKPCNCSSTGSS 595

QY 641 DQLCAGGLCRCPGYGTGTACQCSGPHGFPFPCVPCCHCSAEGSLHAAACDPRSGQCSGRP 700

Db 596 AITCDNTGKCNLNNFAGKQCTLTCTAGYISYPCDLPCHCDSHSGQVSCN-SDGQCLCQP 654

QY 701 RVTGLRCDTCTVPGAYNFPYCEAGSCHPAGLAPVDPALPEAQP-----CMCRAHVEGSPCD 756

Db 655 NFDGRQCDSCXRGFYNFPSCEDCNCDPAGV-IDKFAGCGSVFVGEKCKCKERVTRICN 712

QY 757 RCKPGFWGLSPNPEGCTRCSCDLRGLTGGVAECQPGTGQCFCXPHVCQACASCKDGF 816

Db 713 ECKPLYWNLNTSNTGECIECDWTGDTISALDCTSKSGQCPCPKHTQGRRCQCECRDGT 772

QY 817 GLDQADYFGCRSQRCDIGGALGQSCERTGVCRCRPNTOGPTCSEPARDHYLPDLHLRL 876

Db 773 DLDSASLFGCKDCSDVGGSWQSVCDKISGQCKCHPRITGLACTQPLTTHFFPTLHQFY 832

QY 877 ELEEAATPEGHAYRFGFNPLEFENFWSFGYQAQMAPVQPRIVARLNLTSPLFLVLYRVYN 936

Db 833 EYEDGSLPGSTQVRYDYDEAAFPFGSSKGYVVFNAIQNDVRNEVNFKSSLYRIVLYRVN 892

QY 937 RGAMSVGRVSVREGRSAACANCTAQSQPVAFPPSTEPAFITV--PORGFEPPFLNPG 994

Db 893 PNAENVATISVTSNDPLE-----VDQHVKVLLOPTSEPOFVTVAGPLGVKPSAIVLDPG 947

QY 995 TWALRVEA-EGVLLDYVLLPSAYYEAALLQLRVTEACTYRPSAQSGDNCLLYTHLPD 1053

Db 948 RYVFTTKANKNVMLDYFVLLPAAYYEAGILTRHISNPCEL-----GNMELCRHYKYASVE 1002

QY 1054 GPSPAAGLEALCRQDNLPRPCPTQELSPSHPLIT-----CTGSDVDVQLQVAVPQ 1106

Db 1003 VFSPAA--TPFVIGENSKPTNPVETYTDPHLQIVSHVGDIPVLSGSQNELHYIVDPRS 1060

QY 1107 GRYALVVEY-ANEDARQEVGAVHTPORAPQGLLSLHPCLYSTLCRGRTARDTQDHLAVF 1165

Db 1061 GRYIFVIDYISDRNFPDSYINLKLNDPDSVTSVLLYPCLYSTICR-TSVNEDGMEKSF 1119

QY 1166 HLDSE--ASVRLTA---EQARFFLHGVTLVPIEEFSPFVEPRVSCISSHGAFGPNAAAC 1220

Db 1120 YINKEDLPVVISADIEDGSRFPPIISVTAIPVDQWSIDYINPSPCVI-----HDQOC 1172

QY 1221 LPSRFPKPPQPIILRDCQVPLPPLPLTHAQDLTPATSPAGPRPRPPTAVDPDAEPTLL 1280

Db 1173 ATPKFRSVF-----DSKKIEFE-----TDHEDRIATNKP-----PYASLDERVKLVHL 1215

QY 1281 -REPQATVVFTHV---PTLGRYAFLLHGYQPAHPTFPVEVLINAGR-VWQGHANASFC 1334

Db 1216 DSQNEATIVESKVATKPNL--FVILVKYQPSHPKYQVYITLTAGKNQYDGKFDIQHC 1273

QY 1335 PHGYGCRTLVVCEGOALLDVTHSELITVTVRVEGRWLWLDYLVVVPENVYSFGYLREEPL 1394

Db 1274 PSSSGRGVIRPAGESFEI-DDEFKFTITDRSQSVWLDYLVVVPKQYNDLLVEETF 1332

QY 1395 DKSDFISHCAAQGVHISPSSSSLFCRNLAAASLSLFYNNGARPCGCHVEGATGPTCEPFG 1454

Db 1333 DQTKEFIQNCGHDFHITHNASD-FCKKSVFSLTADYNSGALPCNCDYAGSTSFECHPFG 1391

QY 1455 GQCPCHAHVIGRDCSRCATGYWGFNCRPCDC-GARLCDLGTQOCIPPRTIPTDCLLCQ 1513

Db 1392 GQCQCKPNVIERTCGRSRYGYFPDCKPCKPNSAMCEPTTGCMPNVIIGDLCEKCA 1451

QY 1514 POTFGCHPLVGCCECNCSGPGIQELTDPTCDTSDSQCKCRPNVTGRRCDTCSPGFHGYPR 1573

Db 1452 PNTYGFHQVIGCEECACNPMGIAN-GNSQCDLFGTCECRQNIIEGRACDVCSNGYFNFP 1510

QY 1574 CRPCDCHAGTAPGVCDPLTGQCYCKENVQPKCDQCSLGTSLDAAANPKGCTRCFCFGA 1633

Db 1511 CEQCSCHKPGTELEVCDKIDGACFCCKNVVGRDCDQCVDTYNLQESNPDGCTTCFCFGK 1570

QY 1634 TERCSSSYTRQEFVDMEGVLLSTDRQVVPHERQ-----PGTEM-----LRAD-- 1677

Db 1571 TSRC-DSAYLRVYVNVLLKHVSITTFEF--HEESIKFDMWPVPADEILLNETTLKADFT 1626

QY 1678 LRHVPEAVPEAPPELYWQAPPSYL---GDRVSSYGGTLRYELHSETQRGDVFPVMESRPD 1734

Db 1627 LREVNDERPAYFGVL-----DYLQNQNHISAYGGDLAYTLHFTSGFDGKYI---VAPD 1677

QY 1735 VVLQGNQMSITFLEPAYPTPGHVHRGQLQOLVEGNFRHTETRTNVTYSREELMMVLASLEQLQ 1794

Db 1678 VILFSEHNALVHTSYEQPSRNEPFTNRVIVESNFQ-TISGKPVSRADFMVLRDLKVIF 1736

QY 1795 IRALFSQISSAVSLRRVALEVASPAGQGA-----LASNVELCLCPASYRGSDSCQECAPGF 1849

Db 1737 IRANYWEQTLVTHLSDDVYLTLADEADGTGEYQFLA--VERCSPFGYSGHSCDCAPGY 1794

QY 1850 YRDVKGLFLGRVCPCQCHGHSRDLPGSGVCVDQHNTEGAHCERCQAGFM-SSRDDPSA 1908

Db 1795 YRDPGPGYGGYICPECNHGHSETCDCATGICSKQHGTEGDHCERCVSYYGNATNGTPG 1854

QY 1909 PCVSCPCPLSVPSNNFAEGCVL--RGERTQCLCKPGYAGASCERCAPGFFGNPLVLGSSC 1966

Db 1855 DCMICACPLPFDNSNNFATSCEISESGDIHCECKPGYTGPRCESCANGFYGEPESIGQVC 1914

QY 1967 QPCDCSGNDPNLLFSDCDPLTGACRGLRHTTGPRCEICAPGYGNALLPGNCTRCDC 2026

Db 1915 KPCECSGNINBEDQGS-CDTRTGECLRLNNTFGAACNLCAFGYGDAILKKNQCSCDCD 1973

QY 2027 PCGTEACDPHSGHCLCKAGVTGRRRCRQEGHGFNGCGGCRPCACGPAEGSECHPQSG 2086

Db 1974 DLGTQTCDFVGVCTCHENVIGDRCDRCKPDHYGFESGVGCRACDCCGAASNSTQCDPHTG 2033

QY 2087 QCHCRPGTMGPQCRECAPGYWGLPEQGCRRRCQCPGG-----RCDPHTGRCNCPPLSGER 2141

Db 2034 HCACKSGVTGRQCDRCAVDHWKYEXDGTGTCNQCYSRGFGCNPNTGKCQCLPGVIGDR 2093

QY 2142 CDTCSQHQVPVPGPGVGHSHCEVCHVCVLLDDLERAGALLPAIHEQLRGINASSMA 2201

Db 2094 CDACPNRWLIKDEG-----CQECNNCHHALLDVTDRLMYQIDSV---LEDFNSVTLA 2143

QY 2202 WARLHRLN-----ASIADLQSLRSPPLGPRHET-AQQL 2233

Db 2144 FFTSQKLNYYDQLADELEPKVKLLDPSVDSLSPSKANSELESDAKSYAKQVNTLANAF 2203

QY 2234 EVLEQQSTSLGQDARRLGGQAVGTRDQASQLLAGTEATLGHAKTL-LAAIRAVDRTLSEL 2292

Db 2204 DIRERSSTTLG-NITVAYDEAVKSADQAKAIAASVEAL---SKNLEAAASTKIDAALQEA 2259

QY 2293 MSQTGHLGLANASAPSGEQLLRTLAEVERLLWEMRRARDLGAPQAAAEALAAQRLARV 2352

Db 2260 QHILGQINGTSIELTPNEQVL---EKARKLYE-EVNTLVLPKAKQNSLNALKNDIGBF 2314

QY 2353 QEQLSSLWEENOALATQTRDLRAQHEAGIMDLREALN-RAVDATREAEQELNSRNOERLEE 2411

Db 2315 SDHLEDLFNWSBASQAKSAD-----VERRNVANQKAFD-----NSKFDTVSEQ 2357

QY 2412 ALQRKQEL-SRDNATLQATLHAARDTLASVFRLLHSLDQAKEELERLAASLDGARTPLLQ 2470

Db 2358 KLOAEKNIKDAGNFLINGDL-----TLNQINQKLDLNRDALNELNSFNKNVD-EELPVRE 2411

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:25:32 ; Search time 98.6077 Seconds
(without alignments)
10415.614 Million cell updates/sec

Title: US-10-037-182-4
Perfect score: 19876
Sequence: 1 DLYCKLVGGPVAGGDPNQTI.....QKALTQRHAKPSVSPLLWH 3635

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19876	100.0	3635	5 ABB81589	Abb81589 Mouse lam
2	19876	100.0	3635	5 AAM50357	Aam50357 Mouse lam
3	15839	79.7	3695	5 ABB81588	Abb81588 Human lam
4	15830.5	79.6	3696	5 AAE17310	Aae17310 Human lam
5	15815	79.6	3705	5 AAE17309	Aae17309 Human lam
6	14771	74.3	3600	5 ABB09501	Abb09501 Human lam
7	14706.5	74.0	3597	5 ABB09503	Abb09503 Human lam
8	12354.5	62.2	2743	5 ABB81598	Abb81598 Human lam
9	6643.5	33.4	3332	7 ADE08094	Ade08094 Novel pro
10	6092	30.7	1640	5 ABB09504	Abb09504 Human lam
11	5871.5	29.5	1601	4 AAM39009	Aam39009 Human pol
12	5012.5	25.2	3712	4 ABB64954	Abb64954 Drosophil
13	3968.5	20.0	1486	7 ADE09114	Ade09114 Novel pro
14	3488.5	17.6	953	5 AAM50358	Aam50358 Human lam
15	3325	16.7	908	5 ABB09502	Abb09502 Human lam
16	3096	15.6	3084	3 AAB19796	Aab19796 Mouse lam
17	3096	15.6	3106	3 AAB19795	Aab19795 Mouse lam
18	3096	15.6	3106	7 ADE61792	Ades1792 Rat Prote
19	3022	15.2	3122	7 ADE61794	Ades1794 Human Pro
20	3010.5	15.1	3089	3 AAB19792	Aab19792 Human lam
21	3010.5	15.1	3110	3 AAB19791	Aab19791 Human lam
22	3005	15.1	3088	3 AAB19794	Aab19794 Human lam
23	3005	15.1	3110	2 AAR71730	Aar71730 Merosin m
24	3005	15.1	3110	2 AAY15460	Aay15460 Human lam
25	3005	15.1	3110	3 AAB19793	Aab19793 Human lam

26	3005	15.1	3110	5 AAU84345	Aau84345 Protein L
27	2980	15.0	3070	5 AAO17359	Aao17359 Human lam
28	2925.5	14.7	3150	4 ABG20414	Abg20414 Novel hum
29	2792	14.0	3084	4 AAE11215	Aae11215 Mouse lam
30	2782	14.0	3084	2 AAW50891	Aaw50891 Mouse lam
31	2729.5	13.7	3075	2 AAW50892	Aaw50892 Human lam
32	2531.5	12.7	2901	4 ABG09763	Abg09763 Novel hum
33	2264	11.4	3319	4 ABB70376	Abb70376 Drosophil
34	2185	11.0	1823	5 ABP63020	Abp63020 Human pol
35	2184.5	11.0	1816	7 ADC01879	Adc01879 Human lam
36	2182.5	11.0	1816	7 ADC01877	Adc01877 Human lam
37	2171.5	10.9	1792	3 AAB48443	Aab48443 Human lam
38	2171.5	10.9	1800	3 AAB48445	Aab48445 Human lam
39	2171.5	10.9	1816	3 AAB48442	Aab48442 Human lam
40	2171.5	10.9	1824	3 AAB48444	Aab48444 Human lam
41	2149.5	10.8	1693	3 AAB48459	Aab48459 Human lam
42	2149.5	10.8	1693	3 AAB48457	Aab48457 Human lam
43	2149.5	10.8	1713	3 AAB48458	Aab48458 Human lam
44	2149.5	10.8	1713	6 ABR92102	Abr92102 Human cer
45	2149.5	10.8	1713	7 ADD29904	Add29904 Human lam

ALIGNMENTS

RESULT 1
ABB81589

ID ABB81589 standard; protein; 3635 AA.

XX ABB81589;

DT 19-SEP-2002 (first entry)

DE Mouse laminin alpha 5 amino acid sequence SEQ ID NO:4.

KW Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;
KW tissue repair development; laminin; healing; vascular tissue;
KW re-endothelialisation; vascular injury; cell attachment; cell stasis;
KW proliferation; migration.

XX Mus musculus.

XX WO200250111-A2.

PD 27-JUN-2002.

PF 21-DEC-2001; 2001WO-US051035.

PR 21-DEC-2000; 2000US-0257449P.

PR 28-MAR-2001; 2001US-0279282P.

PR 13-NOV-2001; 2001US-00279282.

XX (BIOS-) BIOSTRATUM INC.

XX Tryggvason K, Doi M, Thyboll J;

XX WPI; 2002-557650/59.

XX N-PSDB; ABQ72907.

XX New human laminin-10 proteins, useful for accelerating the healing of
XX vascular tissue, improving the biocompatibility of grafts, or for
XX promoting re-endothelialization at the site of vascular injuries.

XX Claim 9; Page 94-105; 231pp; English.

XX The present invention describes human laminin alpha 5. Also described is
XX an isolated laminin 10. Laminin 10 has vulnery activity. Laminins are
XX useful in maintaining cell/tissue phenotype as well as promoting cell
XX growth and differentiation in tissue repair development. Specifically,
XX laminin 10 can be used for accelerating the healing injuries of vascular
XX tissue, improving the biocompatibility of grafts useful for treating such
XX injuries, for promoting re-endothelialisation at the site of vascular
XX injuries, and promote cell attachment and subsequent cell stasis,

CC proliferation, differentiation, and/or migration. The present sequence
CC represents mouse laminin alpha 5 which is used in the exemplification of
CC the present invention
XX

SQ	Sequence 3635 AA;	
	Query Match 100.0%; Score 19876; DB 5; Length 3635;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 3635; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 DLYCKLVGGPVAGDPNQTIQGYCDICTAANSNKAHPVSNADIGTERWWQSPPLSRGLE 60	
Db	1 DLYCKLVGGPVAGDPNQTIQGYCDICTAANSNKAHPVSNADIGTERWWQSPPLSRGLE 60	
Qy	61 YNEVNVTLDLGOVPHVAYVLIKFANSRPDLWVLERSTDFGHTYQPWQFFASSKRDCLER 120	
Db	61 YNEVNVTLDLGOVPHVAYVLIKFANSRPDLWVLERSTDFGHTYQPWQFFASSKRDCLER 120	
Qy	121 FGPRTLERTQDDVICTTEYSRIIVPLENGEIVVSLVNGRPGALNPSYSPLLRDTTKATN 180	
Db	121 FGPRTLERTQDDVICTTEYSRIIVPLENGEIVVSLVNGRPGALNPSYSPLLRDTTKATN 180	
Qy	181 IRLRFLRTNTLLGHLMGKALRDPVTTRYYYSIKDISIGGRCVCHGHADVCDKOPLDPF 240	
Db	181 IRLRFLRTNTLLGHLMGKALRDPVTTRYYYSIKDISIGGRCVCHGHADVCDKOPLDPF 240	
Qy	241 RLQACAQHNTCGSCDRCCPGFNQPKPATTDTSANECQSCNCHGHAYDCYYDPEVDRN 300	
Db	241 RLQACAQHNTCGSCDRCCPGFNQPKPATTDTSANECQSCNCHGHAYDCYYDPEVDRN 300	
Qy	301 ASQNDNVYQGGVCLDCQHHTTGINCERCLPGFFRAPDQPLDSPHVCRPCDCESDFTDG 360	
Db	301 ASQNDNVYQGGVCLDCQHHTTGINCERCLPGFFRAPDQPLDSPHVCRPCDCESDFTDG 360	
Qy	361 TCEDLTGRCYCRPNFTGELCAACAEGYTDFPHCYPLPSFPHNDTREQVLPAGQIVNCDN 420	
Db	361 TCEDLTGRCYCRPNFTGELCAACAEGYTDFPHCYPLPSFPHNDTREQVLPAGQIVNCDN 420	
Qy	421 AAGTQGNACRKDPRLGRVCVKPNFRGAHCELCAPIGFHGPSCHPCQCSSPGVANSLCDPES 480	
Db	421 AAGTQGNACRKDPRLGRVCVKPNFRGAHCELCAPIGFHGPSCHPCQCSSPGVANSLCDPES 480	
Qy	481 GQCMCRTGFEGDRCDHCHALGYFHFPLCQLCGCSFAGTLPFGCDDEAGRCQCRPGFDGPHCD 540	
Db	481 GQCMCRTGFEGDRCDHCHALGYFHFPLCQLCGCSFAGTLPFGCDDEAGRCQCRPGFDGPHCD 540	
Qy	541 RCLPGYHGYPDCHACADPRGALDQCGVGGLCHCRPGNTGATCQECSPGFYGFPPSCIPC 600	
Db	541 RCLPGYHGYPDCHACADPRGALDQCGVGGLCHCRPGNTGATCQECSPGFYGFPPSCIPC 600	
Qy	601 HCSADGSLHTTCDPTTGQCRCRPRVTGLHCDMCPVGAIFYNFPYCEAGSCHPAGLAPANPAL 660	
Db	601 HCSADGSLHTTCDPTTGQCRCRPRVTGLHCDMCPVGAIFYNFPYCEAGSCHPAGLAPANPAL 660	
Qy	661 PETQAPCMCRAHVEGPSCDRCXPGYWGSLASNPEGCTRCSCDPRGTLGGVTECQNGQCF 720	
Db	661 PETQAPCMCRAHVEGPSCDRCXPGYWGSLASNPEGCTRCSCDPRGTLGGVTECQNGQCF 720	
Qy	721 CKAHVCGKTCACAKDGGFFGLDYADYFGCRSCRDYGGALGQCEPKTGACRCRPNTQGPT 780	
Db	721 CKAHVCGKTCACAKDGGFFGLDYADYFGCRSCRDYGGALGQCEPKTGACRCRPNTQGPT 780	
Qy	781 CSEPAKDHLYPDLHHRMLEBEAATPEGHAVRFGFNPLEFENFSWRGYAHNMAIQPRIVA 840	
Db	781 CSEPAKDHLYPDLHHRMLEBEAATPEGHAVRFGFNPLEFENFSWRGYAHNMAIQPRIVA 840	
Qy	841 RLNVTSFDLRLVFRYVNRGTSVNGQISVREEGLSSCTNCTEQSQPVAPPPSTEPAFV 900	
Db	841 RLNVTSFDLRLVFRYVNRGTSVNGQISVREEGLSSCTNCTEQSQPVAPPPSTEPAFV 900	
Qy	901 TVPQRGFGEPPVLPNGIWALLVYAEAGVLLDYVWLLPSTYYEALLQHRVTEACTYRPSAL 960	
Db	901 TVPQRGFGEPPVLPNGIWALLVYAEAGVLLDYVWLLPSTYYEALLQHRVTEACTYRPSAL 960	

Qy	961 HSTENCLVYAHLPDLGFFPSAAGTEALCRHDNSLPRPCPTQLSPSHPLATCFGSDVDIQ 1020	
Db	961 HSTENCLVYAHLPDLGFFPSAAGTEALCRHDNSLPRPCPTQLSPSHPLATCFGSDVDIQ 1020	
Qy	1021 LEMAVPQPGQYVLVVEYVGEDSHQEMGVAVHTPQAPQQGVNLNHPCPYSSSLCRSPARDT 1080	
Db	1021 LEMAVPQPGQYVLVVEYVGEDSHQEMGVAVHTPQAPQQGVNLNHPCPYSSSLCRSPARDT 1080	
Qy	1081 QHHLAIFHLDSIASIRLTAEQAHFFLHSLVTLVPVEEFSTEFVEPRVFCVSSHGTNFPSSA 1140	
Db	1081 QHHLAIFHLDSIASIRLTAEQAHFFLHSLVTLVPVEEFSTEFVEPRVFCVSSHGTNFPSSA 1140	
Qy	1141 ACLASRFKPPQPIILKDCQVLPPLPDLPLTQSQELSPGAPPEGPQPRPPTAVDPNAEPT 1200	
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Qy	1201 LLRHPQGTVVFTTQVPTLGRYAFLHGYQVHPSPFPVEVLINGGRIWQHANASFCPHGY 1260	
Db	1201 LLRHPQGTVVFTTQVPTLGRYAFLHGYQVHPSPFPVEVLINGGRIWQHANASFCPHGY 1260	
Qy	1261 GCRTLVLCEGQTMLDVTDNELTIVTVRVEGRWLWLDYVLIVPEDAYSSSYLQEEPLDKSY 1320	
Db	1261 GCRTLVLCEGQTMLDVTDNELTIVTVRVEGRWLWLDYVLIVPEDAYSSSYLQEEPLDKSY 1320	
Qy	1321 DFISHCATQGYHISPSSSSPFCRNAATSLIFYNNGALPCGCHEVGAVSPTCEPFGGQCP 1380	
Db	1321 DFISHCATQGYHISPSSSSPFCRNAATSLIFYNNGALPCGCHEVGAVSPTCEPFGGQCP 1380	
Qy	1381 CRGHVIGRDCSRCATGYWGFNCRPCDCGARLDELGTQCICPPRTVPDCLVCQPQSF 1440	
Db	1381 CRGHVIGRDCSRCATGYWGFNCRPCDCGARLDELGTQCICPPRTVPDCLVCQPQSF 1440	
Qy	1441 CHPLVGCEECNCSPGVQELTDPTCDMDSGQCRPNVAGRRCDTCAPIGFYGYPSCRPCD 1500	
Db	1441 CHPLVGCEECNCSPGVQELTDPTCDMDSGQCRPNVAGRRCDTCAPIGFYGYPSCRPCD 1500	
Qy	1501 CHEAGTMASVCDPLTGQCHCKENQVQSRCDQCRVGTFSLDAAANPKGCTRCFCFGATERCG 1560	
Db	1501 CHEAGTMASVCDPLTGQCHCKENQVQSRCDQCRVGTFSLDAAANPKGCTRCFCFGATERCG 1560	
Qy	1561 NSNLARHEFVDMEGWVLLSSDRQVVPHEHRPEIELLHADLRVADTFSELYWQAPPSYLG 1620	
Db	1561 NSNLARHEFVDMEGWVLLSSDRQVVPHEHRPEIELLHADLRVADTFSELYWQAPPSYLG 1620	
Qy	1621 DRVSSYGGTLHYELHSETQRGDIFIPYESRPDVVLQGNQMSIAFLELAYPPPGQVHRGQL 1680	
Db	1621 DRVSSYGGTLHYELHSETQRGDIFIPYESRPDVVLQGNQMSIAFLELAYPPPGQVHRGQL 1680	
Qy	1681 QLVEGNFRHLETHNPVSREELMMVLAGLEQLQIRALFSQTSSSVSLRRVVLVASEARG 1740	
Db	1681 QLVEGNFRHLETHNPVSREELMMVLAGLEQLQIRALFSQTSSSVSLRRVVLVASEARG 1740	
Qy	1741 PPASNVELCMCPANYRGDSCQECAPGYRDTKGLFLGRVCVPCQCHGSHDRCLPGSGICVG 1800	
Db	1741 PPASNVELCMCPANYRGDSCQECAPGYRDTKGLFLGRVCVPCQCHGSHDRCLPGSGICVG 1800	
Qy	1801 CQHNTEGDQCCRCRPGFVSSDPSNPASPCVSCPCPLAVPSNNFADGCVLRNGRTQCLCRP 1860	
Db	1801 CQHNTEGDQCCRCRPGFVSSDPSNPASPCVSCPCPLAVPSNNFADGCVLRNGRTQCLCRP 1860	
Qy	1861 GYAGASCERCAPGFFGNPLVLGSSCQPCDCSNGNDPNMIFSDCDPLTGACRGLRHTTGP 1920	
Db	1861 GYAGASCERCAPGFFGNPLVLGSSCQPCDCSNGNDPNMIFSDCDPLTGACRGLRHTTGP 1920	
Qy	1921 HCECAPGFYGNALLPGNCTRCDCSPCGTETCDPQSGRCLCKAGVTGQRCRCLRGYFGF 1980	
Db	1921 HCECAPGFYGNALLPGNCTRCDCSPCGTETCDPQSGRCLCKAGVTGQRCRCLRGYFGF 1980	
Qy	1981 EQCQGRPCACGPAKSGECPQSGQCHCQPGTTGFPQCLECAPGYWGLPEKGCRCRCQCP 2040	
Db	1981 EQCQGRPCACGPAKSGECPQSGQCHCQPGTTGFPQCLECAPGYWGLPEKGCRCRCQCP 2040	

2041 GHCDPHTGCTCPPGLSGERCDCSQHQHVPVPGKPGGGHGHCEVCHVCVLLDDDLERA 2100
2041 GHCDPHTGCTCPPGLSGERCDCSQHQHVPVPGKPGGGHGHCEVCHVCVLLDDDLERA 2100
2101 GALLPAIRLOGINASSAAWARLHRLNASIADLQSKLRRPPGPYQAAQQLQTLQOQSI 2160
2101 GALLPAIRLOGINASSAAWARLHRLNASIADLQSKLRRPPGPYQAAQQLQTLQOQSI 2160
2161 SLQODTERLGSQATGVQOAGQLDDTTSTELGRAOKLLESVRAVGRALNELASRMGQGSP 2220
2161 SLQODTERLGSQATGVQOAGQLDDTTSTELGRAOKLLESVRAVGRALNELASRMGQGSP 2220
2221 GDALVPSGEOLRWALAEVERLLWDMRTRDLGAQGAVAEAEALAEQRLMARVQEQLTSFWE 2280
2221 GDALVPSGEOLRWALAEVERLLWDMRTRDLGAQGAVAEAEALAEQRLMARVQEQLTSFWE 2280
2281 ENQSLATHIRDOLAQYESGLMDLREALNQAVNTTREAELNSRNOERVKELQWKQELSQ 2340
2281 ENQSLATHIRDOLAQYESGLMDLREALNQAVNTTREAELNSRNOERVKELQWKQELSQ 2340
2341 DNATLKATLOAASLIIGHVSELLQIDQAKEDLEHLAASLDGAWTPLLKEMQAFSPASSK 2400
2341 DNATLKATLOAASLIIGHVSELLQIDQAKEDLEHLAASLDGAWTPLLKEMQAFSPASSK 2400
2401 VDLVEABAAHAQKLNQALNLSGIILGINQDRFIQRAVEASNAYSSILQAVQAAEDAAGQ 2460
2401 VDLVEABAAHAQKLNQALNLSGIILGINQDRFIQRAVEASNAYSSILQAVQAAEDAAGQ 2460
2461 ALRQASRTWEMVQVQRLAAGAROLLANSALLEETILGHQGRGLGAQGRLOAAGIQLHNWV 2520
2461 ALRQASRTWEMVQVQRLAAGAROLLANSALLEETILGHQGRGLGAQGRLOAAGIQLHNWV 2520
2521 ARKNQLAAQIQEAQAMLAMDTSETSEKIAHAKAVAAEALSTATHVQSLOQGMQKNVERWQ 2580
2521 ARKNQLAAQIQEAQAMLAMDTSETSEKIAHAKAVAAEALSTATHVQSLOQGMQKNVERWQ 2580
2581 SQLGGLQGQDLSQVERDASSVSTLEKTLPLLAKLSRLNENRGVHNASLALSANIGRVRK 2640
2581 SQLGGLQGQDLSQVERDASSVSTLEKTLPLLAKLSRLNENRGVHNASLALSANIGRVRK 2640
2641 LTAQARSAASKVKVSMKFNKSGVRLRPPRDLADLAAYTALKFHIQSPVPAPEPGKNTGD 2700
2641 LTAQARSAASKVKVSMKFNKSGVRLRPPRDLADLAAYTALKFHIQSPVPAPEPGKNTGD 2700
2701 HFVLYMGSQATGDYMGVSLRNQKVHVYRLGKAGPTTSLIDENIGEQAFAVSIDRTLOF 2760
2701 HFVLYMGSQATGDYMGVSLRNQKVHVYRLGKAGPTTSLIDENIGEQAFAVSIDRTLOF 2760
2761 GHMSVTVEKQMVHEIKGDTVAPGSEGLNLHPDDFFVYGGYPSNFTPPEPLRFPYGLGC 2820
2761 GHMSVTVEKQMVHEIKGDTVAPGSEGLNLHPDDFFVYGGYPSNFTPPEPLRFPYGLGC 2820
2821 IEMETLINEEVVSLYNFEQTFMLDTAVDKPCARSKATGDPWLTDGSLDGSGFARISFEKQ 2880
2821 IEMETLINEEVVSLYNFEQTFMLDTAVDKPCARSKATGDPWLTDGSLDGSGFARISFEKQ 2880
2881 FSNTRKRFDOELRLVSYNGIIIFLQKESQFLCLAVQEGTLVLFYDFGSLGKKADPLQPPQA 2940
2881 FSNTRKRFDOELRLVSYNGIIIFLQKESQFLCLAVQEGTLVLFYDFGSLGKKADPLQPPQA 2940
2941 LTAASKAIOVFLLAGNRKRVLRVERATVFSVDQDNMLEMADAYYLGVPPEQLPLSLRQ 3000
2941 LTAASKAIOVFLLAGNRKRVLRVERATVFSVDQDNMLEMADAYYLGVPPEQLPLSLRQ 3000
3001 LFPSCGSGVRCIKGKIKALGKYVDLKRLLNTTGISFGCTADLLVGRMTMTHGHGFLPLALPD 3060
3001 LFPSCGSGVRCIKGKIKALGKYVDLKRLLNTTGISFGCTADLLVGRMTMTHGHGFLPLALPD 3060
3061 VAPITEVVYSGFGFRGTQDNLLYYRTSPDGPYQVSLREGHVTLRFNMQEVETQRFVADG 3120
3061 VAPITEVVYSGFGFRGTQDNLLYYRTSPDGPYQVSLREGHVTLRFNMQEVETQRFVADG 3120
3121 APHYVAFYSNVTGVWLYVDDQLQLVKSHERTTTPMLQLOPPEPSRLLGLLPVSGTFFHNS 3180

3121 APHYVAFYSNVTGVWLYVDDQLQLVKSHERTTTPMLQLOPPEPSRLLGLLPVSGTFFHNS 3180
3181 GCISNVFVQRLRGPQRVFDLHQNMGSVNVSVGCTPAQLIETSRATAQKVSRRSQPSQDL 3240
3181 GCISNVFVQRLRGPQRVFDLHQNMGSVNVSVGCTPAQLIETSRATAQKVSRRSQPSQDL 3240
3241 ACTTPWLPGTIQDAYQFGGPLPSYLFQVGISPSHRNRLHLSMLVRPHAAASQGLLSTAPM 3300
3241 ACTTPWLPGTIQDAYQFGGPLPSYLFQVGISPSHRNRLHLSMLVRPHAAASQGLLSTAPM 3300
3301 SGRSPSLVFLNHHGFVAQTEGPPRLQVQSRQHSRAGQWHRVSVRWGMQQLVVDGSGQ 3360
3301 SGRSPSLVFLNHHGFVAQTEGPPRLQVQSRQHSRAGQWHRVSVRWGMQQLVVDGSGQ 3360
3361 TWSOKALHHRVPRAERPQPYTLVSVGGLPASSYSSKLPVSVGFSGCLKKLQLDKQPLRTPT 3420
3361 TWSOKALHHRVPRAERPQPYTLVSVGGLPASSYSSKLPVSVGFSGCLKKLQLDKQPLRTPT 3420
3421 QMVGVTPCVSGPLEDGLFFPGSEGVVTTLELPKAKMPVVSLELEMRPLAAAGLIHFHIGQAL 3480
3421 QMVGVTPCVSGPLEDGLFFPGSEGVVTTLELPKAKMPVVSLELEMRPLAAAGLIHFHIGQAL 3480
3481 ATPYNQLKVLTEQVLLQANDGAGEPSTWVTYPKLCGRWHRVAVIMGRDTRLREVDVTSN 3540
3481 ATPYNQLKVLTEQVLLQANDGAGEPSTWVTYPKLCGRWHRVAVIMGRDTRLREVDVTSN 3540
3541 HTTGRLPESLAGSPALLHLGSLPKSSTARPELPAVRGCLRKLKLLINGAPVNTVTSVQIQGA 3600
3541 HTTGRLPESLAGSPALLHLGSLPKSSTARPELPAVRGCLRKLKLLINGAPVNTVTSVQIQGA 3600
3601 VGMRCPSGTLALSQKGKALTQORHAKPSVSPLLWH 3635
3601 VGMRCPSGTLALSQKGKALTQORHAKPSVSPLLWH 3635

RESULT 2

AAM50357

ID AAM50357 standard; protein; 3635 AA.

XX

AC AAM50357;

XX

DT 18-FEB-2002 (first entry)

XX

DE Mouse laminin-15 alpha 5 chain.

XX

XX Laminin-15; mouse; retina; eye; therapy; ophthalmological;

KW antiinflammator; rod dystrophy; rod-cone dystrophy;

KW retinitis pigmentosa; macular degeneration; retinal detachment.

XX

OS Mus musculus.

XX

PN WO200183516-A1.

XX

PD 08-NOV-2001.

XX

PF 01-MAY-2001; 2001WO-US013943.

XX

PR 01-MAY-2000; 2000US-0200863P.

XX

PA (MASS-) MASSACHUSETTS GEN HOSPITAL.

XX

PI Burgeson RE, Brunken W, Champlaud M, Hunter D;

XX

DR WPI; 2002-041478/05.

XX

DR N-PSDB; AAI70816.

XX

PT Novel substantially pure preparation comprising laminin having laminin chain alpha 5, beta 2, and gamma 3, useful for treating retinal disorders such as retinitis pigmentosa, macular degeneration, retinal detachment.

PS Disclosure; Fig 1A-B; 58pp; English.

XX

CC The present sequence is that of the alpha 5 chain of mouse laminin-15, a
CC novel member of the laminin family that is produced in the retina. The
CC retina produces 2 novel laminin trimers: laminin-14 (alpha 4, beta 2,
CC gamma 3) and laminin-15 (alpha 5, beta 2, gamma 3). These are expressed
CC within the inter-photoreceptor matrix and in the outer plexiform layer,
CC and may serve to stabilise retinal synapses. The invention provides
CC laminin-15 preparations and cells comprising a nucleic acid encoding the
CC laminin alpha 5, beta 2 and gamma 3 chains, and which are capable of
CC producing laminin-15. The laminin-15 preparation is used in claimed
CC methods of: increasing retina immunophotoreceptor matrix stability;
CC increasing the stability of retina photoreceptor compounds, especially an
CC outer segment, inner segment or synapse; increasing retina adhesion;
CC treating a disorder associated with retina degeneration, especially rod
CC dystrophy, rod-cone dystrophy, retinitis pigmentosa, macular degeneration
CC and retinal detachment; increasing the stability of synapses of the
CC central nervous system or peripheral nervous system; stimulating
CC neuroregeneration, axon outgrowth or synapse formation; preparing an
CC implant, e.g. a catheter, artificial joint, retinal implant, timed
CC releasing device, neural cell growth guide or artificial tissue, by
CC coating with the laminin-15 preparation; and increasing photosensitivity
CC by implanting a tip coated with the laminin-15 preparation into an eye.
CC The laminin may be recombinant, and the 3 chains co-expressed in the same
CC cell or expressed in different cells
XX
SQ

Sequence 3635 AA;

Query Match 100.0%; Score 19876; DB 5; Length 3635;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3635; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	DLYCKLVGGPVAGGDPNQITQGOYCDICTAANSNKAHPVSN	NAIDGTERWQSPPLSRGLE	60
Db	1	DLYCKLVGGPVAGGDPNQITQGOYCDICTAANSNKAHPVSN	NAIDGTERWQSPPLSRGLE	60
Qy	61	YNEVNVTLDLGQVHFVAYVLIKFNANPRPDLWLVERSTDFGHTYQ	WPQWPFASSKRDCLER	120
Db	61	YNEVNVTLDLGQVHFVAYVLIKFNANPRPDLWLVERSTDFGHTYQ	WPQWPFASSKRDCLER	120
Qy	121	FGPRTLERITQDDVICTEYSRIVPLENGEIVVSLVNGRPGALNFS	YSPLLRDFTKATN	180
Db	121	FGPRTLERITQDDVICTEYSRIVPLENGEIVVSLVNGRPGALNFS	YSPLLRDFTKATN	180
Qy	181	IRLRLFRNTLLGLHMGKALRDPVTTRRYYSIKDISIGRCVCHGHAD	VCDKADPLDPF	240
Db	181	IRLRLFRNTLLGLHMGKALRDPVTTRRYYSIKDISIGRCVCHGHAD	VCDKADPLDPF	240
Qy	241	RLQACQHNTCGGSCDRCCPGFNQPPWKPAATDSANEQSCNCHGHAYD	CYYDPEVDRN	300
Db	241	RLQACQHNTCGGSCDRCCPGFNQPPWKPAATDSANEQSCNCHGHAYD	CYYDPEVDRN	300
Qy	301	ASQNDNVYQGGGVCLDCQHTTGINCERCLPGFFRAPDQPLDSPHVC	RPCDESDFTDG	360
Db	301	ASQNDNVYQGGGVCLDCQHTTGINCERCLPGFFRAPDQPLDSPHVC	RPCDESDFTDG	360
Qy	361	TCEDLTGRCYCRPNFTGELCAACAEGYTDFPHCYPLPSPPHNDTREQ	VLPAGQIVNCDN	420
Db	361	TCEDLTGRCYCRPNFTGELCAACAEGYTDFPHCYPLPSPPHNDTREQ	VLPAGQIVNCDN	420
Qy	421	AAGTQGNACRKPRLGRVCVKPNFRGAHCELAPGFHGPSCHPCQCSSPG	VANSICDPES	480
Db	421	AAGTQGNACRKPRLGRVCVKPNFRGAHCELAPGFHGPSCHPCQCSSPG	VANSICDPES	480
Qy	481	GQCMCTGFEGDRCDHCHALGYFHFPLCOLCGCSPAGTLPPEGCD	EAGRCQCRPGDGHCD	540
Db	481	GQCMCTGFEGDRCDHCHALGYFHFPLCOLCGCSPAGTLPPEGCD	EAGRCQCRPGDGHCD	540
Qy	541	RCLPGHYGPDCHACACDPRGALDQCCGVGLCHCRPGNTGATCQECSP	GFYFPFSCIPC	600
Db	541	RCLPGHYGPDCHACACDPRGALDQCCGVGLCHCRPGNTGATCQECSP	GFYFPFSCIPC	600
Qy	601	HCSADGSLHTTCDPTTGQCRPRVTGLHCDMCPVGAYNFPYCEAGSCH	PAGLAPANPAL	660
Db	601	HCSADGSLHTTCDPTTGQCRPRVTGLHCDMCPVGAYNFPYCEAGSCH	PAGLAPANPAL	660

Qy	661	PETQAPCMCRAHVEGSPCDRCKPGYWGSLASNPBEGCTRCSCDPRGTLGGVT	ECQNGQCF	720
Db	661	PETQAPCMCRAHVEGSPCDRCKPGYWGSLASNPBEGCTRCSCDPRGTLGGVT	ECQNGQCF	720
Qy	721	CKAHVCGKTCACAKDGFGLDYADYFGCRSCRCVGGALGQCEPKTGACRC	PNTQGPT	780
Db	721	CKAHVCGKTCACAKDGFGLDYADYFGCRSCRCVGGALGQCEPKTGACRC	PNTQGPT	780
Qy	781	CSEPAKDHLYPLDLHMRLELEAATPEGHAVRFGFNPLEFENFSWRGYAHM	AIQPRIVA	840
Db	781	CSEPAKDHLYPLDLHMRLELEAATPEGHAVRFGFNPLEFENFSWRGYAHM	AIQPRIVA	840
Qy	841	RLNVTSPDLFRLVFRYVNRGSTSVNGQISVREEGKLSSTNCTEQSQP	VAFPPSTEPAFV	900
Db	841	RLNVTSPDLFRLVFRYVNRGSTSVNGQISVREEGKLSSTNCTEQSQP	VAFPPSTEPAFV	900
Qy	901	TVPQRGFGEFVLNPGIWAALLVEAGVLLDYVLLPSTYYEAAALLQHRV	TEACTYRPSAL	960
Db	901	TVPQRGFGEFVLNPGIWAALLVEAGVLLDYVLLPSTYYEAAALLQHRV	TEACTYRPSAL	960
Qy	961	HSTENCLVYAHLPDLGPFSAAGTEALCRHDNSLRPRCPTEQLSPSHPP	PLATCFGSDVDIQ	1020
Db	961	HSTENCLVYAHLPDLGPFSAAGTEALCRHDNSLRPRCPTEQLSPSHPP	PLATCFGSDVDIQ	1020
Qy	1021	LEMAVPPQGOYVLVVEYVGEDSHQEMGVAVHTPORAPQOQVNLNHP	CPYSSLCRSPARDT	1080
Db	1021	LEMAVPPQGOYVLVVEYVGEDSHQEMGVAVHTPORAPQOQVNLNHP	CPYSSLCRSPARDT	1080
Qy	1081	QHHLAIFHLDSEASIRLTAEQAHHFLLHSVTLVPVEEFSTEFVEPR	VFVSVSHGTFNPSSA	1140
Db	1081	QHHLAIFHLDSEASIRLTAEQAHHFLLHSVTLVPVEEFSTEFVEPR	VFVSVSHGTFNPSSA	1140
Qy	1141	ACLASRFPKPPQPIILKDCQVLLPPLDPLTQSOELSPGAPPEGP	QPPRPTAVDPNAEPT	1200
Db	1141	ACLASRFPKPPQPIILKDCQVLLPPLDPLTQSOELSPGAPPEGP	QPPRPTAVDPNAEPT	1200
Qy	1201	LLRHPQGTWVFTTQVPTLGRYAFLLHGYQPVHPSFPVEVLINGGR	IWOQHANASFCPHGY	1260
Db	1201	LLRHPQGTWVFTTQVPTLGRYAFLLHGYQPVHPSFPVEVLINGGR	IWOQHANASFCPHGY	1260
Qy	1261	GCRTLVLCEGQTMLDVTDNELTVTVRVPEGRWLMDVYLIIVPE	DAYSSSYLQEEPLDKSY	1320
Db	1261	GCRTLVLCEGQTMLDVTDNELTVTVRVPEGRWLMDVYLIIVPE	DAYSSSYLQEEPLDKSY	1320
Qy	1321	DFISHCATQGYHISPSSSPFCRNAATSLSFYNNGALPCGCGHE	VAGVAVSPTCEPFGQCP	1380
Db	1321	DFISHCATQGYHISPSSSPFCRNAATSLSFYNNGALPCGCGHE	VAGVAVSPTCEPFGQCP	1380
Qy	1381	CRGHVIGRDCSRCATGYWGFPCNCRPCDCGARLCELTGQICPP	RTVPPDCLVCQPSFG	1440
Db	1381	CRGHVIGRDCSRCATGYWGFPCNCRPCDCGARLCELTGQICPP	RTVPPDCLVCQPSFG	1440
Qy	1441	CHPLVGCEECNCSGPGVQELTPTCDMDSGQCRCPNVAGRRCDT	CAPGFYGYPSCRPCD	1500
Db	1441	CHPLVGCEECNCSGPGVQELTPTCDMDSGQCRCPNVAGRRCDT	CAPGFYGYPSCRPCD	1500
Qy	1501	CHEAGTMASVCDPLTGQCHCKENVQGSRCQCRVGTFSILDAAN	PKGCTRCFCFGATERCG	1560
Db	1501	CHEAGTMASVCDPLTGQCHCKENVQGSRCQCRVGTFSILDAAN	PKGCTRCFCFGATERCG	1560
Qy	1561	NSNLARHEFVDMEGWVLLSSDRQVVPHEHRPEIELLHADLR	SVADTFSELYWQAPPSYLG	1620
Db	1561	NSNLARHEFVDMEGWVLLSSDRQVVPHEHRPEIELLHADLR	SVADTFSELYWQAPPSYLG	1620
Qy	1621	DRVSSYCGTLYELHSETQRGDIPIPYESRDPDVVLQGNQMS	IAFLELAYPPPGQVHRGQL	1680
Db	1621	DRVSSYCGTLYELHSETQRGDIPIPYESRDPDVVLQGNQMS	IAFLELAYPPPGQVHRGQL	1680
Qy	1681	QLVEGNFRHLETHNPVSREELMMVLAGLEQLQIRALFSQTS	SSSVSLRRVVLEVASEAGRG	1740
Db	1681	QLVEGNFRHLETHNPVSREELMMVLAGLEQLQIRALFSQTS	SSSVSLRRVVLEVASEAGRG	1740

QY 1741 PPASNVELCMCPANYRGDSQBCAPGYRDTKGLFLGRCVPCQCHGHSRCLPGSGICVG 1800
Db 1741 PPASNVELCMCPANYRGDSQBCAPGYRDTKGLFLGRCVPCQCHGHSRCLPGSGICVG 1800
QY 1801 COHNTGDCERCRCRPGFVSSDPSPNPASPCVCPCLAVPSNNFADGCVLRNGRTQCLCRP 1860
Db 1801 COHNTGDCERCRCRPGFVSSDPSPNPASPCVCPCLAVPSNNFADGCVLRNGRTQCLCRP 1860
QY 1861 GYAGASCERCAPGFFGNPLVLGSSCQPCDCSNGDGNMIFSDCDPLTGACRCGLRHTTGP 1920
Db 1861 GYAGASCERCAPGFFGNPLVLGSSCQPCDCSNGDGNMIFSDCDPLTGACRCGLRHTTGP 1920
QY 1921 HCERCAPGFYGNALLPGNCTRCDCSPCGTETCDPQSGRCLCKAGVTGQRCDRCLEGYFGF 1980
Db 1921 HCERCAPGFYGNALLPGNCTRCDCSPCGTETCDPQSGRCLCKAGVTGQRCDRCLEGYFGF 1980
QY 1981 EQCQGRPCACGPAKGSCHPSQSGCHCQPGTTGPOCLECAPGYWGLPEKGCRRCCQPR 2040
Db 1981 EQCQGRPCACGPAKGSCHPSQSGCHCQPGTTGPOCLECAPGYWGLPEKGCRRCCQPR 2040
QY 2041 GHCDPHTGHCTCPPGLSGERCDTCSQHQVFPVPGKPGHGIHCEVCDHCVVLLJDDDLERA 2100
Db 2041 GHCDPHTGHCTCPPGLSGERCDTCSQHQVFPVPGKPGHGIHCEVCDHCVVLLJDDDLERA 2100
QY 2101 GALLPAIREQLQGINASSAAWARLHRLNASIADLOSKLRRPPGPRYQAAQLOTLQOQSI 2160
Db 2101 GALLPAIREQLQGINASSAAWARLHRLNASIADLOSKLRRPPGPRYQAAQLOTLQOQSI 2160
QY 2161 SLOQDTERLGSQATGVQGAQQLDDTTTESTLGRAQKLLSVRAVGRALNELASRMGQGSP 2220
Db 2161 SLOQDTERLGSQATGVQGAQQLDDTTTESTLGRAQKLLSVRAVGRALNELASRMGQGSP 2220
QY 2221 GDALVPSGEQLRWALAEVERLLWDMRTRDLGAQGAVAEAEALAEAQRLMARVQEQLTSFWE 2280
Db 2221 GDALVPSGEQLRWALAEVERLLWDMRTRDLGAQGAVAEAEALAEAQRLMARVQEQLTSFWE 2280
QY 2281 ENQSLATHIRDQLAQYESGLMDLREALNQA VNTTREAELNSRNOERVKALQWKQELSQ 2340
Db 2281 ENQSLATHIRDQLAQYESGLMDLREALNQA VNTTREAELNSRNOERVKALQWKQELSQ 2340
QY 2341 DNATLKATLQAASLIIGHVSELLQGIDQAKEDLEHLAASLDGAWTPLLKRMQAFSPASSK 2400
Db 2341 DNATLKATLQAASLIIGHVSELLQGIDQAKEDLEHLAASLDGAWTPLLKRMQAFSPASSK 2400
QY 2401 VDLVEAAEAHAQKLNQLAINLSGII LGINQDRFIQRAVEASNAYSSIIQAVQAAEDAAGQ 2460
Db 2401 VDLVEAAEAHAQKLNQLAINLSGII LGINQDRFIQRAVEASNAYSSIIQAVQAAEDAAGQ 2460
QY 2461 ALRQASRTWEMVVQRLAAGARQLLANSSALEETIIGHQGRGLGAQGRLOAAGIQLHNW 2520
Db 2461 ALRQASRTWEMVVQRLAAGARQLLANSSALEETIIGHQGRGLGAQGRLOAAGIQLHNW 2520
QY 2521 ARKNQLAAQIQEAQAMLAMDTSETSEKIAHAKAVAAEALSTATHVQSQLOGMQKNVERWQ 2580
Db 2521 ARKNQLAAQIQEAQAMLAMDTSETSEKIAHAKAVAAEALSTATHVQSQLOGMQKNVERWQ 2580
QY 2581 SOLGGLQGQDLSQVERDASSVSTLEKTL PQLLAKLSRLENRGVHNASLALSANIGVRK 2640
Db 2581 SOLGGLQGQDLSQVERDASSVSTLEKTL PQLLAKLSRLENRGVHNASLALSANIGVRK 2640
QY 2641 LIAQARSAASKVKVSMKFNRSVRLRPPRDLADLAAYTALKFHIQSPVPAPEPGKNTGD 2700
Db 2641 LIAQARSAASKVKVSMKFNRSVRLRPPRDLADLAAYTALKFHIQSPVPAPEPGKNTGD 2700
QY 2701 HFVLYMGSRQATGDMGVSLRNQKVHVWVYRLGKACPTTLSIDENIGEQAFAVSIDRTLQF 2760
Db 2701 HFVLYMGSRQATGDMGVSLRNQKVHVWVYRLGKACPTTLSIDENIGEQAFAVSIDRTLQF 2760
QY 2761 GHMSVTVEKOMVHEIKGDTVAPGSEGLLNLPDPDFVYVGGYPSNFTPEPLRFPGYLGC 2820
Db 2761 GHMSVTVEKOMVHEIKGDTVAPGSEGLLNLPDPDFVYVGGYPSNFTPEPLRFPGYLGC 2820
QY 2821 IEMETLNEEVVSLYNFETQFMLDTA VDKPCARSKATGDPWLTGDSYLDGSGFARISFEKQ 2880

Db 2821 IEMETLNEEVVSLYNFETQFMLDTA VDKPCARSKATGDPWLTGDSYLDGSGFARISFEKQ 2880
QY 2881 FSNTKRFDDQELRLVSYNGIIFFLKQESQFLCLAVQEGTLVLFYDFGSLKKADPLQPPQA 2940
Db 2881 FSNTKRFDDQELRLVSYNGIIFFLKQESQFLCLAVQEGTLVLFYDFGSLKKADPLQPPQA 2940
QY 2941 LTAASKAIOVFLLAGNRKRVLVRVERATVFSVDQDNMLEMADAYYLGVPPEQLPLSLRQ 3000
Db 2941 LTAASKAIOVFLLAGNRKRVLVRVERATVFSVDQDNMLEMADAYYLGVPPEQLPLSLRQ 3000
QY 3001 LFPSSGSGVRGCIKIGIKALGKVVDLKRLLNTTGISFGCTADLLVGRMTMTHGHGFLPLALPD 3060
Db 3001 LFPSSGSGVRGCIKIGIKALGKVVDLKRLLNTTGISFGCTADLLVGRMTMTHGHGFLPLALPD 3060
QY 3061 VAPITEVVYSGFGERGTQDNLLYYRTSPDGPYQVSI REGHVTLRFMNQEVETQRFVADG 3120
Db 3061 VAPITEVVYSGFGERGTQDNLLYYRTSPDGPYQVSI REGHVTLRFMNQEVETQRFVADG 3120
QY 3121 APHYVAFYSNVTGVWLYVDQQLVKSHERTTPMLQLQPEEPSRLLLGGLPVSGETFNFS 3180
Db 3121 APHYVAFYSNVTGVWLYVDQQLVKSHERTTPMLQLQPEEPSRLLLGGLPVSGETFNFS 3180
QY 3181 GCISNVFVQRLRGPQRFVFDLHQNMGSVNVSVGCTPAQLIETSRATAQKVSRRSRQPSQDL 3240
Db 3181 GCISNVFVQRLRGPQRFVFDLHQNMGSVNVSVGCTPAQLIETSRATAQKVSRRSRQPSQDL 3240
QY 3241 ACTTPWLPGTIQDAYQFGGPLPSYLFQFVGISPSHRNRLHLSMLVRPHAASQGLLLSTAPM 3300
Db 3241 ACTTPWLPGTIQDAYQFGGPLPSYLFQFVGISPSHRNRLHLSMLVRPHAASQGLLLSTAPM 3300
QY 3301 SGRSPSLVFLNHHGHFVAQTEGPGPRLQVQSRQHSRAGQWHRVSVRWGMQIQILVVVDSQ 3360
Db 3301 SGRSPSLVFLNHHGHFVAQTEGPGPRLQVQSRQHSRAGQWHRVSVRWGMQIQILVVVDSQ 3360
QY 3361 TWSOKALHHRVPRAERPQPYTL SVGGLPASSYSSKLPVSVGSGCLKKLQLDKQPLRTPT 3420
Db 3361 TWSOKALHHRVPRAERPQPYTL SVGGLPASSYSSKLPVSVGSGCLKKLQLDKQPLRTPT 3420
QY 3421 QMVGVTPCVSGPLEDGLFFPQSEGVVTTLELPKAKMPYVSLELEMRPLAAAGLIHILGOAL 3480
Db 3421 QMVGVTPCVSGPLEDGLFFPQSEGVVTTLELPKAKMPYVSLELEMRPLAAAGLIHILGOAL 3480
QY 3481 ATPYMQLKVLTEQVLLQANDGAGEFSTWVTYPKLCDGRWHRVAVIMGRDRTLREVDVTQSN 3540
Db 3481 ATPYMQLKVLTEQVLLQANDGAGEFSTWVTYPKLCDGRWHRVAVIMGRDRTLREVDVTQSN 3540
QY 3541 HTTGRLPESLAGSPALLHLGSLPKSSTARPELPA YRGCLRKLLINGAPVNVVTASVQIQGA 3600
Db 3541 HTTGRLPESLAGSPALLHLGSLPKSSTARPELPA YRGCLRKLLINGAPVNVVTASVQIQGA 3600
QY 3601 VGMRGCPSGTLALSQKGKALTQORHAKPSVSPLLMH 3635
Db 3601 VGMRGCPSGTLALSQKGKALTQORHAKPSVSPLLMH 3635
RESULT 3
ABB81588
ID ABB81588 standard; protein; 3695 AA.
XX
AC ABB81588;
XX
DT 19-SEP-2002 (first entry)
XX
DE Human laminin alpha 5 protein SEQ ID NO:2.
XX
KW Laminin alpha 5; laminin 10; vulneryary; cell growth; differentiation;
KW tissue repair development; laminin; healing; vascular tissue;
KW re-endothelialisation; vascular injury; cell attachment; cell stasis;
XX proliferation; migration.
OS Homo sapiens.
XX

PH Key Location/Qualifiers
FT Peptide 1..35
FT /label= signal
FT Protein 36..3695
FT /label= laminin_alpha_5
PN WO200250111-A2.
XX
XX 27-JUN-2002.
PD
XX
PF 21-DEC-2001; 2001WO-US051035.
XX
PR 21-DEC-2000; 2000US-0257449P.
PR 28-MAR-2001; 2001US-0279282P.
PR 13-NOV-2001; 2001US-00279282.
XX
PA (BIOS-) BIOSTRATUM INC.
XX
PI Tryggvason K, Doi M, Thyboll J;
XX
XX WPI; 2002-557650/59.
DR N-PSDB; ABQ72906.
XX
PT New human laminin-10 proteins, useful for accelerating the healing of
PT vascular tissue, improving the biocompatibility of grafts, or for
PT promoting re-endothelialization at the site of vascular injuries.
XX
PS Claim 5; Page 68-79; 231pp; English.
XX
XX The present sequence represents human laminin alpha 5. Also described is
CC an isolated laminin 10. Laminin 10 has vulnerary activity. Laminins are
CC useful in maintaining cell/tissue phenotype as well as promoting cell
CC growth and differentiation in tissue repair development. Specifically,
CC laminin 10 can be used for accelerating the healing injuries of vascular
CC tissue, improving the biocompatibility of grafts useful for treating such
CC injuries, for promoting re-endothelialisation at the site of vascular
CC injuries, and promote cell attachment and subsequent cell stasis,
CC proliferation, differentiation, and/or migration
XX
SQ Sequence 3695 AA;

Query Match 79.7%; Score 15839; DB 5; Length 3695;
Best Local Similarity 79.4%; Pred. No. 0;
Matches 2874; Conservative 277; Mismatches 452; Indels 18; Gaps 8;

QY 1 DLYCKLVGGPVAGDPNQTIGQYCDICTAANSNKAHPVSNNAIDGTERWQSPPLSRGLE 60
Db 79 DLYCKLVGGPVAGDPNQTIRGQYCDICTAANSNKAHPASNAIDGTERWQSPPLSRGLE 138

QY 61 YNEWNVTLDLQGVFHVAYVLIKFNANSPRDLWLERSTDFGHTYQWPQFASSKRDCLER 120
Db 139 YNEWNVTLDLQGVFHVAYVLIKFNANSPRDLWLERSTDFGHTYQWPQFASSKRDCLER 198

QY 121 FGPRTLERITQDDDDVICTEYSRIVPLENGEIVVSLVNGRPGALNFSYSPLLRDFTKATN 180
Db 199 FGPQTLERITRDAAICTEYSRIVPLENGEIVVSLVNGRPGAMNFSYSPLLRDFTKATN 258

QY 181 IRLRFLRTNTLLGHLMGKALRDPVTTRRRYYYSIKDISIGGRVCVCHGHADVCDAKDPDPF 240
Db 259 VRLRFLRTNTLLGHLMGKALRDPVTTRRRYYYSIKDISIGGRVCVCHGHADVCDAKDPDPF 318

QY 241 RLQACQHNTCGGSCDRCCPGFNQPKPATTDSANECQSCNCHGHAYDCYYDPEVDRRN 300
Db 319 RLQCTQHNTCGGTCDRCPCGFNQPWKPATANSANECQSCNCHGHATDCYYDPEVDRRR 378

QY 301 ASQNDNVYQGGVCLDCQHTTGINCERCLPGFFRAPDQPLDSPHVCRCDCESDFTDG 360
Db 379 ASQSLDGTYYQGGVCIDCQHTTAGVNCERCLPGFVRSPNHPDLSPHVCRNCESDFTDG 438

QY 361 TCEDLTGRCYCRPNFTGELCAACAEGYTDFPHCYPLPSFPFHNDRQVLPAGQIVNCDN 420
Db 439 TCEDLTGRCYCRPNFSGERCDCVCAEGFTGFPSCYPFIS-SSNDTREQVLPAGQIVNCDIS 497

QY 421 AAGTQGNACRKDPRGLGRCVCKPNFRGAHCELCAPGFHGPSCHPCQCSSPGVANSLCDPES 480
Db 498 AAGTQGNACRKDPRVGRCLCKPNFQGTCHCELCAPGFYGPQCQCSSPGVADRCDDPT 557

QY 481 GQCMCRTGFEGRDCHCALGYEHFPLCQLCGCSPAGTLPPEGCDAGRCQCRPGFDGPHCD 540
Db 558 GQCRVGVFEGATCDRCAPGYFHFPLCQLCGCSPAGTLPPEGCDAGRCCLCQEFAGPHCD 617

QY 541 RCLPGYHYGYPDCHACADPRGALDQCCGVGGGLCHCRPGTNTGATCQECSPGFYGFPPSPIC 600
Db 618 RCRPGYHGFNQCQACTCDPRGALDQLCGAGGLCHCRPGYTGATCQECSPGFHGFPPSCVPC 677

QY 601 HCSADGSLHTTCDPTTGQCRCRPRVTGLHCDMCPGAYNFPYCEAGSCHPAGLAPANPAL 660
Db 678 HCSAEGSLHAACDPRSGQCSRPRVTGLRCDTCTVPGAYNFPYCEAGSCHPAGLAPVDPAL 737

QY 661 PETQAPCMCRAHVEGPSDCRCKPGYWGSLASNPESGCTRCSCDPRGTLGGVTECO-GNGQC 719
Db 738 PEAQVPCMCRAHVEGPSDCRCKPGFWGLSPSNPEGCTRCSCDLRGLTGGVAECQPGTQC 797

QY 720 FCKAHVCGKTCACAKDGFGLDYADYFGCRSCRCRDVGGALQGCEPKTGACRCRPNTQGP 779
Db 798 FCKPHVCGQACASCKDGFGLDQADYFGCRSCRCRDIGGALGQSCEPRTGVCRCRPNTQGP 857

QY 780 TCSEPAKDHLYPDLHMRLELEEAATPEGHAVRFGFNPLEFENFSWRGYAHMMAIQPRIV 839
Db 858 TCSEPARDHYLPDLHLRLLELEEAATPEGHAVRFGFNPLEFENFSWRGYAQMVPVQPRIV 917

QY 840 ARLNVTSPDLRLVFRVYNRGSTSVNGQISVREEGKLSCTNCTEQSQPVAFPPSTEPAF 899
Db 918 ARLNLTSPDLFWLVFRVYNRGAMSVGRSVREEGRSAAACNCTAQSQPVAFPPSTEPAF 977

QY 900 VTVPRQGFGEFVLNPGIALLVEAEGVLLDYVLLPSTYYEAAALLOHRTVEACTYRPSA 959
Db 978 ITVPQRGFGEFVLNPGTMAIRVEAEGVLLDYVLLPSTYYEAAALLOHRTVEACTYRPSA 1037

QY 960 LHSTENCLVYAHPLDGFPSAAGTEALCRHNSLPRPCPTQLSPSHPPPLATCFGSDVDI 1019
Db 1038 QQSGDNCLLYTHLPDLDFGPPSAAGLEALCRQDNLPRPCPTQLSPSHPPPLITCTGSDVDV 1097

QY 1020 QLEMAVPPQGYVLVVEYVEDSHQEMGVAVHTPQAPQGVNLNHPCPYSSLCRSPARD 1079
Db 1098 QLQVAVPPQGRYALVVEYANEDARQEVGVAVHTPQAPQGVNLNHPCLYSTLCRGTARD 1157

QY 1080 TQHLAIFHLDSEASIRLTAEQAHFFLHSHVTLVPVEEFSTEFVEPRVFCVSSHGTENPSS 1139
Db 1158 TQDHLAVFHLDEASVRLTAEQARFFLHGVTLPVIEEFSPEFVEPRVSCISSHGAFGPNS 1217

QY 1140 AACIASRFPKPPQPIILKDCQVLPPLPDLPLTOSQELSPGAPPEGPQPRPPTAVDPNAEP 1199
Db 1218 AACLPSRFPKPPQPIILRDCQVLPPLPGLPLTHAQDLTPATSPAGPRPRPPTAVDPDAEP 1277

QY 1200 TLRLHPQGTVVFTTQVPTLGRYAFLLHGYQPVHPSFPVEVLINGGRIWQHANASFCPHG 1259
Db 1278 TLRLHPQGTVVFTTQVPTLGRYAFLLHGYQPAHPTFPVEVLINAGRVWQHANASFCPHG 1337

QY 1260 YGKRTLVLCGQTMLDVTDNELTIVRVPEGRWLWLDYVLIIVPEDAYSSSYLQEEPLDKS 1319
Db 1338 YGKRTLVLCGQTMLDVTDNELTIVRVPEGRWLWLDYVLIIVPEDAYSSSYLQEEPLDKS 1397

QY 1320 YDFISHCATQGYHISPSSSSPFCRNAATSLSFYNNGALPCGCHEVGAVSPICEPFGGQC 1379
Db 1398 YDFISHCAAQGYHISPSSSSLFCRNAASLSLFYNNGARPCGCHEVGATGPTCEPFGGQC 1457

QY 1380 PCRGHVIGRDCSRCATGYWGFPPNCRPCDCGARLDCDELTCQICPPRTVPPDCLVCQPQSF 1439
Db 1458 PCRAHVIGRDCSRCATGYWGFPPNCRPCDCGARLDCDELTCQICPPRTIPPDCLLCQPQTF 1517

QY 1440 GCHPLVGCEECNCSGPGVQELTDPTCDMDSGQCRCPNVAGRRCDTCAPGFYGPYPSCRPC 1499
Db 1518 GCHPLVGCEECNCSGPGVQELTDPTCDTDSGQCRCPNVAGRRCDTCAPGFYGPYPSCRPC 1577

QY 1500 DCHEAGTMASVCDPLTGTQCHCKENVOGSRCDQCRVGTFFSLDAANPKGCTRCFCFGATERC 1559

Db	1578	DCHEAGTAPGVCDPLTGTQCYCKENVQPKDCQCSLGTFSLDAANPKGCTRCFCFGATERC	1637
Qy	1560	GNSNLARHEFVDMEGVLLSSDRQVVPHEHRPEIELLHADLR---SVADTFSELYWQAP	1615
Db	1638	RSSSYTRQEFVDMEGVLLSTDQVVPHERQPGTEMLRADLRHVPEAVPEAFPELYWQAP	1697
Qy	1616	PSYLGDRVSSYGGTLHYELHSETQRGDIFIPYESRPDVVLQGNQMSIAFLELAYPPPGQV	1675
Db	1698	PSYLGDRVSSYGGTLRYELHSETQRGDVFPWMESRPDVVLQGNQMSITFUEPAYPTPGHV	1757
Qy	1676	HRGQLQLVEGNFRHLETHNPVSREELMMVLAGLEQLQIRALFSQTSSTSSVSLRRVVLEVAS	1735
Db	1758	HRGQLQLVEGNFRHTETRTNTVSREELMMVLASLEQLQIRALFSQISSAVSLRRVALEVAS	1817
Qy	1736	EAGRGPASNVELCMCPANYRGDSCQECAPGYRDTKGLFLGRVCVPCQCHGSHDRCLPGS	1795
Db	1818	PAGQALASNVELCLCPASYRGDSCQECAPGFYRDKGLFLGRVCVPCQCHGSHDRCLPGS	1877
Qy	1796	GICVGCQHNTEGDQCERCPRPGFVSSDPSPASPCVSCPCPLAVPSNNFADGCVLRNGRTQ	1855
Db	1878	GVCVDCQHNTEGAHCERCQAGFMSS-RDDSPAPCVSCPCPLSVPSNNFAEGCVLRGGRTQ	1936
Qy	1856	CLCRPGYAGASCERCAPGFFGNPLVLGSSQPCDCSNGDPMIFSDCDPLTGACRGCLR	1915
Db	1937	CLCKPGYAGASCERCAPGFFGNPLVLGSSQPCDCSNGDPMNLLFSDCDPLTGACRGCLR	1996
Qy	1916	HTTGPHCERCAPGFYGNALLPGNCTRCDCSPCGTETCDPQSGRCLCKAGVTGQRCDRCLE	1975
Db	1997	HTTGPRCEICAPGFYGNALLPGNCTRCDCPCGTEACDPHSGHCLCKAGVTGRRCDRCQE	2056
Qy	1976	GYFGFEQCQGRPCACGPAAGSECHPSQSGQCHCQPGTTGPPQCLECAPGYWGLPEKGRR	2035
Db	2057	GHFGFNGCGGRPCACGPAAGSECHPSQSGQCHCPRPGTMGPQCRECAPGYWGLPEQGRR	2116
Qy	2036	CQCPRGHCDPHTGHTCTCPPGLSGERCDCSCQHQVVPVPGKPGGHHCEVCDHCWVLLD	2095
Db	2117	CQCPGGRCDPHTGRCNCPPLGSGERCDCSCQHQVVPVPGGPGVGHSHCEVCDHCWVLLD	2176
Qy	2096	DLERAGALLPAIREQLQGINASSAAWARLHRLNASIADLQSKLRRPPGPRYQAAQQLQTL	2155
Db	2177	DLERAGALLPAIHEQLRGINASSMAWARLHRLNASIADLQSLRSPLGPRHETAQQLQVL	2236
Qy	2156	EQQSISLQDTERLGSQATGVQOQAGQLDTESTLGRAQKLLSVRAVGRALNELASRM	2215
Db	2237	EQQSTSLGQDARRLGGQAVGTRDQASQLLAGTEATLGHAKTLLAAIRAVDRTLSELMST	2296
Qy	2216	QGQSPGDALVPSGEQLRWALAEVERLLWDMETRDILGAQGAVAEAEAEAOQLMARVQEQ	2275
Db	2297	GHGLANASAPSGEQLLRTLAEVERLLWENRARDLGAPOAAAEAEELAAOQLLARVQEQ	2356
Qy	2276	TSFWEENQSLATHIRDQAOYESGLMDLREALNQAVNTTREAEEELNSRQERVKEALQWK	2335
Db	2357	SSLWEENQALATQTRDRLAQHEAGLMDLREALNRAVDATREAQELNSRQERLEALQRK	2416
Qy	2336	QELSQDNATLKATLQAAASLILGHVSELQGDQAKEDLEHLAASLDGAWTPLLKRMQAFS	2395
Db	2417	QELSRDNATLQATLHAARDTLASVFRLLHSLDQAKEELERLAASLDGARTPLLQRMQTFS	2476
Qy	2396	PASSKVDLVEAAEAHAQKLNQLAINLSGIILGINQDRFIQRAVEASNAYSILQAVQAAE	2455
Db	2477	PAGSKLRLVEAAEAHAQQLGQLALNLSIILDVNDQRLTQRAIEASNAYSRILQAVQAAE	2536
Qy	2456	DAAGQALRQASRTWVVRGLAAGARQLLANSSALEETILGHQGRGLGAQRLQAAAGIQ	2515
Db	2537	DAAGQALQOQADHTWTVVRQGLVDRAQQLLANSTALEEAMLOEQQLGLVYWAALQGARTQ	2596
Qy	2516	LHNVWARKNQALAAQIQEAQAQAMLAMDTSETSEKIAHAKAVAAEALSTATHVQSQIQGMQKN	2575
Db	2597	LRDVRAKQDQLEAHIQAAQAQAMLAMDTDETSKKIAHAKAVAAEAQDTATRVQSQIQAMQEN	2656
Qy	2576	VERWQSQGLGQGDLSQVERDASSSVSTLEKTLPLQALLKLSRLNRGVHNASIALSANI	2635

Db	2657	VERWQGYEGLRGQDLGQAVLDAGHSVSTLEKTLPLQALLAKSLILENRGVHNASLALSASI	2711
Qy	2636	GRVREKLIAQARSAASKVKYSMKFNGRSGVRLRPPRDLADLAAYTALKFHIQSPVPAPEPG	2695
Db	2717	GRVRELIAQARGAASKVKVPMKFNGRSGVQLRTPRDLADLAAYTALKFYLOG--PEPEPG	2774
Qy	2696	KNTGDHFVLYMGSRQATGDMGVSLRNQKVHVYRLKGAGPTTILSIDENIGEQAFAAVSID	2755
Db	2775	QGTEDRFVYMGSRQATGDMGVSLRDKKVHVYQLGEAGPAVLSDIDEDIGEQAFAAVSLD	2834
Qy	2756	RTLQFGHMSVTVEKOMVHEIKGDTVAPGSEGLLNHLHPDDFVYVGGYPNSFTTPEPLRFP	2815
Db	2835	RTLQFGHMSVTVERQMIQETKGTVPAPGAEGLLNLRPDDFVYVGGYPSTFTTTPPLLRFP	2894
Qy	2816	GVLGCIEMETLNEEVVSLYNEBOTFMFLDTAVDKPCARSKATGDPWLTDGSLYDGSGFARI	2875
Db	2895	GVRGCIEMDTLNEEVVSLYNEFERTFQLDTAVDRPCARSKSTGDPWLTDGSLYDGTGFARI	2954
Qy	2876	SFEKQFSNTKRFDOELRLVSYNGIIFFLKOESQFCLAVQEGTLVLFYDFGSGLKKADPL	2935
Db	2955	SFDSQISTTKRFEQELRLVSYGVLFLLKQSQFCLAVQEGSLVLLYDFGAGLKKAVPL	3014
Qy	2936	QPQALTAASKAIQVFLLAGNRKRVLRVERATVFSVDQDNMLEMADAYYLGVPPEQLP	2995
Db	3015	QPPPLTSASKAIQVFLGGRKRVLRVERATVYSVEQDNLELADAYYLGVPDPQLP	3074
Qy	2996	LSLRQLFPSSGSGVRGCIKGIKALGKYVDLKLRLNTTGISFGCTADLLVGRMTTFHGHGFLP	3055
Db	3075	PSLRWLFPPTGSGVRGCVGIGIKALGKYVDLKLRLNTTGVSAAGTADLLVGRAMTFHGHGFLR	3134
Qy	3056	LALPDVAPITEVYSGFGRGTQDNLLYYRTSPDGPYQVSLREGHVTLRFMNQEVETQR	3115
Db	3135	LALSNVAPLTGNVYSGFHFSAQDSALLYYRASPDGLCQVSLQQGRVSLQLLRTEVKTOA	3194
Qy	3116	VFADGAPHYVAFYSNVTGVWLYVDDQLQLVKSHERTTLMQLQLOPEEPSRLLLGGLPVSGT	3175
Db	3195	GFADGAPHYVAFYSNATGVWLYVDDQLQOMKPHRGPPPELQOPQPEGPPRLLLGGLPESGT	3254
Qy	3176	FHNFGGCIISNVFQRLRGPQRVFDLHQNMGSVNVSVGCTPAQLIETS-----RATAQK	3228
Db	3255	IYNFGGCIISNVFQRLRGPQRVFDLQNLGSVNVSTGCAPALQAQTPGLGPRGLQATARK	3314
Qy	3229	VSRRSRQPSQDLACTTPWLPGTIQDAYQFGGLPSPYQFVGISPSHRNRLHLMLVRPHA	3288
Db	3315	ASRRSRQPARHPACMLPPHLRTRTDSYQFGGSLSSHLEFVGILARHNWPSLSMHVLPRL-	3373
Qy	3289	ASQGLLLSTAPMSGRSPSLVFLNHHGHFVAQTEGPGPRLQVQSRQHSRAGQWHRVSVRWG	3348
Db	3374	SSRGLLLFTARLRPGSPSLALFLSNHGHFVAQMEGLGTRLRAQSRQSRPGRWHKVSVRWE	3433
Qy	3349	MQIQLVVDGSGQTSQKALHHRVPRAPERPPYTLVSGGLPASSYSKKLPVSVGFSGCLKK	3408
Db	3434	KNRILLVTDGARAWSQEGPHRQHQAEPHPQHTLTFVGGLPASSSHSSKLPVTVGFSGCVKR	3493
Qy	3409	LQLDKQPLRTPQTMVGVTCPVSGPLEDGLFFPGSEGVVTLLELPKAKMPYVSLELEMRPLA	3468
Db	3494	LRLHGRPLGAPTRMAGVTPCILGPLEAGLFFPGSGGVITLLEFGATLPDVGLELEVRPLA	3553
Qy	3469	AAGLIHFLGQALATPYMQLKVLTEQVLLQANDGAGEFSTWVTPK-LCDGRWHRVAVIMG	3527
Db	3554	VTGLIFHLGQARTPPYLQQLVTEKQVLLRADDGAGEFSTVTRPSVLCDGQWHRLAVMKS	3613
Qy	3528	RDILRLEVDTQSNHTTGRLPESLAGSPALLHLGSLPKSSTARPELPAYRGCLRKLILINGA	3587
Db	3614	GNVLRLEVDAQSNHTVGPLLAAAGAPAPLYLGLLPEPMAVQWPWPAYCGCMRRRLAVNRS	3673
Qy	3588	PVNVITASVQIQGAVGMRGCPSS	3608
Db	3674	PVAMTRSVVEHGAVGASGCPA	3694

RESULT 4
AAE17310

AAE17310 standard; protein; 3696 AA.
AAE17310;
18-APR-2002 (first entry)
Human laminin alpha protein, sbg417005LAMININ_ALPHA #2.
Human; therapy; wound healing disorder; vaccine; cancer; infection;
autoimmune disorder; haematopoietic disorder; inflammation; arthritis;
Parkinson's disease; Huntington's chorea; schizophrania; antiarrhythmic;
multiple sclerosis; Alzheimer's disease; analgesic; cardiant; asthma;
ischaemia; stroke; AIDS; bone disease; atherosclerosis; brain disorder;
depression; cardiovascular disease; myocardial infarction; renal failure;
respiratory disease; liver disorder; Fanconi's syndrome; spleen disorder;
type II diabetes mellitus; skeletal muscle disorder; immunosuppressive;
hypersplenism; renal disease; hypoglycaemia; gastrointestinal disease;
nootropic; cirrhosis; Hodgkin's disease; neuroleptic; antiinflammatory;
haemostatic; vulnery; anticonvulsant; antirheumatic; neuroprotective;
nephrotropic; hypotensive; vasotropic; cytostatic; cerebroprotective;
allergy; laminin alpha protein.
Homo sapiens.
WO200198342-A1.
27-DEC-2001.
22-JUN-2001; 2001WO-US019929.
22-JUN-2000; 2000US-0213156P.
22-JUN-2000; 2000US-0213161P.
(SMIK) SMITHKLINE BEECHAM CORP.
(SMIK) SMITHKLINE BEECHAM PLC.
(GLAX) GLAXO GROUP LTD.
Agarwal P, Cogswell JP, Kabnic KS, Lai Y, Martensen SA,
Murdock PR, Smith RF, Strum JC, Xiang Z, Xie Q, Rizni SK,
WPI; 2002-139783/18.
N-PSDB; AAD27805.
Novel secreted and membrane-associated polypeptides and polynucleotides
useful for preventing, ameliorating or correcting dysfunction or disease
including diabetes, cancer, hypertension and growth abnormalities.
Claim 1; Page 115-122; 138pp; English.
The invention relates to secreted and membrane-associated polypeptides
and polynucleotides. The sequences of the invention are useful in
diagnostic assays for detecting diseases associated with inappropriate
activity or levels of these polynucleotides, and in identifying their
agonists and antagonists that are potentially useful in therapy. The
sequences of the invention are useful as vaccines for inducing
immunological response. The sequences of the invention are useful for
treating cancers, infections, autoimmune disorders, haematopoietic
disorders, wound healing disorders, cholesterol ester storage disease,
inflammation, congenital muscular dystrophy, junctional epidermolysis
bullosa, Parkinson's disease, Huntington's chorea, multiple sclerosis,
viral and bacterial infections, Alzheimer's disease, asthma, arthritis,
allergies, schizophrania, inflammatory bowel disease, transplant rejection,
septicaemia, psoriasis, ischaemia, stroke, acute respiratory disease,
graft versus host disease, bone disease, bone diseases, atherosclerosis,
syndrome, restenosis, brain injury, AIDS, bone diseases, atherosclerosis,
brain disorders including parasupranuclear palsy, myotonic dystrophy,
depression, anxiety disorders and sleep disorders, cardiovascular
diseases including congestive heart failure and myocardial infarction,
respiratory diseases including chronic obstructive pulmonary disease,
acute bronchitis and adult respiratory distress syndrome, liver disorders
including hypercholesterolaemia, hypertriglyceridaemia, cirrhosis, viral
and non-viral hepatitis, type II diabetes mellitus, renal disease
including acute and chronic renal failure, glomerulonephritis, Fanconi's

CC syndrome, cystinuria, skeletal muscle disorders including hypoglycaemia
CC and tendinitis, gastrointestinal diseases including intestinal
CC obstruction and tropical sprue, spleen disorders including hypersplenism,
CC Hodgkin's disease and malignant lymphoma, testicular cancer, male
CC reproductive diseases including low testosterone and male infertility.
CC The present sequence is human laminin alpha protein
XX
SQ Sequence 3696 AA;
Query Match 79.6%; Score 15830.5; DB 5; Length 3696;
Best Local Similarity 79.3%; Pred. No. 0;
Matches 2874; Conservative 279; Mismatches 450; Indels 19; Gaps 9;
QY 1 DLYCKLVGGPVAGDPNQTIOGYCDICTAANSNKAHPVSNADGTERWWQSPPLSRGLE 60
DB 79 DLYCKLVGGPVAGDPNQTIRGOYCDICTAANSNKAHPASNAIDGTERWWQSPPLSRGLE 138
QY 61 YNEVNVTLDLGQVFHVAYVLIKFAANSRPPDLWVLERSTDFGHTYQWQFFASSKRDCLER 120
DB 139 YNEVNVTLDLGQVFHVAYVLIKFAANSRPPDLWVLESMDFGRTYQWQFFASSKRDCLER 198
QY 121 FGPRTLERITQDDDVICTEYSRIVPLENGEIVVSLVNGRPGALNPSYSPLLRDTKATN 180
DB 199 FGPRTLERITRDAAICTEYSRIVPLENGEIVVSLVNGRPGAMNFSYSPLLRDTKATN 258
QY 181 IRLRFLRTNTLLGHLMGKALRDPVTTRRYYSIKDISIGRCVCHGHADVCDKDLDPDF 240
DB 259 VRLRFLRTNTLLGHLMGKALRDPVTTRRYYSIKDISIGRCVCHGHADACDAKDPDFF 318
QY 241 RLQACQHNNTCGSCDRCCPGFNQWPKPATTDSANECSCNCHGHAYDCYYDPEVDRN 300
DB 319 RLQCTCQHNNTCGTCDRCPPGFNQWPKPATANSANECSCNCHGHATDCYYDPEVDRR 378
QY 301 ASQNDNVYQGGVCLDCQHHTTGINCERCLPGFFRAPDPLDSPHVCRCPCDCESDFTDG 360
DB 379 ASQSLDGTYYGGVCLDCQHHTTGINCERCLPGFYRSPNHLDSPHVCRRCNCESDFTDG 438
QY 361 TCEDLTGRCYCRPNFTGELCAACAEGYTDFPHCYPLPSFPHNDTREQVLPAGQIVNCDN 420
DB 439 TCEDLTGRCYCRPNFSGERCDCVCAEGFTGFPSCYPTPS-SSNDTREQVLPAGQIVNCDN 497
QY 421 AAGTQGNACRKPRLGRVCCKPNFRGAHCELCAFGHGSCHPCQCSSPGVANSILCDPES 480
DB 498 AAGTQGNACRKPRLGRVCCKPNFRGAHCELCAFGHGSCHPCQCSSPGVANSILCDPES 557
QY 481 GQCMCRTEGEGDRCDHCAFGYFHFPLCQCGSPAGTLPPEGDEAGRCQCRPGDGPCHD 540
DB 558 GQCMCRTEGEGDRCDHCAFGYFHFPLCQCGSPAGTLPPEGDEAGRCQCRPGDGPCHD 617
QY 541 RCLPGYHGYPDCHACADPRGALDQCGVGLCHCRPNTGATCQECSPGFYFPSCIPC 600
DB 618 RCRPGYHGFNCQACTCDPRGALDQCGVGLCHCRPNTGATCQECSPGFYFPSCIPC 677
QY 601 HCSADGSLHTTCDPTTGQCRCRPRVTGLHCDMCPVPGAYNFPYCEAGSCHPAGLAPANPAL 660
DB 678 HCSAEGSLHAACTDPRSGQCSRCRPRVTGLRCDTCVPGAYNFPYCEAGSCHPAGLAPANPAL 737
QY 661 PETQAPCMCAHVEGPSDCRCKPGYWGSLASNPEGCTRCSDPRGTLGGVTECO-GNGQC 719
DB 738 PEAVQPCMAHVEGPSDCRCKPGYWGSLASNPEGCTRCSDPRGTLGGVTECO-GNGQC 797
QY 720 FCKAHVCGKTCACAKDGGFFGLDYADYFGCRSCRCVGGALGQGCPEKGTGACRCPNTQGP 779
DB 798 FCKPHVCGKTCACAKDGGFFGLDYADYFGCRSCRCVGGALGQGCPEKGTGACRCPNTQGP 857
QY 780 TCSEPAKHVLPDLHLMRLELEEAATPEGHAVRFGFNPLEFENFWSRGYAHMMAIQPRIV 839
DB 858 TCSEPAKHVLPDLHLMRLELEEAATPEGHAVRFGFNPLEFENFWSRGYAHMMAIQPRIV 917
QY 840 ARLNVTSPDLFRLVFRYVNRGSTSVNGQISVREEGKLSCTNCTEQSQPVAFPPSTEPAF 899
DB 918 ARLNVTSPDLFRLVFRYVNRGSTSVNGQISVREEGKLSCTNCTEQSQPVAFPPSTEPAF 977

Db 3135 RLALSNVAPLTGNVSGFGPHSAQDSALLYRRASPDGLCQVSLQQGRVSLQLLRTEVKTQ 3194
QY 3115 RVFADGAPHYVAFYSNVTVGWLYVDDQLQLVKSHERTTPTMLQLQPEEPSRLLLGGLPVSG 3174
Db 3195 AGFADGAPHYVAFYSNATGWLYVDDQLQOMKPHRGPPPELQPOPEGPRLLGGLPESG 3254
QY 3175 TFHNFSGCISNVFQRLGEPQORVFDLHONMGSVNVSVGCTPAQLIETS-----RATAQ 3227
Db 3255 TIYNFSGCISNVFQRLGEPQORVFDLQNLGSVNVSTGCAPALQAQTPLGPRGLQATAR 3314
QY 3228 KVSRRSQPSQDLACTTWPPLGCTIQDAYQFGGPLPSYLFQVGISPSHNRPLHLSMLVRPH 3287
Db 3315 KASRRSQPARHPACMLPPHLTRTDSYQFGGSLSSHLEFVGILARHNPWPSLSMHVLP 3374
QY 3288 AASQGLLLSTAPMSGRSPSLVFLNTHGHFVAQTEGPPRQLQVQSRQHSRAGQWHRVSVRW 3347
Db 3375 -SSRGLLLFTARLRPGSPSLALFLSNGHFEVAQMEGLTRLRAQSRQRSPRGRWHKVSVRW 3433
QY 3348 GMOQIQLVVDGSGQTSQKALHHRVPRAPERQPYTLVGGPLPASSYSSKLPVSVGFGCLK 3407
Db 3434 EKNRILLVTDGARAWSQEGPHRQHQAEHPQPHLTFVGGPLPASSHSHKLPVTVGFGCVK 3493
QY 3408 KLQLDKQPLRTPQMVGTPTCVSGPLEDGLFFPGSGEVVTLPLPKAKMPYVLSLEMRPL 3467
Db 3494 RLRLHGRPLGAPTRMAGVTPCILGPLLEAGLFFPGSGGVITLPLGATLDDVGLLEVRPL 3553
QY 3468 AAAGLIFHLGQALATPYMQLKVLTEQVLLQANDGAGEFSTWVTPK-LCDGRWHRVAVIM 3526
Db 3554 AVTLGIFHLGQARTPPYLQVTEKQVLLRADGAGEFSTVTRPSVLCDGQWHLAVMK 3613
QY 3527 GRDLRLVDTQSNHTTGRLPESLAGSPALLHLGLSPKSTARPELPAYRGCLRKLLING 3586
Db 3614 SGNVLRLEVDQAQSNHTVGPLLAAAGAPAPLYLGLPEPMAVQWPPPAYCGMRLAVNR 3673
QY 3587 APVNVTVASVQIQGAVGMRGCP 3608
Db 3674 SPVAMTRSEVHGAVGAGGCPA 3695

RESULT 5

AAE17309
ID AAE17309 standard; protein; 3705 AA.
AC AAE17309;
XX
XX 18-APR-2002 (first entry)
XX Human laminin alpha protein, sbg417005LAMININ_ALPHA #1.
DE Human; therapy; wound healing disorder; vaccine; cancer; infection;
XX autoimmune disorder; haematopoietic disorder; inflammation; arthritis;
KW Parkinson's disease; Huntington's chorea; schizophrenia; antiarrhythmic;
KW multiple sclerosis; Alzheimer's disease; analgesic; cardiac; asthma;
KW ischaemia; stroke; AIDS; bone disease; atherosclerosis; brain disorder;
KW depression; cardiovascular disease; myocardial infarction; renal failure;
KW respiratory disease; liver disease; Fanconi's syndrome; spleen disorder;
KW type II diabetes mellitus; skeletal muscle disorder; immunosuppressive;
KW hypersplenism; renal disease; hypoglycaemia; gastrointestinal disease;
KW nootropic; cirrhosis; Hodgkin's disease; neuroleptic; antiinflammatory;
KW haemostatic; vulnery; anticonvulsant; antirheumatic; neuroprotective;
KW nephrotropic; hypotensive; vasotropic; cytostatic; cerebroprotective;
allergy; laminin alpha protein.

Homo sapiens.

WO200198342-A1.

27-DEC-2001.

22-JUN-2001; 2001WO-US019929.

22-JUN-2000; 2000US-0213156P.

22-JUN-2000; 2000US-0213161P.

XX (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
XX Agarwal P, Cogswell JP, Kabnic KS, Lai Y, Martensen SA;
PI Murdock PR, Smith RF, Strum JC, Xiang Z, Xie Q, Rizni SK;
XX WPI; 2002-139783/18.
DR N-PSDB; AAD27804.
XX Novel secreted and membrane-associated polypeptides and polynucleotides
PT useful for preventing, ameliorating or correcting dysfunction or disease
PT including diabetes, cancer, hypertension and growth abnormalities.
XX Claim 1; Page 107-114; 138pp; English.
XX The invention relates to secreted and membrane-associated polypeptides
CC and polynucleotides. The sequences of the invention are useful in
CC diagnostic assays for detecting diseases associated with inappropriate
CC activity or levels of these polynucleotides, and in identifying their
CC agonists and antagonists that are potentially useful in therapy. The
CC sequences of the invention are useful as vaccines for inducing
CC immunological response. The sequences of the invention are useful for
CC treating cancers, infections, autoimmune disorders, haematopoietic
CC disorders, wound healing disorders, cholesteryl ester storage disease,
CC inflammation, congenital muscular dystrophy, junctional epidermolysis
CC bullosa, Parkinson's disease, Huntington's chorea, multiple sclerosis,
CC viral and bacterial infections, Alzheimer's disease, asthma, arthritis,
CC allergies, schizophrenia, sbg42445PROA-associated disorders,
CC septicemia, psoriasis, inflammatory bowel disease, transplant rejection,
CC graft versus host disease, ischaemia, stroke, acute respiratory disease
CC syndrome, restenosis, brain injury, AIDS, bone diseases, atherosclerosis,
CC brain disorders including paraspranuclear palsy, myotonic dystrophy,
CC depression, anxiety disorders and sleep disorders, cardiovascular
CC diseases including congestive heart failure and myocardial infarction,
CC respiratory diseases including chronic obstructive pulmonary disease,
CC acute bronchitis and adult respiratory distress syndrome, liver disorders
CC including hypercholesterolaemia, hypertriglyceridaemia, cirrhosis, viral
CC and non-viral hepatitis, type II diabetes mellitus, renal disease
CC including acute and chronic renal failure, glomerulonephritis, Fanconi's
CC syndrome, cystinuria, skeletal muscle disorders including hypoglycaemia
CC and tendinitis, gastrointestinal diseases including intestinal
CC obstruction and tropical sprue, spleen disorders including hypersplenism,
CC Hodgkin's disease and malignant lymphoma, testicular cancer, male
CC reproductive diseases including low testosterone and male infertility.
CC The present sequence is human laminin alpha protein
XX Sequence 3705 AA;

Query Match 79.6%; Score 15815; DB 5; Length 3705;
Best Local Similarity 79.1%; Pred. No. 0;
Matches 2873; Conservative 279; Mismatches 451; Indels 28; Gaps 9;

QY 1 DLYCKLVGGPVAGGDPNQTIGQYCDICTAANSNKAHPVSNADGTERWWQSPPLSRGLE 60
Db 79 DLYCKLVGGPVAGGDPNQTIGQYCDICTAANSNKAHPVSNADGTERWWQSPPLSRGLE 138
QY 61 YNEVNVTLDLGQVHFVAYVLIKFNANSPRPDLWVLERSTDFGHTYQWPQFFASKRDCLER 120
Db 139 YNEVNVTLDLGQVHFVAYVLIKFNANSPRPDLWVLERSTDFGHTYQWPQFFASKRDCLER 198
QY 121 FGPRTLERTQDDDVICTEYSRIVPLENGEIVVSLVNGRPGALNFYSPLRFTKATN 180
Db 199 FGPQTLERTRDDAAICTEYSRIVPLENGEIVVSLVNGRPGAMNFYSPLRFTKATN 258
QY 181 IRLRFLRTNTLLGLHMGKALRDPVTVTRRYYSIKDISIGRCVCHGHADVCDAKDFDPF 240
Db 259 VRLRFLRTNTLLGLHMGKALRDPVTVTRRYYSIKDISIGRCVCHGHADVCDAKDFDPF 318
QY 241 RLQACQHNTCGSGCDRCPCGFNQPKPATDTSANECQSCNCHGHAYDCYDPEVDRRN 300
Db 319 RLQCTQHNTCGGTCDCRCPCGFNQPKPATANSANECQSCNCHGHATDCYDPEVDRRR 378

Db 2537 RILQAVQAAEDAAQALQQAADHTWATVVRQGLVDRAQQLLANSTALEEAMLEQEQRLGLV 2596
QY 2506 QGRLOAAGIQLHNWARKNOLAAQIQEAQAMLAMDTSETSEKIAHAKAVAAEALSTATHV 2565
Db 2597 WAALQARTQLRDVRAKQDLEAHIQAAQAMLAMDTDETSKIAHAKAVAAEAQDTATRV 2656
QY 2566 QSOLQGMQKNVERWQSLGGLQGDLSQVERDASSVSTLEKTLPLLAKLSRLNRGVH 2625
Db 2657 QSOLQAMQENVERWQGYEGLRGQDLGQAVLDAGHSVSTLEKTLPLLAKLSILENRGVH 2716
QY 2626 NASLALSANIGRVKRLIAQARSAASKVKVSMKFNKRGSGVRLRPPRDLADLAAAYTALKFHI 2685
Db 2717 NASLALSASIGRVRELIAQARGAASKVKVPMKFNKRGSGVQLRTPRDLADLAAAYTALKFYL 2776
QY 2686 QSPVPAPEPGKNTGDHFLVLYMGSRQATGDYMGVSLRNQKVHWYRLGKAGPTTLSIDENI 2745
Db 2777 QG--PEPEPGQGTEDRFVYMGSRQATGDYMGVSLRDKKVHWYQLGEAGPAVLSIDEDI 2834
QY 2746 GEQFAAVSIDRTLQFGHMSVTVKEQMVHEIKGDTVAPGSEGLNLNHPDDFVFYVGGYPSN 2805
Db 2835 GEQFAAVSLDRTLQFGHMSVTVVERQMIQBTGKDTVAPGAEGLLNLRPDDFVFYVGGYEST 2894
QY 2806 FTPPEPLRFPFYGLCIEMETLNEEVVSLYNFEQTFMLDITAVDKPCARSKATGDPWLTDCS 2865
Db 2895 FTPPPLLRFPFYGCIEMDTLNEEVVSLYNFEFTFQLDITAVDRPCARSKSTGDPWLTDCS 2954
QY 2866 YLDGSGFARISFEKQFSNTKRFQDELRLVSYNGIIFFLKQESQFLCLAVQEGTLVLFYDF 2925
Db 2955 YLDGTGFARISFDSQISTTKRFEQELRLVSYSGVFLFLKQSQFLCLAVQEGSLVLLYDF 3014
QY 2926 GSGLKKADPLQPPQALTAASKAIQVFLLAGNRKRVLRVERATVFSVDQDNMLEMADAYY 2985
Db 3015 GAGLKKAVPLQPPPLTSASKAIQVFLGGSRKRVLRVERATVYSVEQDNDLELADAYY 3074
QY 2986 LGVPPEQLPLSLRQLFPPSGSVRGCIKIGIKALGKYVDLKRNLNTTGISFGCTADLLVGR 3045
Db 3075 LGGVPPDQLPPLSLRRLFPPTGGSVRGCVKIGIKALGKYVDLKRNLNTTGVSACTADLLVGRA 3134
QY 3046 MTFHGHGFLPLALPDVAPITEVYSGFGFRGTQDNNLLYYRTSPDGPYQVSLRREGHVTLR 3105
Db 3135 MTFHGHGFLRLALSNAVPLTGNVYSGFGFHSQAQDSALLYRASPDGLCQVSLQQGRVSLQ 3194
QY 3106 FMNQEVETQRFADGAPHYVAFYSNVTGMVLYVDDQLQLVKSHERTPMLQLQPEEPSRL 3165
Db 3195 LLRTEVKTQAGFADGAPHYVAFYSNATGMVLYVDDQLQMKPHRGPPPELQPOEGPPRL 3254
QY 3166 LIGGLPVSGTFHNFSGCISNVFVQRLRGPQRVFDLHONMGSVNVSVGCTPAQLIETS --- 3222
Db 3255 LIGGLPESGTIYNFSGCISNVFVQRLRGPQRVFDLQONLGSVNVSTGCAPALQAQTPGLG 3314
QY 3223 ----RATAQKVSRRSQPSQDLACTTPWLPGTIQDAYQFGGGLPLSYLQFVGISPSHRNRL 3278
Db 3315 PRGLQATARKASRRSRQPARHPACMLPPLHLRTTRDSYQFGGSLSSHLEFVGILARHNWP 3374
QY 3279 HLSMLVRPHAAASQGLLSTAPMSGRSPSLVFLNHHGFVAQTEGPGPRQLQVQSRQHSRAG 3338
Db 3375 SLSMHVLP-R-SSRGLLLFTARLRPGSPSLALFLSNHGFVAQMEGLGTFLRAQSRQSRPG 3433
QY 3339 QWHRVSVRWGMQIQIQLVVDGSGQTSQKALHHRVPRAEPRQPYTLTVSGGLPASSYSSKLPV 3398
Db 3434 RWHKVSVRWEKNRILLVTDGARAWSQEGPHRQHQAEHPQPHTLTVGGGLPASSHSSKLPV 3493
QY 3399 SVGFSGCLKQLQDKQLRTPTQMVGVTPCVSGPLEDGLFFPGSGEVVLELPPKAMPYV 3458
Db 3494 TVGFSGCVKRLRLHGRPLGAPTRMAGVTPCILGLEAGLFFPGSGGVITLDLPGATLPDV 3553
QY 3459 SLELEMRPLAAAGLFIHLGQALATPYMQKVLVTEQVLLQANDGAGEFSTWVTYPK-LCDG 3517
Db 3554 GLELEVRPLAVTGLFIHLGQARTPPYLQVTEKQVLLRADDDGAGEFSTSVTRPSVLCDG 3613
QY 3518 RWHRVAVIMGRDTRLREVDVTQSNHTTGRLPESLAGSPALLHLGSLPKSSTARPELPAYRG 3577

Db 3614 QWHLAVMKSNGVLRLEVDQAQSNHTVGPLLAAAGAPAPLYLGLPEPMAVQWPWPAYCG 3673
QY 3578 CLRKLLINGAPVNVTTASVQIQGAVGMRGCCPS 3608
Db 3674 CMRR LAVNRSPVATRSVEVHGAVGASGCCPA 3704
RESULT 6
ABB09501
ID ABB09501 standard; protein; 3600 AA.
XX
AC ABB09501;
XX
DT 01-NOV-2002 (first entry)
XX
DE Human laminin alpha-5-like NOV1a protein, SEQ ID NO:2.
XX
KW Human; NOVX; neurological disorder; Alzheimer's disease;
KW Huntington's disease; Parkinson's disease; pain; behavioural disorder;
KW addiction; tuberous sclerosis; cancer; immune disorder; allergy;
KW autoimmune disease; myasthenia gravis; asthma; arthritis; diabetes;
KW thyroiditis; cardiovascular disease; hypertension; reproductive disorder;
KW endometriosis; incontinence; psoriasis; scleroderma; alopecia; ulcer;
KW pancreatitis; cirrhosis; glomerular endotheliosis; bacterial infection;
KW polycystic kidney disease; endocrine disorder; obesity; cardiomyopathy;
KW atherosclerosis; cell signal processing-related disorder;
KW metabolic pathway regulation disorder; cytostatic; neuroprotective;
KW antiinflammatory; immunosuppressive; analgesic; antiatherosclerotic;
KW dermatological; antibacterial; antiarthritic; hepatotropic; neurogenesis;
KW differentiation; proliferation; motility; haematopoiesis; wound healing;
KW angiogenesis; forensic biology; transgenic animal; drug screening;
KW gene therapy; NOV1a; laminin alpha-5-like; chromosome 20.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..14
FT Protein /label= Signal_peptide
FT 15..3600
FT /note= "Mature NOV1a protein"
WO200253742-A2.
11-JUL-2002.
07-JAN-2002; 2002WO-US000375.
05-JAN-2001; 2001US-0260018P.
08-JAN-2001; 2001US-0260360P.
28-FEB-2001; 2001US-0272411P.
02-MAR-2001; 2001US-0272817P.
05-JUL-2001; 2001US-0303231P.
12-JUL-2001; 2001US-0305060P.
10-SEP-2001; 2001US-0318405P.
12-SEP-2001; 2001US-0318700P.
04-JAN-2002; 2002US-00037417.
(CURA-) CURAGEN CORP.
PI Kekuda R, Alsobrook JP, Tchernev VT, Liu X, Spytek KA;
PI Patturajan M, Grosse WM, Lepley DM, Burgess CE, Vernet CAM, Li L;
PI Gorman L, Edinger S, Sciore P, Ellerman K, Malyankar U;
PI Rothenberg M, Stone D, Boldog F, Guo X, Shenoy S, Anderson D;
PI Padigar M, Taupier RJ, Miller CE, Eisen A;
XX
DR WPI; 2002-583619/62.
DR N-PSDB; ABQ93879.
XX
PT Novel polypeptides and nucleic acids homologous to transmembrane
PT receptor, thymosin, neuromodulin-like family of proteins for diagnosing,
PT treating cancer, atherosclerosis, neurological, skin and autoimmune
PT disorders.
XX

PS Claim 1c; Page 14-15; 323pp; English.

XX The invention relates to 24 novel human proteins designated NOV1-NOV14

CC (ABB09501-ABB09524), collectively referred to as NOVX proteins, and

CC nucleic acids encoding them (ABQ93879-ABQ93902). NOVX proteins and

CC nucleotides are useful in the treatment, diagnosis or prevention of NOVX-

CC associated disorders or in the manufacture of a medicament for treating

CC such disorders, with specific applications described for each of the 24

CC NOVX proteins, based on their homology to known proteins. Various

CC disorders are associated with NOVX proteins including neurological

CC disorders (e.g., Alzheimer's, Huntington's and Parkinson's diseases),

CC pain, behavioural disorders, addiction, tuberculous sclerosis, cancers

CC (e.g., colorectal cancer, leukaemia and osteosarcoma), immune disorders

CC (e.g., allergies and autoimmune diseases), myasthenia gravis, asthma,

CC various forms of arthritis, diabetes, thyroiditis, cardiovascular disease

CC (e.g., hypertension), reproductive disorders, endometriosis,

CC incontinence, psoriasis, scleroderma, alopecia, ulcers, pancreatitis,

CC cirrhosis, glomerular endotheiosis, polycystic kidney disease, endocrine

CC disorders, obesity, bacterial infections and particularly cardiomyopathy,

CC atherosclerosis, cell signal processing-related disorders and disorders

CC of metabolic pathway regulation. NOVX nucleic acids and polypeptides may

CC be used to identify cellular receptors or downstream effectors which

CC binds to a NOVX protein, and are also useful as targets for the

CC identification of small molecules that modulate or inhibit processes such

CC as neurogenesis, cell differentiation, cell motility, cellular

CC proliferation, haematopoiesis, wound healing and angiogenesis. NOVX

CC nucleic acid sequences can be used to identify a cell or tissue type and

CC are useful as a source of primers or probes for forensic biology and for

CC identifying and cloning NOVX homologues in other cell types. Cells

CC comprising NOVX nucleic acids are useful for producing non-human

CC transgenic animals which are useful for studying the function and

CC activity of NOVX proteins and for identifying and evaluating modulators

CC of NOVX activity. The present sequence represents the laminin alpha-5-

CC like protein NOV1a. The gene encoding NOV1a is located on chromosome 20

XX Sequence 3600 AA;

SQ Query Match 74.3%; Score 14771; DB 5; Length 3600;
Best Local Similarity 74.8%; Pred. No. 0;
Matches 2739; Conservative 275; Mismatches 472; Indels 178; Gaps 26;

QY 1 DLYCKLVGGPVAGGDPNQTIOGYCDICTAANSNKAPVSNADIGTERWWQSPPLSRGLE 60

Db 58 DLYCKLVGGPVAGGDPNQTIOGYCDICTAANSNKAPVSNADIGTERWWQSPPLSRGLE 117

QY 61 YNEVNTLDLGQVHFVAYVLIKFPANSPRDLWVLERSTDFGHTYQWPQFFASSKRDCLER 120

Db 118 YNEVNTLDLGQVHFVAYVLIKFPANSPRDLWVLERSTDFGHTYQWPQFFASSKRDCLER 177

QY 121 FGPRTLERITQDDDVICTEYSRIVPLENGEIVVSLVNGRPGALNFSYSPLLRDFTKATN 180

Db 178 FGPQTLERITRDAAICTEYSRIVPLENGEIVVSLVNGRPGALNFSYSPLLRDFTKATN 237

QY 181 IRLRFLRTNTLLGLHMGKALRDPVTTRRYYSIKDISIGGRCVCHGHADVCDADKPLDPF 240

Db 238 VRLRFLRTNTLLGLHMGKALRDPVTTRRYYSIKDISIGGRCVCHGHADACDAKPLDPF 297

QY 241 RLQACQHNTCGGSCDRCCPGFNQOPWKPAATTDSANECQSCNCHGHAYDCYDPEVDRRN 300

Db 298 RLQCTQHNTCGGTCDRCCPGFNQOPWKPATANSANECQ-CECYGHATDCYDPEVDRRR 356

QY 301 ASQNDNVYQGGVCLDCQHTTGINCERCLPGFFRAPDQPLDSPHVCRCDCESDFTDG 360

Db 357 ASQSLDGTYYQGGVCLDCQHTTGINCERCLPGFFRSPNHPDLSPHVCRGCNCESDFTDG 416

QY 361 TCEDLTGRCYCRPNFTGELCAACAEGYTDFPHCYPLPSPPHNDTREQVLPAQIVNCDN 420

Db 417 TCEDLTGRCYCRPNFSGERCVDVCAEGFTGFPSCY-REHLPGNNDTREQVLPAQIVSCDCS 475

QY 421 AAGTQGNACRKDPRLGRVCVKPNFRGAHCELCAPGFHGPSCHPCQCSS---PGVANSLCD 477

Db 476 AAGTQGNACRKDPRVGRCLCKPNFQGTCELCAPGFYGPGC-PASVPALEWEMTAVTLTQ 534

QY 478 PESGQCMCRGTG-----FEGDRCDHCALGYFHFPL-CQLCGCSPAGTLPEGCDEAG 526

Db 535 ASAGAEWASRGPHVIAVPPATFTSLASH-----PLRSVAVCGCSPAGTLPEGCDEAG 586

QY 527 RCQCRPGFDGPHCDRCLPGYHGYDPDCHACACDPRGALDQCCGVGGLCHCRPNTGATCQE 586

Db 587 RCLCQPEFAGPHCDRCPRGYHGFNCAACTCDPRGALDQCCGAGGLCRCPGYTGTACQE 646

QY 587 CSPGFYGFPPSCIPCHCSADGSLHTTC-----DPTTGQCRCP-RVTGL-H-CDMCPGAYN 639

Db 647 CSPGFHGFPS-----CPATALLKAPCTQPVTPGVGSAAGPVRGCGVTHVCPVPTSPTA 701

QY 640 FPYCEAGSCHPAGLAPANPALPETQAPCMCRAHVEGPSCDRCCKPGYWGLSASNPEGTRC 699

Db 702 KPLFTAGSCHPAGLAPVDPALPEVSPPCMCRAHVEGPSCDRCCKPGFWGLSPSNPEGTRC 761

QY 700 SCDPRGTGGVTECQNGQCFCFAHVCGKTCACAKDGFGLDYADYFGCRSCRCDVGGAL 759

Db 762 SCDLRGTGGVAECQGTGQCFCFKPHVCGQACASCKDGFGLDQADYFGCRSCRCDIGGAL 821

QY 760 GQCEPKTGACRCRPNTOGPTCSEPAKDHLYLPDLHMKLELEEAATPEGHAVRFGFNPLE 819

Db 822 GQCEPRTGVCRCRPNTOGPTCSEPAKDHLYLPDLHMKLELEEAATPEGHAVRFGFNPLE 881

QY 820 FENFSWRGYAHMAIQPRIVARLNVTSPLDLFRLVFRYVNRGTSVNGQISVREEGLSSC 879

Db 882 FENFSWRGYAQMVPQPRIVARLNLTSPLDLFWLFRYVNRGAMSVSGRVSVREGRSATC 941

QY 880 TNCTEQSQPVAFPPSTEPAFVTPQRGFGEFVLNPGIALLVEAEGVLLDYVVLPLSTY 939

Db 942 ANCTAQSQPVAFPPSTEPAFITVPQRGFGEFVLNPGFWALRVEAEGVLLDYVVLPSAY 1001

QY 940 YEALLQHRVTEACTYRPSALHSTENCLVYAHLPDLGPPSAAGTEALCRHDSNLPRCPT 999

Db 1002 YEALLQLRVTEACTYRPSAQSPSCLLYTHLPDLGPPSAAGLEALCRQDNLSPRCPT 1061

QY 1000 EQLSPSPHPPLATCFGSDVDIQLMAVPPQGVYVVEYVGEDSHQEMGVAVHTPQRAPOQ 1059

Db 1062 EQLSPSPHPPLITCTGSDVDVLQVAVPPQGRYALVVEYANEDARQEVGVAVHTPQRAPOQ 1121

QY 1060 GVLNLHPCPYSSSLCRSPARDTQHHLIAIFHLDSEASIRLTAEQAHFFLHSVTLVPVEEFS 1119

Db 1122 GLLSLHPCLYSTLCRGRTARDTQDHLAVFHLDSSEASVRLTAEQARFFLHGVTLPVEEFS 1181

QY 1120 EFVEPRVFCVSSHGTENPSSAAACLASRFPKPPQPIILKDCQVLPPLPDLPLTQSOELSPG 1179

Db 1182 EFVEPRVSCISSHGAFGPNSSAACLPSPRFPKPPQPIILRDCQVLPPLPDLPLTHAQLTFA 1241

QY 1180 APPEGPQPRPPTAVDPNAEPTLLRHQPQGVFTTQVPTLGRYAFLLHGYQPVHPSFFVEV 1239

Db 1242 MSPAGERPRPPTAVDPAEPTLLREPOQATVFTTTHVPTLGRYAFLLHGYQPAHPTFFVEV 1301

QY 1240 LINGRIWQGHANASFCPHGYGCRCTLVCEGQTMLDVTDNELTIVTVRVEGRWLWLDYVL 1299

Db 1302 LINAGRVMQGHANASFCPHGYGCRCTLVCEGQALLDVTHSELTVTVRVPKRWLWLDYVL 1361

QY 1300 IVPEDAYSSSYLQEEPLDKSYDFISHCATQGYHISPSSSSPFCRNAATSLSLFYNNGALP 1359

Db 1362 VVPENVYSFGLREEPLDKSYDFISHCAAQGYHISPSSSSLFCRNAASLSLFYNNGARP 1421

QY 1360 CGCHEVGAVSPTCEPFGGQPCRGHVIIGRDCSRCATGYWGFPPNCRPCDCGARLCELTGQ 1419

Db 1422 CGCHEVGATGPTCEPFGGQPCCHAHVIGRDCSRCATGYWGFPPNCRACDCGARLCELTGQ 1481

QY 1420 CICPRTVPPDCLVCQPSFGCHPLVGCEECNCSGPGVQELTDPTCDMSGQCRCPNVA 1479

Db 1482 CICPRTIPPDCLLCQPTFGCHPLVGCEECNCSGPGIQLTDPTCDTDSGQCRCPNVT 1541

QY 1480 GRRCDTCAPGFYGYPSRCPCDCHEAGTMASVCDPLTGOCHCKENVOGSRCDQCRVGTFSL 1539

Db 1542 GRRCDTCSPGFHGYPRCPCDCHEAGTAPGVCDPLTGQCYCKENVOGPKDCQCSLGTFSL 1601

QY 1540 DAANPKGCTRCFCGATERCGNSNLARHEFVDMEGWLLSSDRQVVPHEHRPEIELLHAD 1599

2645	RGQDLGQAVLDAGSAVSTLEKTLPLQLAKLSILENRGVHNASLALSASIGRVRELIAQAR	2704
2647	SAASK-VKVSMPKNGRSGVRLRPPRLADLAAYTALKFHIQSPVPAPEPGKNTGDHFVLY	2705
2705	GAASKVVKVPKPNKNGRSGVQLRTPRDLADLAAYTALKFYLQG--PEPEPGQGTEDRFVWY	2762
2706	MGSROATGDYMGVSLRNQKVHVYRLGKAGPTTILSIDENIGEOPAAVSDIRTLQFGHMSV	2765
2763	MGSROATGDYMGVSLRDKKVHVYQLGEAGPAVLSDIDIGEOPAAVSLDRTLQFGHMSV	2822
2766	TVEKQMVHEIKGDTVAPGSEGLNLNHPDDFFVYVGGYPSNFTTPEPLRFPFGYLGCIEMET	2825
2823	TVERQMIQETKXGDTVAPGAEGLLNLRPDDFFVYVGGYPSFTTTPPLLRFPFGYRGCIEMDT	2882
2826	LNEEVVSLYNFEQTFMLDTAVDKPCARSKATGDPWLTDGSYLDGSGFARISFEKQFSNTK	2885
2883	LNEEVVSLYNFEQTFQDLTAVDRPCARSKSTGDPWLTDGSYLDGTGFARISFDSQISITTK	2942
2886	RFDQELRLVSNGIIFFLKQESQFCLAVQEGTILVLYDFDGSGLKKADPLQPPQALTAAS	2945
2943	RPEQELRLVSYSGLVFLFKQSQFCLAVQEGSLVLLYDFGAGLKKAVLPQPPPLTSAS	3002
2946	KAIQVFLLAGNRKRVLRVERATVFSVDQDNMLEMADAYYLGVPPEQLPLSLRQLFPGS	3005
3003	KAIQVFLGGSRKRVLRVERATVYSVEQDNLELADAYYLGVPVPPDQLP-SLRRLFPPTG	3061
3066	GSVRGCIKIGIKALGYVDLKLRLNTTGISFGCTADLLVGRMTTFHGHGFLPLALPDVAPIT	3065
3062	GSVRGCVKIGIKALGYVDLKLRLNTTGVSAGCTADLLVGRAMTFHGHGFLRLALSNAVPLT	3121
3066	EVVYSGFGRGTQDNLLYYRTSPDGPYQVSLREGHVTLRFMNQEVETQRFVADGAPHYV	3125
3122	GNVYSGFGFHASQDSALLYYRASVPVRPHQVSLQQGRVSLQLLRTEVKTQAGFADGAPHYV	3181
3126	AFYSNVTGVWLYVDDQLQLVKSHERTTTPMLQLQPEEPSRLJLGGLPVSGTTFHNFSGCISN	3185
3182	AFYSNATGVWLYVDDQLQMKPHRGPPPELOQPGEPPRLLJLGGLPESGTIYNFSGCISN	3241
3186	VFVQRLRGPQRVEDLHQNMGSVNVSVGCTPAQLIETSRATAKVSRRSRQPSQDLACTTP	3245
3242	VFVQRLRGPQRVEDLQQNLGSVNVSVCAPALQACTPGLGPRQASRRSRQPARHPACMLP	3301
3246	WLPGTIQDAYQFGGELPSYLOFVGISPSHRNRLHLSMLVRPHASQGLLLSTAPMSGRSP	3305
3302	PHLRTTRDSYQFGGSLSSHLEFVGILARHN-----	3332
3306	SLVFLFNHGHFVAQTEGPGPRLOVQSRQHSRAGQWHRVSVRWGMQOIQLVVDGSGQTSQK	3365
3333	-----VSVRWKXNRILLVTDGARAWSQE	3355
3366	ALHHRVPRAEPPQYTLVSVGGLPASSYSSKLPVSVGFSGLKKLQDKQPLRTPQMVG	3425
3356	GPHRQHQAEPHPHTLFFVGGLPASSHSSKLPVTVGFGCVKRLRHLGRPLGAPTRMAGV	3415
3426	TPCVSGPLEDGLFFPGSEGVVTLPLPKAMPYVSLSEMRPLAAAGLIFHLGQALATPYM	3485
3416	TPCILGPLEAGLFFPGSGGVITLGLPGATLPLDVGLELEVRPLAVTGLIFHLGQARTPPYL	3475
3486	QLKVLTEQVLLQANDGAGEFSTWVTPK-LCDGRHVRVAVINGRDTLRLEVDTQSNHHTTG	3544
3476	QLQVLPQVLLRADGAGEFSTSVTRPSVLCDGQWHRLAVMKSGNVLRLEVDAQSNHTVG	3535
3545	RLPESLAGSPALLHLGLSPKSSSTARPELPAIRGCLRKLLINGAPVNVITASVQIQGAVGMR	3604
3536	PLAAAGAPAPLYLGLLEPMAVQPPFPAYCGCMRRLAVNRSPVAMTRSVVEHGAVGAS	3595
3605	GCPS 3608	
3596	GCFA 3599	

RESULT 7
ABB09503

ID	ABB09503	standard; protein; 3597 AA.
XX	ABB09503;	
AC	01-NOV-2002	(first entry)
XX	Human laminin alpha-5-like NOV1c protein, SEQ ID NO:6.	
DT	Human; NOVX; neurological disorder; Alzheimer's disease;	
XX	Huntington's disease; Parkinson's disease; pain; behavioural disorder;	
DE	addiction; tuberculous sclerosis; cancer; immune disorder; allergy;	
XX	autoimmune disease; myasthenia gravis; asthma; arthritis; diabetes;	
XX	thyroiditis; cardiovascular disease; hypertension; reproductive disorder;	
XX	endometriosis; incontinence; psoriasis; scleroderma; alopecia; ulcer;	
XX	pancreatitis; cirrhosis; glomerular endotheliosis; bacterial infection;	
XX	polycystic kidney disease; endocrine disorder; obesity; cardiomyopathy;	
XX	atherosclerosis; cell signal processing-related disorder;	
XX	metabolic pathway regulation disorder; cytostatic; neuroprotective;	
XX	antiinflammatory; immunosuppressive; analgesic; antiatherosclerotic;	
XX	dermatological; antibacterial; antiarthritic; hepatotropic; neurogenesis;	
XX	differentiation; proliferation; motility; haematopoiesis; wound healing;	
XX	angiogenesis; forensic biology; transgenic animal; drug screening;	
XX	gene therapy; NOV1c; laminin alpha-5-like; chromosome 20.	
OS	Homo sapiens.	
XX	Key	Location/Qualifiers
FH	Peptide	1..14
FT		/label= Signal_peptide
FT	Protein	15..3597
FT		/note= "Mature NOV1c protein"
XX	WO200253742-A2.	
PN	11-JUL-2002.	
XX	07-JAN-2002; 2002WO-US000375.	
PF	05-JAN-2001; 2001US-0260018P.	
XX	08-JAN-2001; 2001US-0260360P.	
PR	28-FEB-2001; 2001US-0272411P.	
PR	02-MAR-2001; 2001US-0272817P.	
PR	05-JUL-2001; 2001US-0303231P.	
PR	12-JUL-2001; 2001US-0305060P.	
PR	10-SEP-2001; 2001US-0318405P.	
PR	12-SEP-2001; 2001US-0318700P.	
PR	04-JAN-2002; 2002US-00037417.	
XX	(CURA-) CURAGEN CORP.	
PA	Kekuda R, Alsbrook JP, Tchernev VT, Liu X, Spytek KA;	
XX	Patturajan M, Grosse WM, Lepley DM, Burgess CE, Vernet CAM, Li L;	
PI	Gorman L, Edinger S, Sciore P, Ellerman K, Malyankar U;	
PI	Rothenberg M, Stone D, Boldog F, Guo X, Shenoy S, Anderson D;	
PI	Padigaru M, Taupier RJ, Miller CE, Eisen A;	
XX	WPI; 2002-583619/62.	
DR	N-PSDB; ABQ93881.	
DR	Novel polypeptides and nucleic acids homologous to transmembrane	
XX	receptor, thymosin, neuromodulin-like family of proteins for diagnosing,	
PT	treating cancer, atherosclerosis, neurological, skin and autoimmune	
PT	disorders.	
PT	Claim 1c; Page 20-21; 323pp; English.	
XX	The invention relates to 24 novel human proteins designated NOV1-NOV14	
PS	(ABB09501-ABB09524), collectively referred to as NOVX proteins, and	
XX	nucleic acids encoding them (ABQ93879-ABQ93902). NOVX proteins and	
CC	nucleotides are useful in the treatment, diagnosis or prevention of NOVX-	
CC	associated disorders or in the manufacture of a medicament for treating	
CC	such disorders, with specific applications described for each of the 24	
CC	NOVX proteins, based on their homology to known proteins. Various	

disorders are associated with NOVX proteins including neurological disorders (e.g., Alzheimer's, Huntington's and Parkinson's diseases), pain, behavioural disorders, addiction, tuberosus sclerosis, cancers (e.g., colorectal cancer, leukaemia and osteosarcoma), immune disorders (e.g., allergies and autoimmune diseases), myasthenia gravis, asthma, various forms of arthritis, diabetes, thyroiditis, cardiovascular disease (e.g., hypertension), reproductive disorders, endometriosis, incontinence, psoriasis, scleroderma, alopecia, ulcers, pancreatitis, cirrhosis, glomerular endotheliosis, polycystic kidney disease, endocrine disorders, obesity, bacterial infections and particularly cardiomyopathy, atherosclerosis, cell signal processing-related disorders and disorders of metabolic pathway regulation. NOVX nucleic acids and polypeptides may be used to identify cellular receptors or downstream effectors which binds to a NOVX protein, and are also useful as targets for the identification of small molecules that modulate or inhibit processes such as neurogenesis, cell differentiation, cell motility, cellular proliferation, haematopoiesis, wound healing and angiogenesis. NOVX nucleic acid sequences can be used to identify a cell or tissue type and are useful as a source of primers or probes for forensic biology and for identifying and cloning NOVX homologues in other cell types. Cells comprising NOVX nucleic acids are useful for producing non-human transgenic animals which are useful for studying the function and activity of NOVX proteins and for identifying and evaluating modulators of NOVX activity. The present sequence represents the laminin alpha-5-like protein NOV1c. The gene encoding NOV1c is located on chromosome 20

xx
SQ Sequence 3597 AA;

Query Match	74.0%;	Score 14706.5;	DB 5;	Length 3597;
Best Local Similarity	74.5%;	Pred. No. 0;		
Matches 2729;	Conservative 274;	Mismatches 482;	Indels 177;	Gaps 25;

QY	1	DLYCKLVGGPVAGGDPNQTIQGYCDICTAANSNKAHPVSN	NAIDGTERWQSPPLSRGLE	60
DB	58	DLYCKLVGGPVAGGDPNQTIQGYCDICTAANSNKAHPASNA	IDGTERWQSPPLSRGLE	117
QY	61	YNEVNVTLDLGOVHFVAYVLIKFANSRPDLWVLERSTDFGHTYQ	WPQWFFASKRDCLE	120
DB	118	YNEVNVTLDLGOVHFVAYVLIKFANSRPDLWVLESMDFGRTYQ	WPQWFFAASKRDCLE	177
QY	121	FGPRTLERITODDDVICTEYSRIVPLENGEIVVSLVNGRPGALNFSY	SPLLRDFTKATN	180
DB	178	FGPQTLERITRDDAAICTEYSRIVPLENGEIVVSLVNGRPGAMNFSY	SPLLRDFTKATN	237
QY	181	IRLFLRNTNLLGLHMGKALRDPVTTRRYYSIKDISIGGRVCVCHGAD	VCDAKDPDPP	240
DB	238	VLRLFLRNTNLLGLHMGKALRDPVTTRRYYSIKDISIGGRVCVCHGAD	ACDAKDPDPP	297
QY	241	RLQACQHNTCGSGCDRCPPGFNQPKPATDSANECQSCNCHGHAYDCY	YDPEVDRRN	300
DB	298	RLQCTQHNTCGTCDRCPPGFNQPKPATANSANECQ-CECYGHATDCY	YDPEVDRRR	356
QY	301	ASQNQDNVYQGGVCLDCQHHTTGINCERCLPGFFRAPDQPLDSPHVC	RPCDCESDFTDG	360
DB	357	ASQSLDGTYYQGGVCLDCQHHTTGIVNCERCLPGFYRSPNHPPLDSPH	VCRGNCESDFTDG	416
QY	361	TCEDLTGRCYCRPNFTGELCAACAEGYTDFFHCYPLPSPFPHNDTRE	QVLPAGQIVNCDN	420
DB	417	TCEDLTGRCYCRPNFSGERCDVCAEGFTGFPPSCY-REHLPNGNDTRE	QVLPAGQIVSCDCS	475
QY	421	AAGTQGNACRKPRLGRVCVCKPNFRGAHCELCAPGFHGPSCHPCQCSS	---PGVANSLCD	477
DB	476	AAGTQGNACRKPDRVGRCLCKPNFQTHCELCAPGFYGPGC-PASVPALE	WPMTAVTLTQ	534
QY	478	PESGQCMCRTG-----FEGDRCDHCAALGYFHFPL-CQLCGCSPAGT	LPEGCDEAG	526
DB	535	ASAGAEWASRGPHVIAVPATFTLSASH-----PLRSVAVCGCSPAGT	LPEGCDEAG	586
QY	527	RCQCRPGFDGPHCDRCLUPGYHYGYPDCHACACDPRGALDQQCGVGLCH	CRPGNTGATCQE	586
DB	587	RCLCQPEFAGPHCDRCPGYPHYGFPNCAACTCDPRGALDQLCGAGGLCR	CRPGYGTGATCQE	646
QY	587	CSPGFYGFPPSCIPCHCSADGSLHTTC-----DPTTGTQCRCPRTV	GLHCDMCPGAYNFPY	642

Db 647 CSPGFHGFPS-----CPATALLKAPCTQPTVPFGVGSAAAGP-VRGCGVTRVCVPVPTTSPT 700

Qy 643 CEAGSCHPAGLAPANPALPETQAPCMCRAHVEGSPCDRCKPGYWGLSASNPEGCTRCSGD 702

Db 701 AKLALATLPVWPPVPDPALPEAQVPCMCRAHVEGSPCDRCKPGFWGLSPSNPEGCTRCSGD 760

Qy 703 PRGTLGGVTECO-GNGQCFCKAHVCGKTCACAKDGFFGLDYADYFGCRSCRDVGGALGO 761

Db 761 LRGTGGVAECQPGTGCFCKPHVCGQACASCKDGFFGLDQADYFGCRSCRDIGGALGO 820

Qy 762 GCEPKTGACRCRPNTOGPTCSEPAKDHYPDLFHMRLLEEEAATPEGHAVRFGFNPLEFE 821

Db 821 SCEPRTGVCRCRPNTOGPTCSEPAKDHYPDLFHMRLLEEEAATPEGHAVRFGFNPLEFE 880

Qy 822 NFSWRGYAHMAIQPRIVARLNVTSPLDFRLVFRVYNRGSTSVNGQISVREEGKLSSCTN 881

Db 881 NFSWRGYAQMAMPVQPRIVARLNLTSPLDFLWVFRVYNRGAMSVSGRVSVREEGRSAACAN 940

Qy 882 CTEQSQPVAFPPSTEPAFVTVPORGFGEFVLNPGIWALLVEAEGVLLDYVVLPLSTYYE 941

Db 941 CTAQSQPVAFPPSTEPAFITVPORGFEFVLNPGTWALRVEAEGVLLDYVVLPLSAYYE 1000

Qy 942 AALLQHRVTEACTYRPSALHSTENCLVYAHPLDGFPSAAGTEALCRHDNSLPRPCPTEQ 1001

Db 1001 AALLQLRVTEACTYRPSAQSPSCLLYTHPLDGFPSAAGLEALCRQDNSLPRPCPTEQ 1060

Qy 1002 LSPSHPPPLATCFGSDVDIQLEMAVPQPGQYVLVVEYVGEDSHQEMGVAVHTPQAPQOQV 1061

Db 1061 LSPSHPPPLITCTGSDVDVQLQVAVPQPGRYALVVEYANEDARQEVGVAVHTPQAPQOGL 1120

Qy 1062 LNLHPCPYSSLCRSPARDTOHHLAIFHLDSEASIRLTAEQAHFFLHSVTLPVVEEFSTEF 1121

Db 1121 LSLHPCLYSTLCRGHTARDTDHDLAVFHLDSSEASVRLTAEQARFFLHGVTLPVPIEEFSPEF 1180

Qy 1122 VEPRVFCVSSHGTENPSSAACLASRFKPPQPIILKDCQVLPPLPDLPTQSOELSPGAP 1181

Db 1181 VEPRVSCISSHGAFGENSAAACLPSPFKPPQPIILRDCQVILPPLPGLPLTHAODLTPAMS 1240

Qy 1182 PEGPQRPPTAVDPNAPETLLRHPQGTVVFTTQVPTLGRYAFLLHGGYQPVHPSPFVEVLI 1241

Db 1241 PAGPRRPPTAVDPDAEPTLLREPQATVVFTTHVPTLGRYAFLLHGGYQPAHPTFPFVEVLI 1300

Qy 1242 NGGRIWQGHANASFCPHGYGCRTLVLCEGQTMLDVTDNELTVTVRVEGRWLWLDYVLIV 1301

Db 1301 NAGRVWQGHANASFCPHGYGCRTLVWCEGQALLDVTHSELVTVTVRVEKRWLWLDYVLVV 1360

Qy 1302 PEDAYSSSYLOEEPLDKSYDFISHCATQGYHISPSSSSPFCRNAATSLSLFYNNGALPCG 1361

Db 1361 PENVYSFGYLREEPLDKSYDFISHCAAQGYHISPSSSSLFRCNAAASLSLFYNNGARPCG 1420

Qy 1362 CHEVGAVSPTCEPFGGQPCRGHVIGRDCSRCATGYWGFNCRPCDCGARLCDELGTQCI 1421

Db 1421 CHEVGATGPTCEPFGGQPCCHAHVIGRDCSRCATGYWGFNCRACDCGARLCDELGTQCI 1480

Qy 1422 CPPRTVPPDCLVCQPSFGCHPLVGCEEENCSGPGVQELTDPTCDMDSGQCRCPNVAGR 1481

Db 1481 CPPRTIPPDCLLCQPTFGCHPLVGCEEENCSGPGIQELTDPTCDTDSGQCRCPNVTGR 1540

Qy 1482 RCDTCAPGFYGYPSRCPCDCHEAGTMASVCDPLTGQCHCKENVOGSRCDQCRVGTFSLDA 1541

Db 1541 RCDTCSPGFHGYPRCPCDCHEAGTAPGVCDPLTGQCYCKENVOGPKCDQCSLGTFSLDA 1600

Qy 1542 ANPKGCTRCFCFGATERCNGSNLARHEFVDMEGWVLLSSDRQVVPHEHRPEIELLHADLR 1601

Db 1601 ANPKGCTRCFCFGATERCRESSYTRQEFVDMEGWVLLSTDQVVPHERQPCGTEMLRADLR 1660

Qy 1602 ----SVADTFSELYWQAPPSYLGDRVSSYGGTLHYELHSETQRGDIFITYESRPDVVLQ 1657

Db 1661 HYPEAVPEAFPPELYWQAPPSYLGDRVSSYGGTLRYELHSETQRGDVFPVMESRPDVVLQ 1720

Qy 1658 NQMSIAFLELAY2PPPGVHRGQQLQLVGEGNFRHLETHNPVSREELMMVLASLEQLQIRALF 1717

Db 1721 NQMSITFLEPAYPTPGHVHRGQQLQLVGEGNFRHTETRTNTVSRREELMMVLASLEQLQIRALF 1780

Qy 1718 SQTSSSVSLRRVLEVASEAGRPPASNVELCMCPANRYRGSDSCQECAPGYRDTKGLFLG 1777

Db 1781 SQISSAVFLRRVALEVASPAGQALASNVELCLCPASYRGSDSCQECAPGYRDKGLFLG 1840

Qy 1778 RCVPCQCHGHSRCLPGSGICVGCQHNTGECQECRCRPGFVSSDSPSNPASPVCSCPCPLA 1837

Db 1841 RCVPCQCHGHSRCLPGSGVCV-CQHNTGEGHCHERCQAGFVSS-RDDPSAPVCSCPCPLS 1898

Qy 1838 VPSNPFADGCVLRNRTQCLCRPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSGNDPN 1897

Db 1899 VPSN-----RCAPGFFGNPLVLGSSCQPCDCSGNDPN 1931

Qy 1898 MIFSDCDPLTGACRCGLRHTTTPHCERCAPGYGNALLPGNCTRCDCSPCGTETCDPQSG 1957

Db 1932 LLFSDCDPLTGACRCGLRHTTTPRCEICAPGYGNALLPGNCTRCDCCTPCGTEACDPHSG 1991

Qy 1958 RCLCKAGVTGQRCRCLEGYFGEQCGQCRPCACGPAAGSECHPQSGQCHCQPGTTGPQ 2017

Db 1992 HCLCKAGVTGRRCDRCQEGHFGFDGCGGCRPCACGPAAGSECHPQSGQCHCRPGTMGPQ 2051

Qy 2018 CLECAPGYWGLPEKGCRRCCQPRGHCDPHTGHCTCPPGLSGERCDCSCQHQHVVPKPG 2077

Db 2052 CRECAPGYWGLPEQGCRRCCQPGRCDPHTGRCNCPPGLSGERCDCSCQHQHVVPGGPV 2111

Qy 2078 GHGIHCEVCDHCVVLLDDDLERAGALLPAIREQLQGINASSAAWARLHRLNASIADL--- 2134

Db 2112 GHSIHCEVCDHCVVLLDDDLERAGALLPAIHEQLRGINASSMAWARLHRLNASIADLQVL 2171

Qy 2135 -----QSKLRRPPGPRYQAAQQLQTLQEQQSISLQODTERLGSQAT 2174

Db 2172 SVLAFFPPQPGPVQAFTRLPQSQLRSPGLPRHETAQQLVLEQQSTSLP-----PQAV 2224

Qy 2175 GVQSQAGQLLDTTTESTLGRAQKLLSVAVGRALNELASRMGQSGPGDALVPSGEQLRWA 2234

Db 2225 GTRDQASQLLAGTEATLGHAKTLLAAIRAVDRDTLSELMSQTGHLGLANASAPSGEQLLRT 2284

Qy 2235 LAEVERLLWDMRTRDLGAQGAVAEAEAEAEAOILMARVQEQLTSFWEENQSLATHIRDOLA 2294

Db 2285 LAEVERLLWEMRARDLGAPQAAAEAEAEAAQORVLARVQEQLSSLWEENQALATQTRDLA 2344

Qy 2295 QYESGLMDLREALNOAVNTTREAEEELNSRNOBRVKEALQWKQELSDNATLKATLQAASL 2354

Db 2345 QHEAGLMDLREALNRAVDATREAQELNSRNOBRLEALQKQELSRDNATLQATLHAARD 2404

Qy 2355 ILGHVSELLQIDQAK-EDLEHLAASLDGAWTPLLKRMQAFSPASSKVDLVVEAAEAHAQK 2413

Db 2405 TLASVFRLLLEGSLPLKFQELERLAASLDGARFLLQRMQTFSPAGSKLRLVEAAEAHAQK 2464

Qy 2414 LNQLAINLSGIILGINQDRFIQRAVEASNAYSSILQAVQAAEDAAGQALRQASRTWEMV 2473

Db 2465 LGQLALNLS-IILDVNQDRLTQRAIEASNAYSRIQAVQAAEDAAGQALQOQADHTWTW 2523

Qy 2474 QRLAAGARQLLANSSALEETILGHQGRGLAQ-----GRLQAAGIQLHNVWARKNQALAA 2528

Db 2524 RQGLVDRAQQLLANSTALEEAMLQEQORLGLGECWAPMGALRPAGTQLRDVRAKDKDLEA 2583

Qy 2529 QIQEAQAMLAMDTSETSEKIAHAKAVAAEAALSTATHVQSOLQGMQKNVERWQSQGLQ 2588

Db 2584 HIQAAQAMLAMDTGETSKIAHAKAVAAEAQDTATRVQSOLQAMQENVERWQCYEGLRG 2643

Qy 2589 QDLSQOVERDASSSVSTLEKTLPLLAKLSRLENRGVHNASLALSANIGRVRKLIQAARSA 2648

Db 2644 QDLGQAVLDAGSAVSTLEKTLPLLAKLSILENRGVHNASLALSASIGRVRBELIAQARGA 2703

Qy 2649 ASK-VKVSMMKFNGRSGVRLRPPRDLADLAAYTALKFHIQSPVPAPEPGKNTGDHFVLYMG 2707

Db 2704 ASKVVKVPMKFNGRSGVQLRTPRDLADLAAYTALKFYLG--PEPEPGGTEDRFVYMG 2761

Qy 2708 SRQATGDMGVSLRNQKVHVYRLGKAGPTTILSIDENIGEQAFAAVISIDRTLOFGHMSVT 2767

Db 2762 SRQATGDMGVSLRDKKVHVYQLGEAGPAVLSIDEDIGEQAFAAVSLDRTLOFGHMSVT 2821

QY 301 ASQNDNVYQGGVCLDCQHHTTGINCERCLPGFFRAPDQPLDSPHYCRPCDCESDFTDG 360
Db 379 ASQSLDGTQGGVCIDCQHHTAGVNCERCLPGFVRSPNHPLDSPHYCRRNCESDFTDG 438
QY 361 TCEDLTGRCYCRPNFTGELCAACAEGYTDFPHCYPLPSFPHNDRTEQVLPAGQIVNDCN 420
Db 439 TCEDLTGRCYCRPNFSGERCDCVCAEGFTGFPSYCPFPS-SSNDTREQVLPAGQIVNDCS 497
QY 421 AAGTCGNACRKPRLGRVCVKPNFRGAHCELCAPEGHGPSCHPCQCSCSSPGVANSLCDPES 480
Db 498 AAGTCGNACRKPVRGRCLCKPNFQGTCHCELCAPGFVPGCQPCQCSCSSPGVADDRCDPDT 557
QY 481 GQCMCRGTGFEGRCDHCHALGALYFHFPLCLQCGCSPAGTLPPEGCDEAGRCQCPCPFDPGPHCD 540
Db 558 GQCRVGFEGATCDRCAPGYFHFPLCLQCGCSPAGTLPPEGCDEAGRCCLQCFEAGPHCD 617
QY 541 RCLPGYHGYPDCHACACDPRGALDQOCGVGGLCHCRPGNTGATCQECSPGYFPSPCIPC 600
Db 618 RCRPGYHGFPCQACTCDPRGALDQLCGAGGLCRCPGYTGATCQECSPGFHFPSCVPC 677
QY 601 HCSADGSLHTTCDPTTGQCRCPRTVTGLHCDMCPVGAIFYCEAGSCHPAGLAPANPAL 660
Db 678 HCSAEGSLHAACDPRSGQSCRCRPRVTGLRCDTCVPGAIFYCEAGSCHPAGLAPVDPAL 737
QY 661 PETQAPCMCRAHVEGPSDCRCKPGYWGLSASNPEGCTRCSDPRGTLGGVTECQ-GNGQC 719
Db 738 PEAQVPCMRAHVEGPSDCRCKPGFWGLSPSNPEGCTRCSDLRGTLGGVABCQFGTGQC 797
QY 720 FCKAHVCGKTAACKDGGFFGLDYADYFGCRSCRDVGALGQGCCEPKTGACRCRPNTOGP 779
Db 798 FCKPHVCGQACASCKDGGFFGLDQADYFGCRSCRDIGGALGQSCCEPKTGACRCRPNTOGP 857
QY 780 TCSEPAKDHVLPDLHLRLLELEBAATPEGHAVRFGFNPLEFENFSWRGYAHNMAIQPRIV 839
Db 858 TCSEPARDHVLPDLHLRLLELEBAATPEGHAVRFGFNPLEFENFSWRGYAQMVPVQPRIV 917
QY 840 ARLNVTSPDLFRLVFRYYNRGTSVNGQISVREEGLSSCTNCTEQSQPVAFPPSTEPAF 899
Db 918 ARLNLTSPDLFWLVFRYYNRGMSVSGRVSVREEGRSAACTAQSQPVAFPPSTEPAF 977
QY 900 VTVPQRGFGEFVLPNGIWAIVYAEAGVLLDYVWLLPSTYYEALLQHRVTEACTYRPSA 959
Db 978 ITVPQRGFGEFVLPNGITWALRVEAEGVLLDYVWLLPSAYEALLQLRVTEACTYRPSA 1037
QY 960 LHSTENCLVYAHPLPDGFPSAAGTEALCRHNSLPRPCPTQELSPSHPLATCFGSDVDI 1019
Db 1038 QOSGDNCLLYTHPLPDGFPSAAGLEALCRQDNLPRPCPTQELSPSHPLITCTGSDVDV 1097
QY 1020 QLEMAVQPQGVYLVVEYVEDSHQEMGVAVHTPQAPQGVNLNHPYSSLCRSPARD 1079
Db 1098 QLOVAVQPQGRYALVVEYANEDARQEVGVAVHTPQAPQGLLSLHPCLYSTLCRGTARD 1157
QY 1080 TQHLALPHLDSEASIRLTAEQAHFHLSVTLVPVEEFSTEFVEPRVFCVSSHGTFNPSS 1139
Db 1158 TQDLAVPHLDSEASVRLTAEQARFHLGVTLVPIEEFSPFVEPRVSCISSHGAFGPS 1217
QY 1140 AACLASRFPKPPQPIILKDCQVLPPLPDLPLTQSQELSPGAPPEGPQPRPPTAVDPNAEP 1199
Db 1218 AACLPSPRFPKPPQPIILRDCQVPLPPLGLPLTHAQDLTPATSPAGPRPPTAVDPDAEP 1277
QY 1200 TLLRHPQGTVVFTTQVPTLGRYAFLLHGYQPVHPSFPFVVLINGGRIWQGHANASFCPHG 1259
Db 1278 TLLREPQATVVFTTHVPTLGRYAFLLHGYQPAHPTFFPVVVLINAGRVWQGHANASFCPHG 1337
QY 1260 YGCRTLVLCBQTMLDVTDNELVTVRVPEGRWLWDYVLVPEDAYSSSYLQEEFLDKS 1319
Db 1338 YGCRTLVVCBQALLDVTHSELVTVRVPEGRWLWDYVLVPENVYSFGLYLRREEFLDKS 1397
QY 1320 YDFISHCATQGYHISPSSSPFCRNAATSLSLFYNNGALPCGCHEVGAVSPTCEPFGGQC 1379
Db 1398 YDFISHCAAQGYHISPSSSLFCRNAASLSLFYNNGARPCGCHEVGATGPTCEPFGGQC 1457
QY 1380 PCRGHVIGRDCSRCATGYWGFNCRPCDCGARLDELGTQCICPPRTVPPDCLVCQPQSF 1439

Db 1458 PCHAHVIGRDCSRCATGYWGFNCRPCDCGARLDELGTQCICPPRTIPPPDCLLCQPQTF 1517
QY 1440 GCHPLVGCBEECNCSGPGVQBELDPTCDMDSGQCRCPNVAGRRCDTCAPGFYGYPSRCRPC 1499
Db 1518 GCHPLVGCBEECNCSGPGIQLDPTCDTDSGQCKRPNVTGRRCDTCSPGFHGYPRCRPC 1577
QY 1500 DCHAGTMASVCDPLTGQCHCKENVQSGRCDQCRVGTFSLDAAANPKGCTRCFCFGATERC 1559
Db 1578 DCHAGTAPGVCDDLGTQCYCKENVQGPCKDCQCSLGTFSLDAAANPKGCTRCFCFGATERC 1637
QY 1560 GNSNLARHEFVDMEGWVLLSSDRQVVPHEHRPEIELLHADLR----SVADTFSELYWQAP 1615
Db 1638 RSSSYTRQEFVDMEGWVLLSTDRQVVPHERQPGTETMLRADLRHVPEAVPEAFPELYWQAP 1697
QY 1616 PSYLGDRVSSYGGTLHYELHSETQRGDIPIPYESRPDVVLQGNQMSIAFLELAYPPPGQV 1675
Db 1698 PSYLGDRVSSYGGTLRYELHSETQRGDVFPVPMESRPDVVLQGNQMSITFLEPAYPTPGHV 1757
QY 1676 HRGQLQVVEGNFRHLETHNPVSREELMMVLAGLEQLQIRALFSQTSSSSVSLRRVVLEVAS 1735
Db 1758 HRGQLQVVEGNFRHTETRTNTVSREELMMVLASLEQLQIRALFSQISSAVSLRRVLEVAS 1817
QY 1736 EAGRGPASNVELCMCPANVRGDSQCECAPGYRYRDKGLFLGRVCVPCQCHGSHDRCLPGS 1795
Db 1818 PAGQALASNVELCLCPASVYRGDSQCECAPGYRYRDKGLFLGRVCVPCQCHGSHDRCLPGS 1877
QY 1796 GICVGCQHNTEGDQCERCRCRPGVSSDPSPNPASPCVSCPPLAVPSNNFADGCVLRNGRTQ 1855
Db 1878 GVCVDCQHNTEGAHCERCQAGFMSS-RDDPSAPCVSCPPLSVPSNNFAEGCVLRNGRTQ 1936
QY 1856 CLCRPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSGNGDPNMFSDCDPLTGACRGCLR 1915
Db 1937 CLCKPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSGNGDPNLLFSDCDPLTGACRGCLR 1996
QY 1916 HTTGPHCERCAPGYGNALLPGNCTRCDCSPCGTETCDPQSGRCLCKAGVTGQRCDRCLE 1975
Db 1997 HTTGPRCEICAPGYGNALLPGNCTRCDCTPCGTEACDPHSGHCLCKAGVTGRRCDRCQE 2056
QY 1976 GYFGFEQCGCRPCACGPAKSGSECHPQSGQCHCQPGTTPGQCLECAPGYWGLPEKGR 2035
Db 2057 GHFGFNGCGCRPCACGPAKSGSECHPQSGQCHCQPGTTPGQCRECAPGYWGLPEKGR 2116
QY 2036 CQCPRGHCDPHTGHCTCPPGLSBERCDTCSQQHQVPVPGKPGGHIHCEVCDHCVVLLLD 2095
Db 2117 CQCPGGRCDPHTGRCNCPGLSBERCDTCSQQHQVPVPGPGVGHSHIHCVECDHCVVLLLD 2176
QY 2096 DLERAGALLPAIREQLOGINASSAAWARLHRLNASIADLQSKLRRPPGPRYQAAQLOTL 2155
Db 2177 DLERAGALLPAIHEQLRGINASSMAWARLHRLNASIADLQSLRSPGLGRHETAQOQLEVL 2236
QY 2156 EQQSISLQDTERLGSQATGVQOAGQLDTTTESTLGRAKILLESVRAVGRALNELASRM 2215
Db 2237 EQQSTSLGQDARRLGGQAVGTRDQASQLLAGTEATLGHAKTLLAAIRAVDRTLSEMSQT 2296
QY 2216 GQSGPDALVPSGEQLRWALAEVERLLWDMRTRDLGAQGAFAEAEAEAEAEAEAEAEAEAE 2275
Db 2297 GHLGLANASAPSGEQLLRTLAEVERLLWEMRARDLGAPQAAAFAEAEAEAEAEAEAEAE 2356
QY 2276 TSFWEENQSLATHIRDQLAQYESGLMDLREALNQAVNTTREAEEELNSRNQERVKEALQWK 2335
Db 2357 SSLWEENQALATQTRDLRAQHEAGLMDLREALNRAVDATREAQELNSRNQERLEEALQK 2416
QY 2336 QELSQDNATLKATLOAASLILGHVSELLOQIDQAKEDLEHLAASLDGAWTPLLKRMQAFS 2395
Db 2417 QELSRDNATLQATLHAARDTTLASVFRLLHSLDQAKEELERLAASLDGARTPLLQRMQTF 2476
QY 2396 PASSKVDLVEAAEAAHAQKLNQNLAINLSGIILGINQDRFIQRAVEASNAYSSILQAVQAAE 2455
Db 2477 PAGSKLRLVEAAEAAHAQQLGQLALNLSIILDVNQDRLTQRTAEASNAYSRILOAVQAAE 2536
QY 2456 DAAGQALRQASRTWEMVQVRGLAAGARQLLANSSALEETILGHQGRGLGAQGRLOAAGIQ 2515

Db	2537	DAAGQALQADHTWATVVRQGLVDRAQQLLANSTALEEAMLQEQRGLGLVWAALQGARTQ	2596
QY	2516	LHNVTWARKNQLAAQIQEAQAMLAMDTSETSEKIAHAKAVAAEALSTATHVQSOLQGMQKN	2575
Db	2597	LRDVRAKKQLEAHIQAAQAMLAMDTDETSKIAHAKAVAAEAQDTATRVQSOLQAMQEN	2656
QY	2576	VERWQSOLGGLQGQDLQSVERDASSSVSTLEKILPQLIAKLSRLENRGVGNASLALSANI	2635
Db	2657	VERWQGYEGLRGQDLGQAVLDAGHSVSTLEKILPQLIAKLSILENRGVGNASLALSASI	2716
QY	2636	GRVRKLIQAARSAASKVKVSMKFNGRS	2662
Db	2717	GRVRELIAQARGAASKVKVPMKFNGRS	2743

RESULT 9
ADE08094
ID ADE08094 standard; protein; 3332 AA.
XX
AC ADE08094;
XX
DT 29-JAN-2004 (first entry)
XX
DE Novel protein (useful for identifying genetic disorders) #249.
XX
KW novel gene; novel protein; tissue marker; molecular weight marker;
KW chromosome marker; genetic disorder.
XX
OS Unidentified.
XX
PN WO2003054152-A2.
XX
PD 03-JUL-2003.
XX
PF 10-DEC-2002; 2002WO-US039555.
XX
PR 10-DEC-2001; 2001US-0339739P.
PR 11-DEC-2001; 2001US-0339453P.
PR 14-MAR-2002; 2002US-0365091P.
PR 14-MAR-2002; 2002US-0365384P.
PR 12-APR-2002; 2002US-0372381P.
PR 12-APR-2002; 2002US-0372615P.
PR 22-APR-2002; 2002US-00128558.
PR 24-APR-2002; 2002US-0376045P.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;
PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
XX
DR WPI; 2003-569235/53.
DR N-PSDB; ADE07183.

XX
PT New polynucleotides, useful for expressing recombinant proteins for
PT analysis, characterization or therapeutic use, or as markers for tissues
PT in which the corresponding protein is preferentially expressed.

XX
PS Claim 20; SEQ ID NO 1160; 1177pp; English.
XX
CC The invention comprises the amino acid and coding sequences of novel
CC proteins. The DNA and protein sequences of the invention are useful as:
CC markers for tissues in which the corresponding protein is preferentially
CC expressed; as molecular weight markers on gels; as chromosome markers or
CC tags; to identify chromosomes or to map related gene positions; and to
CC compare with endogenous DNA sequences in patients to identify potential
CC genetic disorders. The present amino acid sequence represents a protein
CC of the invention.
XX
SQ Sequence 3332 AA;

Query Match 33.4%; Score 6643.5; DB 7; Length 3332;
Best Local Similarity 38.6%; Pred. No. 0;

	Matches	1434;	Conservative	537;	Mismatches	1175;	Indels	567;	Gaps	77;
QY	1	DLCKLVGGPVAGGDPNQTIQGYCDICTAANSNKAHPVSN	1	DLCKLVGGPVAGGDPNQTIQGYCDICTAANSNKAHPVSN	1	DLCKLVGGPVAGGDPNQTIQGYCDICTAANSNKAHPVSN	1	DLCKLVGGPVAGGDPNQTIQGYCDICTAANSNKAHPVSN	1	DLCKLVGGPVAGGDPNQTIQGYCDICTAANSNKAHPVSN
Db	79	ELYCKLVGGPTAPGS-GHTIQGFCDYCNSEDPRKAHPVTNAIDGSE	79	ELYCKLVGGPTAPGS-GHTIQGFCDYCNSEDPRKAHPVTNAIDGSE	79	ELYCKLVGGPTAPGS-GHTIQGFCDYCNSEDPRKAHPVTNAIDGSE	79	ELYCKLVGGPTAPGS-GHTIQGFCDYCNSEDPRKAHPVTNAIDGSE	79	ELYCKLVGGPTAPGS-GHTIQGFCDYCNSEDPRKAHPVTNAIDGSE
QY	61	YNEVNTLDLGQVHFVAYLIKFA NSPRPDLWLERSTDFGHTYQ	61	YNEVNTLDLGQVHFVAYLIKFA NSPRPDLWLERSTDFGHTYQ	61	YNEVNTLDLGQVHFVAYLIKFA NSPRPDLWLERSTDFGHTYQ	61	YNEVNTLDLGQVHFVAYLIKFA NSPRPDLWLERSTDFGHTYQ	61	YNEVNTLDLGQVHFVAYLIKFA NSPRPDLWLERSTDFGHTYQ
Db	138	YNRVNTLDLGQVHFVAYLIKFA NSPRPDLWLERSVDFGSTYSP	138	YNRVNTLDLGQVHFVAYLIKFA NSPRPDLWLERSVDFGSTYSP	138	YNRVNTLDLGQVHFVAYLIKFA NSPRPDLWLERSVDFGSTYSP	138	YNRVNTLDLGQVHFVAYLIKFA NSPRPDLWLERSVDFGSTYSP	138	YNRVNTLDLGQVHFVAYLIKFA NSPRPDLWLERSVDFGSTYSP
QY	121	FGPRTLERITQDDDDVICTEYSRIVPLENGEIVVSLVNGRPGALN	121	FGPRTLERITQDDDDVICTEYSRIVPLENGEIVVSLVNGRPGALN	121	FGPRTLERITQDDDDVICTEYSRIVPLENGEIVVSLVNGRPGALN	121	FGPRTLERITQDDDDVICTEYSRIVPLENGEIVVSLVNGRPGALN	121	FGPRTLERITQDDDDVICTEYSRIVPLENGEIVVSLVNGRPGALN
Db	198	FGREANMAVTRDDDLVLCVTEYSRIVPLENGEIVVSLVNGRPGALN	198	FGREANMAVTRDDDLVLCVTEYSRIVPLENGEIVVSLVNGRPGALN	198	FGREANMAVTRDDDLVLCVTEYSRIVPLENGEIVVSLVNGRPGALN	198	FGREANMAVTRDDDLVLCVTEYSRIVPLENGEIVVSLVNGRPGALN	198	FGREANMAVTRDDDLVLCVTEYSRIVPLENGEIVVSLVNGRPGALN
QY	181	IRLRLTNTLLGHLMGKALDDPTVTRRYYSIKDISIGRCVCHGHAD	181	IRLRLTNTLLGHLMGKALDDPTVTRRYYSIKDISIGRCVCHGHAD	181	IRLRLTNTLLGHLMGKALDDPTVTRRYYSIKDISIGRCVCHGHAD	181	IRLRLTNTLLGHLMGKALDDPTVTRRYYSIKDISIGRCVCHGHAD	181	IRLRLTNTLLGHLMGKALDDPTVTRRYYSIKDISIGRCVCHGHAD
Db	258	IRLRLTNTLLGHLISKAQDPTVTRRYYSIKDISIGRCVCHGHAD	258	IRLRLTNTLLGHLISKAQDPTVTRRYYSIKDISIGRCVCHGHAD	258	IRLRLTNTLLGHLISKAQDPTVTRRYYSIKDISIGRCVCHGHAD	258	IRLRLTNTLLGHLISKAQDPTVTRRYYSIKDISIGRCVCHGHAD	258	IRLRLTNTLLGHLISKAQDPTVTRRYYSIKDISIGRCVCHGHAD
QY	241	RLQACQHNTCGGSCDRCCPGFNQPKPATTDSANECSCNCHGHAYD	241	RLQACQHNTCGGSCDRCCPGFNQPKPATTDSANECSCNCHGHAYD	241	RLQACQHNTCGGSCDRCCPGFNQPKPATTDSANECSCNCHGHAYD	241	RLQACQHNTCGGSCDRCCPGFNQPKPATTDSANECSCNCHGHAYD	241	RLQACQHNTCGGSCDRCCPGFNQPKPATTDSANECSCNCHGHAYD
Db	318	R--CEQHHTCGETCDRCCTGYNQRRWRPAAWEQSHCEACNCHGHAS	318	R--CEQHHTCGETCDRCCTGYNQRRWRPAAWEQSHCEACNCHGHAS	318	R--CEQHHTCGETCDRCCTGYNQRRWRPAAWEQSHCEACNCHGHAS	318	R--CEQHHTCGETCDRCCTGYNQRRWRPAAWEQSHCEACNCHGHAS	318	R--CEQHHTCGETCDRCCTGYNQRRWRPAAWEQSHCEACNCHGHAS
QY	301	ASQNDNVYQGGVCLDCQHHTTGINCERCLPGFFRAPDPLDSPHVCR	301	ASQNDNVYQGGVCLDCQHHTTGINCERCLPGFFRAPDPLDSPHVCR	301	ASQNDNVYQGGVCLDCQHHTTGINCERCLPGFFRAPDPLDSPHVCR	301	ASQNDNVYQGGVCLDCQHHTTGINCERCLPGFFRAPDPLDSPHVCR	301	ASQNDNVYQGGVCLDCQHHTTGINCERCLPGFFRAPDPLDSPHVCR
Db	376	ASLNTQGIYAGGVCCINCHQNTAGVNCCEQCAKGYRYPYVPVADP	376	ASLNTQGIYAGGVCCINCHQNTAGVNCCEQCAKGYRYPYVPVADP	376	ASLNTQGIYAGGVCCINCHQNTAGVNCCEQCAKGYRYPYVPVADP	376	ASLNTQGIYAGGVCCINCHQNTAGVNCCEQCAKGYRYPYVPVADP	376	ASLNTQGIYAGGVCCINCHQNTAGVNCCEQCAKGYRYPYVPVADP
QY	361	TCEDLTGRCYCRPNFTGELCAACAEGYTDFPHCYPLPSFPHNDTRE	361	TCEDLTGRCYCRPNFTGELCAACAEGYTDFPHCYPLPSFPHNDTRE	361	TCEDLTGRCYCRPNFTGELCAACAEGYTDFPHCYPLPSFPHNDTRE	361	TCEDLTGRCYCRPNFTGELCAACAEGYTDFPHCYPLPSFPHNDTRE	361	TCEDLTGRCYCRPNFTGELCAACAEGYTDFPHCYPLPSFPHNDTRE
Db	436	-CEQSGRCHCKPNFHDNCEKCAIGY-NFPFCLRTPIFPVSTPSS	436	-CEQSGRCHCKPNFHDNCEKCAIGY-NFPFCLRTPIFPVSTPSS	436	-CEQSGRCHCKPNFHDNCEKCAIGY-NFPFCLRTPIFPVSTPSS	436	-CEQSGRCHCKPNFHDNCEKCAIGY-NFPFCLRTPIFPVSTPSS	436	-CEQSGRCHCKPNFHDNCEKCAIGY-NFPFCLRTPIFPVSTPSS
QY	421	AAGTQGNACRKDPRLGRVCVCKPNFRGAHCELCA PGFHGFSCHPC	421	AAGTQGNACRKDPRLGRVCVCKPNFRGAHCELCA PGFHGFSCHPC	421	AAGTQGNACRKDPRLGRVCVCKPNFRGAHCELCA PGFHGFSCHPC	421	AAGTQGNACRKDPRLGRVCVCKPNFRGAHCELCA PGFHGFSCHPC	421	AAGTQGNACRKDPRLGRVCVCKPNFRGAHCELCA PGFHGFSCHPC
Db	494	L-----	494	L-----	494	L-----	494	L-----	494	L-----
QY	481	GQCMCRITGEGDRCDHCALGYHFHPLCQCGSPAGTLP	481	GQCMCRITGEGDRCDHCALGYHFHPLCQCGSPAGTLP	481	GQCMCRITGEGDRCDHCALGYHFHPLCQCGSPAGTLP	481	GQCMCRITGEGDRCDHCALGYHFHPLCQCGSPAGTLP	481	GQCMCRITGEGDRCDHCALGYHFHPLCQCGSPAGTLP
Db	495	-----EGVLEICDAHGRCLCRPGVEGRCD	495	-----EGVLEICDAHGRCLCRPGVEGRCD	495	-----EGVLEICDAHGRCLCRPGVEGRCD	495	-----EGVLEICDAHGRCLCRPGVEGRCD	495	-----EGVLEICDAHGRCLCRPGVEGRCD
QY	541	RCLPGYHGYDDCHACADPRGALDQCGVGGGLCHCRPGNTGATC	541	RCLPGYHGYDDCHACADPRGALDQCGVGGGLCHCRPGNTGATC	541	RCLPGYHGYDDCHACADPRGALDQCGVGGGLCHCRPGNTGATC	541	RCLPGYHGYDDCHACADPRGALDQCGVGGGLCHCRPGNTGATC	541	RCLPGYHGYDDCHACADPRGALDQCGVGGGLCHCRPGNTGATC
Db	521	-----TCRSGFYSPFICQAC	521	-----TCRSGFYSPFICQAC	521	-----TCRSGFYSPFICQAC	521	-----TCRSGFYSPFICQAC	521	-----TCRSGFYSPFICQAC
QY	601	HCSADGSLHTTCDPTTGQCRCRPRVTGLHCDMCPGAVNFPYCE	601	HCSADGSLHTTCDPTTGQCRCRPRVTGLHCDMCPGAVNFPYCE	601	HCSADGSLHTTCDPTTGQCRCRPRVTGLHCDMCPGAVNFPYCE	601	HCSADGSLHTTCDPTTGQCRCRPRVTGLHCDMCPGAVNFPYCE	601	HCSADGSLHTTCDPTTGQCRCRPRVTGLHCDMCPGAVNFPYCE
Db	536	WCSALGSYQMPCCSVTGQCECRPGVTGQRCRCLSGAYDFPHCQ	536	WCSALGSYQMPCCSVTGQCECRPGVTGQRCRCLSGAYDFPHCQ	536	WCSALGSYQMPCCSVTGQCECRPGVTGQRCRCLSGAYDFPHCQ	536	WCSALGSYQMPCCSVTGQCECRPGVTGQRCRCLSGAYDFPHCQ	536	WCSALGSYQMPCCSVTGQCECRPGVTGQRCRCLSGAYDFPHCQ
QY	659	ALPETQAPCMCRAHVEGSPCDCKPGYWGWSASNPEGCTRCSCD	659	ALPETQAPCMCRAHVEGSPCDCKPGYWGWSASNPEGCTRCSCD	659	ALPETQAPCMCRAHVEGSPCDCKPGYWGWSASNPEGCTRCSCD	659	ALPETQAPCMCRAHVEGSPCDCKPGYWGWSASNPEGCTRCSCD	659	ALPETQAPCMCRAHVEGSPCDCKPGYWGWSASNPEGCTRCSCD
Db	596	GY-----CQCKLHVEGPTCSRCKLLYWNLDKENPSGCC	596	GY-----CQCKLHVEGPTCSRCKLLYWNLDKENPSGCC	596	GY-----CQCKLHVEGPTCSRCKLLYWNLDKENPSGCC	596	GY-----CQCKLHVEGPTCSRCKLLYWNLDKENPSGCC	596	GY-----CQCKLHVEGPTCSRCKLLYWNLDKENPSGCC
QY	718	QCFCKAHVCGKTCACAKDGFGLDYADYFGCRSCRCDVGGALG	718	QCFCKAHVCGKTCACAKDGFGLDYADYFGCRSCRCDVGGALG	718	QCFCKAHVCGKTCACAKDGFGLDYADYFGCRSCRCDVGGALG	718	QCFCKAHVCGKTCACAKDGFGLDYADYFGCRSCRCDVGGALG	718	QCFCKAHVCGKTCACAKDGFGLDYADYFGCRSCRCDVGGALG
Db	650	DCHCKSHVGGSDCTCEDGYFALEKSNYFGCQCQCDIGGALL	650	DCHCKSHVGGSDCTCEDGYFALEKSNYFGCQCQCDIGGALL	650	DCHCKSHVGGSDCTCEDGYFALEKSNYFGCQCQCDIGGALL	650	DCHCKSHVGGSDCTCEDGYFALEKSNYFGCQCQCDIGGALL	650	DCHCKSHVGGSDCTCEDGYFALEKSNYFGCQCQCDIGGALL
QY	778	GPTCSEPAKDHVLPDLHMRLELEEAATPEGHAVRFGNPLEFEN	778	GPTCSEPAKDHVLPDLHMRLELEEAATPEGHAVRFGNPLEFEN	778	GPTCSEPAKDHVLPDLHMRLELEEAATPEGHAVRFGNPLEFEN	778	GPTCSEPAKDHVLPDLHMRLELEEAATPEGHAVRFGNPLEFEN	778	GPTCSEPAKDHVLPDLHMRLELEEAATPEGHAVRFGNPLEFEN
Db	710	GKVCQRPENNYFPDLHMKYEIEDGSTPNGRDLRFGDPLAFPE	710	GKVCQRPENNYFPDLHMKYEIEDGSTPNGRDLRFGDPLAFPE	710	GKVCQRPENNYFPDLHMKYEIEDGSTPNGRDLRFGDPLAFPE	710	GKVCQRPENNYFPDLHMKYEIEDGSTPNGRDLRFGDPLAFPE	710	GKVCQRPENNYFPDLHMKYEIEDGSTPNGRDLRFGDPLAFPE
QY	838	IVARLV--TSPDLFRLVFRYVNRGTSVNGQISVREEGKLSCTN	838	IVARLV--TSPDLFRLVFRYVNRGTSVNGQISVREEGKLSCTN	838	IVARLV--TSPDLFRLVFRYVNRGTSVNGQISVREEGKLSCTN	838	IVARLV--TSPDLFRLVFRYVNRGTSVNGQISVREEGKLSCTN	838	IVARLV--TSPDLFRLVFRYVNRGTSVNGQISVREEGKLSCTN
Db	770	VRITLVGKSSGSLFRVILRYVNPCTEAVSGHITIYPSWGAA	770	VRITLVGKSSGSLFRVILRYVNPCTEAVSGHITIYPSWGAA	770	VRITLVGKSSGSLFRVILRYVNPCTEAVSGHITIYPSWGAA	770	VRITLVGKSSGSLFRVILRYVNPCTEAVSGHITIYPSWGAA	770	VRITLVGKSSGSLFRVILRYVNPCTEAVSGHITIYPSWGAA
QY	896	EPAFVTPQKGEGEPFLNPGIALLVEAEGVLLDYVVLPLSTY	896	EPAFVTPQKGEGEPFLNPGIALLVEAEGVLLDYVVLPLSTY	896	EPAFVTPQKGEGEPFLNPGIALLVEAEGVLLDYVVLPLSTY	896	EPAFVTPQKGEGEPFLNPGIALLVEAEGVLLDYVVLPLSTY	896	EPAFVTPQKGEGEPFLNPGIALLVEAEGVLLDYVVLPLSTY
Db	823	EPAFVTLPGNGFADPFSTIPGMWVACIKAEGLLDYVLLPRD	823	EPAFVTLPGNGFADPFSTIPGMWVACIKAEGLLDYVLLPRD	823	EPAFVTLPGNGFADPFSTIPGMWVACIKAEGLLDYVLLPRD	823	EPAFVTLPGNGFADPFSTIPGMWVACIKAEGLLDYVLLPRD	823	EPAFVTLPGNGFADPFSTIPGMWVACIKAEGLLDYVLLPRD
QY	956	RPSALHSTENCLVYAHPLDGFPSAAGTEALCRHD--NSLPR	956	RPSALHSTENCLVYAHPLDGFPSAAGTEALCRHD--NSLPR	956	RPSALHSTENCLVYAHPLDGFPSAAGTEALCRHD--NSLPR	956	RPSALHSTENCLVYAHPLDGFPSAAGTEALCRHD--NSLPR	956	RPSALHSTENCLVYAHPLDGFPSAAGTEALCRHD--NSLPR
Db	883	---AGPPQENCLLYQHLPVTRFPCTRSCEA--RHFLLDGE	883	---AGPPQENCLLYQHLPVTRFPCTRSCEA--RHFLLDGE	883	---AGPPQENCLLYQHLPVTRFPCTRSCEA--RHFLLDGE	883	---AGPPQENCLLYQHLPVTRFPCTRSCEA--RHFLLDGE	883	---AGPPQENCLLYQHLPVTRFPCTRSCEA--RHFLLDGE
QY	1014	GSDVDIQLEMAVPOPGQVVLVVEYVGEDSHQEMGVAVHTP	1014	GSDVDIQLEMAVPOPGQVVLVVEYVGEDSHQEMGVAVHTP	1014	GSDVDIQLEMAVPOPGQVVLVVEYVGEDSHQEMGVAVHTP	1014	GSDVDIQLEMAVPOPGQVVLVVEYVGEDSHQEMGVAVHTP	1014	GSDVDIQLEMAVPOPGQVVLVVEYVGEDSHQEMGVAVHTP
Db	938	GREVELHLRVIPQVGPVYVYVVEYSTEAAQLFVVDANV	938	GREVELHLRVIPQVGPVYVYVVEYSTEAAQLFVVDANV	938	GREVELHLRVIPQVGPVYVYVVEYSTEAAQLFVVDANV	938	GREVELHLRVIPQVGPVYVYVVEYSTEAAQLFVVDANV	938	GREVELHLRVIPQVGPVYVYVVEYSTEAAQLFVVDANV

Db 2886 LGG-----SNFEGCISNVFVQRLSLSPVEVLDTSNSLKRDSVSLGGCSLNKPPFLMLLK 2938

QY 3221 TSRATAQKVSRRSRQPSQDLACTTPWLPGTIQDAYQFGGPLP-----SYLQFVGISPSH 3274

Db 2939 GSTRFNKTKTFRINQLQDTPVASPRSVKVMQDAC---SPLPKTQANHGAHQFGDIPDISH 2995

QY 3275 RNRLHLSMLVRPHA-----ASQGLLLSTAPMSGRSPSLVLFNLHGHFVAQTEGPGP 3325

Db 2996 LLFKLPQELLKPRSQFAVDMQTTSSRGLVFHTGT---KNSFMALYLSKGRLVFALGTDGK 3052

QY 3326 RLQVQSRQHSRAGQWHRVSVRWGMQIQLVVDGSGQTSQKALHHRVPRAPRPQPYTLISVG 3385

Db 3053 KLRIKSKEKNDGKWHTVVFGHDGEGKRLVVDGL-----RAREGSLPGNSTISIR 3102

QY 3386 ----GLPASSYSSKLPVSGFSGCKKLQLDKQPLRPTQMVGVTPCVSGPLEDGLFFP 3440

Db 3103 APVYLGSPSGKPKSLPTN-SFVGCLKNFQLDKPLYPSSSFGVSSCLGGLPKGIYFS 3161

QY 3441 GSEGVVTLPLPKAMPYVVSLEEMRPLAAAGLIFHLQALATPYMQLVLTB--QVLLQA 3498

Db 3162 BEGCHVVLASHVLLGPEFKLVFSIRPSRLTGILIHIG---SQPGKHLVCVYLEAGKVTASM 3218

QY 3499 NDGAGEFSTWVTPK--LCDGRWHRVAVIMGRDTRLRLVDTQSNHHTTGRLPESLAGSPAL 3556

Db 3219 DSGAGGTSTSVT-PKQSLCDQWHSVAVTIKQHILHLELDTDSSYTAGQIIPFPASTQEP 3277

QY 3557 LHLSLPSKSTAR--PELPAYRGCLRKLKLLINGAPVNVNTASVQIQGAVGMRGCP 3607

Db 3278 LHLGAPANLTLTRIPVWKSFGLRNHIVHPVPTAELEVQGPVSLNGCP 3330

RESULT 10

ABB09504

ID ABB09504 standard; protein; 1640 AA.

XX ABB09504;

AC

XX

DT 01-NOV-2002 (first entry)

XX

DE Human laminin alpha-5-like NOVld protein, SEQ ID NO:8.

XX

KW Human; NOVX; neurological disorder; Alzheimer's disease;

KW Huntington's disease; Parkinson's disease; pain; behavioural disorder;

KW addiction; tuberous sclerosis; cancer; immune disorder; allergy;

KW autoimmune disease; myasthenia gravis; asthma; arthritis; diabetes;

KW thyroiditis; cardiovascular disease; hypertension; reproductive disorder;

KW endometriosis; incontinence; psoriasis; scleroderma; alopecia; ulcer;

KW pancreatitis; cirrhosis; glomerular endotheliosis; bacterial infection;

KW polycystic kidney disease; endocrine disorder; obesity; cardiomyopathy;

KW atherosclerosis; cell signal processing-related disorder;

KW metabolic pathway regulation disorder; cytostatic; neuroprotective;

KW antiinflammatory; immunosuppressive; analgesic; antiatherosclerotic;

KW dermatological; antibacterial; antiarthritic; hepatotropic; neurogenesis;

KW differentiation; proliferation; motility; haematopoiesis; wound healing;

KW angiogenesis; forensic biology; transgenic animal; drug screening;

KW gene therapy; NOVld; laminin alpha-5-like; chromosome 20.

XX

OS Homo sapiens.

XX

PN WO200253742-A2.

XX

PD 11-JUL-2002.

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PF 07-JAN-2002; 2002WO-US0000375.

XX

PR 05-JAN-2001; 2001US-0260018P.

PR 08-JAN-2001; 2001US-0260360P.

PR 28-FEB-2001; 2001US-0272411P.

PR 02-MAR-2001; 2001US-0272817P.

PR 05-JUL-2001; 2001US-0303231P.

PR 12-JUL-2001; 2001US-0305060P.

PR 10-SEP-2001; 2001US-0318405P.

PR 12-SEP-2001; 2001US-0318700P.

PR 04-JAN-2002; 2002US-00037417.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Kekuda R, Alsobrook JP, Tchernen VT, Liu X, Spytek KA;

PI Patturajan M, Grosse WM, Iepley DM, Burgess CE, Vernet CAM, Li L;

PI Gorman L, Edinger S, Sciore P, Ellerman K, Malyankar U;

PI Rothenberg M, Stone D, Boldog F, Guo X, Shenoy S, Anderson D;

PI Padigar M, Taupier RJ, Miller CE, Eisen A;

XX

DR WPI; 2002-583619/62.

DR N-PSDB; ABQ93882.

XX

PT Novel polypeptides and nucleic acids homologous to transmembrane

PT receptor, thymosin, neuromodulin-like family of proteins for diagnosing,

PT treating cancer, atherosclerosis, neurological, skin and autoimmune

PT disorders.

XX

PS Claim 1c; Page 23; 323pp; English.

XX

CC The invention relates to 24 novel human proteins designated NOV1-NOV14

CC (ABB09501-ABB09524), collectively referred to as NOVX proteins, and

CC nucleic acids encoding them (ABQ93879-ABQ93902). NOVX proteins, and

CC nucleotides are useful in the treatment, diagnosis or prevention of NOVX-

CC associated disorders or in the manufacture of a medicament for treating

CC such disorders, with specific applications described for each of the 24

CC NOVX proteins, based on their homology to known proteins. Various

CC disorders are associated with NOVX proteins including neurological

CC disorders (e.g., Alzheimer's, Huntington's and Parkinson's diseases),

CC pain, behavioural disorders, addiction, tuberculous sclerosis, cancers

CC (e.g., colorectal cancer, leukaemia and osteosarcoma), immune disorders

CC (e.g., allergies and autoimmune diseases), myasthenia gravis, asthma,

CC various forms of arthritis, diabetes, thyroiditis, cardiovascular disease

CC (e.g., hypertension), reproductive disorders, endometriosis,

CC incontinence, psoriasis, scleroderma, alopecia, ulcers, pancreatitis,

CC cirrhosis, glomerular endotheliosis, polycystic kidney disease, endocrine

CC disorders, obesity, bacterial infections and particularly cardiomyopathy,

CC atherosclerosis, cell signal processing-related disorders and disorders

CC of metabolic pathway regulation. NOVX nucleic acids and polypeptides may

CC be used to identify cellular receptors or downstream effectors which

CC binds to a NOVX protein, and are also useful as targets for the

CC identification of small molecules that modulate or inhibit processes such

CC as neurogenesis, cell differentiation, cell motility, cellular

CC proliferation, haematopoiesis, wound healing and angiogenesis. NOVX

CC nucleic acid sequences can be used to identify a cell or tissue type and

CC are useful as a source of primers or probes for forensic biology and for

CC identifying and cloning NOVX homologues in other cell types. Cells

CC comprising NOVX nucleic acids are useful for producing non-human

CC transgenic animals which are useful for studying the function and of NOVX

CC activity. The present sequence represents the laminin alpha-5-like

CC protein NOVld. The gene encoding NOVld is located on chromosome 20

XX

SQ Sequence 1640 AA;

Query Match 30.7%; Score 6092; DB 5; Length 1640;

Best Local Similarity 72.7%; Pred. No. 0;

Matches 1197; Conservative 156; Mismatches 278; Indels 16; Gaps 5;

QY 1970 CDRLEGYGFGEQCGCRPCACGPAAGSECHPQSGQCHCQPGTTGQCLECAPGYWGLP 2029

Db 1 CDRCQEGHFGNGCGCRPCACGPAAGSECHPQSGQCHCQPGTTGQCLECAPGYWGLP 60

QY 2030 EKGRCRCQCPRGHCDPHTGHTCTPPGLSGERCDCSTCSQHQVVPVPGKPGGGHICVCDHC 2089

Db 61 EQGRCRCQCPGGRCDPHTGRCNCPPGLSGERCDCSTCSQHQVVPVPGGVPVGHSHICEVCDHC 120

QY 2090 VVLLDDLERAGALLPAIREQLQGINASSAAWARLHRLNVIADLQSKLRRPPGPRYQAA 2149

Db 121 VVLLDDLERAGALLPAIHEQLRGINASSMAWARLHRLNVIADLQSKLRSPLGRHETA 180

QY 2150 QQLQTLQQSISLQDTERLGSOATGVQGOAGQLLDTTSTLGRAQKLLSVRAVGRLN 2209

Db 181 QQLEVLEQQSTSLGQDARRLGQAVGTRDQASQLLAGTEATLGHAKTLAAIRA VDRITLS 240

QY 2210 ELASRMGQSGPGDALVPSGEQIRWALAEVERELLWDMRTRDLGAQGA VAEAEALAEAO RLMA 2269

Db 241 ELMSTQCHLGLANASAPSGEQLLRTLAEVERELLWEMRARDLGAPQAAAEAEALAAQORLLA 300

QY 2270 RVQEQLTSEWENQSLATHIRDQLAQYESGLMDLREALNQAVNTTPEABEELNSRNOERVK 2329

Db 301 RVQEQLSLWEENQALATQTRDRLAQHEAGLMDLREALNRAVDATPEAQEELNSRNOERLE 360

QY 2330 EALQWKQELSODNATLKATLQAAASLILGHVSELLQIGIDQAKEDLEHLAASLDGAWTPLLK 2389

Db 361 EALQKQELS RDNATLQATLHAARDTTLASVFFLLHSLDQAKEELERLAASLDGARTPLLQ 420

QY 2390 RMOAFSPASSKVDLVEAAEAHAQKLNQNLAINLSGIILGINQDRFTIQRAVEASNAYSSILQ 2449

Db 421 RMOQTFSPAGSKLRLVEAAEAHAQQLQLALNLSIILDVNQDLRTQRAIEASNAYSRILO 480

QY 2450 AVQAAEDAAGQALRQASRTWEMVQVQGLAAGARQLLANSSALEETILGHQGRGLGAQGRLL 2509

Db 481 AVQAAEDAAGQALQQADHTWATVVRQGLVDRQQLLANSTALEEAMLQEQQRGLGLVWAAL 540

QY 2510 QAAGIQIHNVWARKNQLAQIQEAAQAMLMDTSETSEKIAHAKAVAAEALSTATHVQSOL 2569

Db 541 QGARTQLRDVRAKDDQLEAHIQAAQAAMLMDTDETSKKIAHAKAVAAEAQDTATRVQSOL 600

QY 2570 QGMQKNVERWQSLGGLQGDLSQVERDASSVSTLEKTLPLLAKLSRLNENRGVHNASL 2629

Db 601 QAMQENVERWQGYEGLRGQDLGQAVLDAGHSVSTLEKTLPLLAKLSILENENRGVHNASL 660

QY 2630 ALSANIGRVRKLIQAARSAASKVKVSMKFNKRGSGVRLRPPRDLADLAAYTALKFHIQSPV 2689

Db 661 ALSASIGRVRRELIQAARGAASKVKVPMKFNKRGSGVQLRTPRDLADLAAYTALKFYLQ-- 718

QY 2690 PAPEPGKNTGDHFVLYMGSRQATGDYMGVSLDNQKVHWYRLGKAGPTTLSIDENIGE QF 2749

Db 719 PEPEPGQGTEDRFVYMGSRQATGDYMGVSLDQKVVHWYQLGEAGPAVLSDIDEDIGE QF 778

QY 2750 AAVSIDRTLQFGHMSVTVEKQMVHEIKGDTVAPGSEGLLNLPDDFFVYVGGYPSNFTPP 2809

Db 779 AAVSLDRTLQFGHMSVTVERQMIQETKGTIVAPGAEGLLNLRPDDFFVYVGGYPSFTTPP 838

QY 2810 EPLRFPGLGCIEMETLNEEWSLYNFEQTFMLD TAVDKPCARSKATGDPWLTDGSYLDG 2869

Db 839 PLLRFPGYRGCIEMDTLNEEWSLYNFERTFQD TAVDRPCARSKSTGDPWLTDGSYLDG 898

QY 2870 SGFARISFEKQFSNTKRFDOELRLVSYNGIIFFLKQESQFLCLAVQEGTLVLFYDFGSGL 2929

Db 899 TGFARISFDSQISTTKRFEQELRLVSYSGVLFPLKQSQFLCLAVQEGSLVLLYDFGAGL 958

QY 2930 KKADPLQPPQALTAASKAIQVFLLAGNRKRVLRVERATVFSVDQDNMLEMADAYYLG V 2989

Db 959 KKA VPLQPPPLTSASKAIQVFLLGSRKRVLRVERATVYSVEQNDLELADAYYLG V 1018

QY 2990 PPEQLPLSLRLQFPSSGSGVRCIKGIKALGVYDLKRLNTTGISFGCTADLLVGRMTTFH 3049

Db 1019 PPDQLPPSLRLWLPFGSGSVRGCVKGIKALGVYDLKRLNTTGVSAGTADLLVGRMTTFH 1078

QY 3050 GHGFLPLALPDVAPITEVVYSGFGFRGTQDNLLYYRTSPDGPYQVSLREGHVTLRFMNQ 3109

Db 1079 GHGFLRLALSNVAPLTGNVYSGFGFHSAQDSALLYRASPDGLCQVSLQQGRVSLQLLRT 1138

QY 3110 EVETQRFVADGAPHYVAFYSNVTGVWLYVDQLQLVKSHERTTPEMLQLOPEEPSRLLLG 3169

Db 1139 EVKTQAGFADGAPHYVAFYSNATGVWLYVDQLQQMKPHRGPPELQPOPEGPPRLLLG 1198

QY 3170 LPVSGTFHNFSGCISNVFVQRLRGPQRFVLIHQNMGSNVSVGCTPAQLIETS----- 3222

Db 1199 LPESGTIYNFSGCISNVFVQRLRLLGPQRFVLIHQNMGSNVSTGCAPALQAQTPLGLPRGL 1258

QY 3223 RATAQKVSRRSRQPSQDLACTTPWLPGTIQDAYQFGGPLPSYLFQVIGSPSHRNLHLSM 3282

Db 1259 QATARKASRRSRQPARHPACMLPPHLRTRTDSYQFGGSLSSHLEFVFGILARHNWP SLSM 1318

QY 3283 LVRPHAAASQGLLLSTAPMSGRSPSLVLFNLHGHFVAQTEGPPRLQVQSRQHSRAGQWHR 3342

Db 1319 HVLPR-SSRGLLFTARLRPGSPSLALFLSNHGFVAQMEGLGTLRLRAQSRQSRPGRWHK 1377

QY 3343 VSVRWGMQIQLVVDGSGQTSQKALHHRVPRAE RPPQYTL SVGGLPASSYSKLPVSVGF 3402

Db 1378 VSVRWEXNRILLVTDGARAWSEQEPHRHQHQAEPHPQHTL FVGGLPASSHSSKLPVTVGF 1437

QY 3403 SGCLKKLQLDKQPIRTPTQMVGVTPCVSGPLEDGLFFPGSEGVVTLLELPKAKMPYVSLEL 3462

Db 1438 SGCVKRLRLHGRPLGAPTRMAGVTPCILGPLEAGLFFPGSGGVITL DLPGATLPDVGLEL 1497

QY 3463 EMRPLAAAGLIFHLGQALATPYMQLVLTBQVLLQANDGAGEFSTWVTPK-LCDGRWHR 3521

Db 1498 EVRPLAVTGLIFHLGQARTPPYLQL-----QVLLRADDDGAGEFSTVTRPSVLC DQGWHR 1552

QY 3522 VAVIMGRDTRLREVDTSQSNHTTGRLPESLAGSPALLHLGSLPKSSTARPELPAYRGCLR K 3581

Db 1553 LAVMKSGNVLRLEVD AQSNHTVGPLLLAAAGAPAPLYLGLPEPMAVQPPPPAYCGCMRR 1612

QY 3582 LLINGAPNVNTASVQIQGAVGMRGCP S 3608

Db 1613 LAVNRSPVAMTRSV EHVGA VGASGCPA 1639

RESULT 11

AAM39009

ID AAM39009 standard; protein; 1601 AA.

XX

AC AAM39009;

XX

DT 22-OCT-2001 (first entry)

XX

DE Human polypeptide SEQ ID NO 2154.

XX

KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia.

XX

OS Homo sapiens.

XX

PN WO200153312-A1.

XX

PD 26-JUL-2001.

XX

PF 26-DEC-2000; 2000WO-US034263.

XX

PR 23-DEC-1999; 99US-00471275.

PR 21-JAN-2000; 2000US-00488725.

PR 25-APR-2000; 2000US-00552317.

PR 20-JUN-2000; 2000US-00598042.

PR 19-JUL-2000; 2000US-00620312.

PR 03-AUG-2000; 2000US-00653450.

PR 14-SEP-2000; 2000US-00662191.

PR 19-OCT-2000; 2000US-00693036.

PR 29-NOV-2000; 2000US-00727344.

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PA (HYSE-) HYSEQ INC.

XX

PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;

PI Zhou P, Goodrich R, Drmanac RT;

XX

WP1; 2001-442253/47.

DR N-PSDB; AAI58165.

XX

Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.

PT

PT

XX

Example 4: SEQ ID NO 2154; 10078pp; English.

The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with neurotrophic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification

sequence 1601 AA:

every Match	29.5%;	Score 5871.5;	DB 4;	Length 1601;
st Local Similarity	72.5%;	Pred. No. 0;		
atches 1161;	Conservative	155;	Mismatches	275;
			Indels	11;
			Gaps	4;

QY	2015	GPQCLECAPGYWGLPEKGCRRCCQPRGHCDPHTGHTCTCPPGLSGERCDDTCSQQHQVBPVG	2074
Db	2	GPQCRECAPGYWGLPEQGCRRCCQPGGRCDPHTGRNCNCPGLSGERCDDTCSQQHQVBPVG	61
QY	2075	KPGGHIHCEVCDHCVVLLDDLERAGALLPAIREQLOGINASSAAWARLHRLNASTADL	2134
Db	62	GPVGHSIHCEVCDHCVVLLDDLERAGALLPAIHEQLRGINASSMAWARLHRLNASTADL	121
QY	2135	QSKLRPPGPRYQAAQQLQTLFQQSISLQODTERIGSQATGVQQAQQLDDTTTESTLGRA	2194
Db	122	QSOLRSPLGPRHETAQQLFVLEQQSTSLGQDARRLGGQAVGTRDQASQLLAGTEAULGHA	181
QY	2195	QKLLSVRAVGRALNELASRMGGSPGDALVPSGEQIRWALAEVERLLWDMRTRDLGAQG	2254
Db	182	KTLAAIRAVDRTLSELMSTQTHLGLANASAPSGEQLLRTLAEVERLLWEMRARDLGAPO	241
QY	2255	AVAEAEALAEARLMARVQEQLTSFWEENQSLATHIRDOLAQYESGLMDLREALNQAVNTT	2314
Db	242	AAAEAEALAAQRLLARVQEQLSSLWEENQALATQTRDLAQHEAGLMDLREALNRAVDAT	301
QY	2315	REAEELNSRNOERVKEALQWKQELSODNATLQATLQAAASLILGHVSELQGIQAKEDLE	2374
Db	302	REAQELNSRNOERLEEALQRKQELSRDNATLQATLHAARDTLASVFRLLHSLDQAKEELE	361
QY	2375	HLAASLDGAWTPLLKRMQAFSPASSKVDLVEAAEAHAQKLNQLAINLSGIIILGINODRFI	2434
Db	362	RLAASLDGARTPLLQRMCTFSPAGSKRLVEAAEAHAQQLALNLSIIILDVNQDRLT	421
QY	2435	QRAVEASNAYSIIQAVQAAEDAAGQALRQASRTWVMVQVQGLAAGARQLLANSSALEET	2494
Db	422	QRAIEASNAYSRIIQAVQAAEDAAGQALQADHTWATVVRQGLVDRAQQLLANSTALEEA	481
QY	2495	ILGHQGRIGLAQQRLOQAAGIQLHNVWARKNQLAAQIQEAQAMLAMDTSETSEKIAHAKAV	2554
Db	482	MLQEQQRIGLVVAALQGARTQLRDVRAKQDQLEAHIQAAQAMLAMDTDETSKKIAHAKAV	541
QY	2555	AAEALSTATHVQSILQGMQKNVERWQSQLGGQGLQGDLSQVERDASSSVSTLEKTLQOLLA	2614
Db	542	AAEAQDTATRVQSILQAMQENVERWQGYEGLRGQDLGQAVLDAGHSVSTLEKTLQOLLA	601
QY	2615	KLRLLENRGVHNASLALSANIGRVRKLIQAQARSAAKVKVSMKFNGRSGVRLRPPRDLAD	2674
Db	602	KLSSILENRGVHNASLALSASIGRVRELIAQARGAASKVKVPMKFNGRSGVQLRTPRDLAD	661
QY	2675	LAAYTALKFHIQSPVPAPPEPGKNTGDHFVLYMGSRQATGDYMGVSLRNQKVHVTVRLGKA	2734
Db	662	LAAYTALKFYLQG--PEPEPGQGTEDRFVVMYMGSRQATGDYMGVSLRDKKKVHVTVQLGEA	719
QY	2735	GPTTLLSIDENIGEOPAAVSIDRTLQFGHMSVTVEKOMVHEIKGDTVAPGSEGLNLNHPDD	2794

Db 1540 VGRDCQCVDTYNLQESNPDGCTTCFCFGKTSRCD SAYLRVYNVSLLKHSVITTPFEHE 1599
QY 1572 MEGWVLLSSDRQVVPHEHPEIEL---LHAD--LRSVADTFSELYWQAPPSYLG----- 1620
Db 1600 ES-----IKFDMWPVPAD---EILLNETTLKADFTLREVND-----ERPAYFGVLDYL 1644
QY 1621 ----DRVSSYGGTLHYELHSETQGDIFIPYESRPDVLVQGNQMSIAFLELAYPPPGQVH 1676
Db 1645 LNCNNHISAYGGDLAYTLHTFTSGPDGKYI---VAPDVILFSEHNALVHTSYEQPSRNEPF 1701
QY 1677 RQQLQVLEGNFRHLETHNPVSRBELMMVLAGLEQLQIRALFSQTSSTSSVSRLRVLEVASE 1736
Db 1702 TNRVNIVESNFQTI-SGKPVSRADFMVLRDLKVIFIRANYWEQTLVTHLSDVYLTILADE 1760
QY 1737 AGRGPPASN--VELCMCPANVRGSDCOECAPGYIRDTKGLFLGRVCVPCQCHGSHSDRCLP 1793
Db 1761 DADGTGEYQFLAVERCSCPPGISGHSCEDCAPGYIRDPSPGYGICYIPCPCNCGHSETCDC 1820
QY 1794 GSGICVGCQHNTGDCQERCRCRPFVSSDPSNPASPCVSCPCPLAVPSNPNFADGCVLRNGR 1853
Db 1821 ATGICSKQHGTGHDHCERCVSQYGNATNGTPGDCMICACPLPFDNSNPFATSCISESG 1880
QY 1854 TQ--CLCRPGYAGASCERCAPGFPGNPLVLGSSCQPCDCSGNDPDMIFSDCDPLTGACR 1911
Db 1881 DQIHCECKPGYTGPRCESCANPGYGEPESIGQVCKPCESGNINPEDQGS-CDTRTGECL 1939
QY 1912 GCLRHTTGPHCERCAPGYGNALLPGNCTRCDCSPCCTETCDPQSGRCLCKAGVTGQRCD 1971
Db 1940 RCLNNTFGAACNLCAPGFYGDAIKLKNQSCDCDDLTGTCTDPPFVGVCCTCHENVIGDRCD 1999
QY 1972 RCLEGYGFGEQCGCRPCACGPAAGSECHPQSGQCHCQPGTTGPQCLECAPGWGLPEK 2031
Db 2000 RCKPDHYGFESGVGRACDCGAASNSTQCDPHTGHCACKSGVTGRQCDRCADVHWKYEKD 2059
QY 2032 GCRRCQCPRGH----CDPHTGHCTCPPGLSGERCDCSCQHQVVPVPGKPGGHGHCVEVC 2086
Db 2060 GCTPCNCNQGYSRGFGCNPNTGKCQCLPGVIGDRCDACPNRW---VLIKDEG----CQEC 2112
QY 2087 DHCVVLLDDLERAGALLPAIREQLQGINASSAAWARLRLN-----ASIADQSKLRRP 2141
Db 2113 NNCHHALLDVDRMRYQIDSV---LEDFNSVTLAFTSQXLYNYDQLADELEPKVKLLDP 2169
QY 2142 PGPYQAAQQLQTLQEQSISLQDTERLGSQATGVQGAQGLDDTTTESTLGRAQKLLSV 2201
Db 2170 ----NSVDLSPSKKANSELESDAKSYAKQVNTLANAFDIRERSSTTLGNITVAY--- 2220
QY 2202 RAVGRALNELASRMGQSGPDALVPSGEQLRWALAEVERLLWDMRTRDLGAQGAVAEAE 2261
Db 2221 -----DEAVKSADQAKEAIAASVEALSKNLE----AAASTKIDAAL 2256
QY 2262 AEQRLMARVQ-----EOLTSFWEENQSLATHIRDQ---LAQYESGLMDLRE 2305
Db 2257 EQAQHILQINGTSIELTPNEQVLEKARKLYEEVNTLVLPIKAQNKS LNALKNDIGEFSD 2316
QY 2306 ALNQA VNTTREAEBELNSRNOERVKEALQWKQELSQDNATLKATLQA-----A 2352
Db 2317 HLEDLFNWS-EASQAKSADVERRNVANQKAFDNSKFDTVSEQKQAEKNIKDAGNFLING 2375
QY 2353 SLILGHVSELLOGIDQAKEDLEHLAASLDGAWTPLLKRMQAFSPASSKVDLVEABEHAHQ 2412
Db 2376 DLTNLQINQKLDNLRDALNELNSFNKNVD---EELPVREDQHEADALTDQAE-----Q 2426
QY 2413 KLNQLAINLSGIILG-INQDRFIQPAVEASNAYSSILQAVQAEDAAGQALRQASRTWEM 2471
Db 2427 KAAELAIKAQDLAAQYDTMTASAEPAIKAATAYS GIVEAVEARAQKLSQDAISAAGNATDX 2486
QY 2472 ---VVQRLGAA--GARQLLANS-SALBEETILGHQRLGLAQGLQAAAGIQLHNWARKNQ 2525
Db 2487 TDGIERAHLADTGSTDLLQRARQSLQKVQDDLEPRLNASAGKVQ-----KISAVNNA 2539
QY 2526 LAAQIQEAQAMLAMDTSETSEKI-AHAKAVAAEALSTATHVQSOLQGMQKNVERWQSQLG 2584

Db 2540 TEHQDKDINKLIDQLPAESQDWMKNSNANASDALBILKNVLEILEPVSQVTPKLEKAH 2599
QY 2585 G-----LQODLSQVER---DASSSVSTLEKTLPLLAKLSRLNRRGVHNASLANSANI 2635
Db 2600 GINRDLDLTNKDVSOANKQLDDVEGVS KLSE-----LAEDIEEQHRVGSQSRQLGQEI 2654
QY 2636 GRVRKLIQAARSAASKVKVSMKFNRSRGVRLRPPRDLADLAAYTALKFHIQSPVPAPBEPG 2695
Db 2655 ENLKAQVEAARQLANSIKVGVNFKPSTILELKTPEKTXLLATRTNLSTYFRTTPTS----- 2710
QY 2696 KNTGDHFVLYMG-----SRQATGDMGVSLRNQKVHVVRIGKAGPPTLSIDENI--GBOF 2749
Db 2711 ----GFLLYLGNNDNKTAQKNDFVAIVEINGYPILITDLGN-GPERITSDKYVADGRWY 2764
QY 2750 AAVSIDRTLQFGHMSVTVEKQMVHEIKGDTVAPGSEGLN-----LHPD-DFVIFYVGGYP 2803
Db 2765 QAV-VDR--MGPNAKLTIREELPN---GDVVEHSKSGYLEGSQNLHV DKNRSLFVGGYP 2818
QY 2804 --SNFTPEPELRFPGYLGCIEMETLNEEVVSLYNF-----EQTFMLDTAVDKPC 2850
Db 2819 GISDFNAPPDLTNNSFGDIEDLKIGDESGLWNFVYVGDNDQGARERDVLLKXKPVTVG 2878
QY 2851 ARSKATGDPWLTDG SYLDGSGFARISFEKQFSNTKRFDELRLVSYNGIIFFLKQESQFL 2910
Db 2879 LRFKNGYVQLNATSNLKSRSSTQFSF-----KADKD---TSNGLLFFYGRDKHYM 2926
QY 2911 CLAVQEGTLVLFYDFGSGLKKADPLQPPQALTAASKAIQVFLLAGNRKRV-----LVRV 2964
Db 2927 SIEMIDGAIFFNISLGE-----GGVQ-----SGSDRYNDNQWHKVQA 2965
QY 2965 ER-----ATVFSVDQDNMLEMADAYLGGVPPE-QLPLSLRQLFPSPGGSV 3008
Db 2966 ERENRLGLKVDDIVISRTNAPLEADLELPKRLRYFGHPRRLNTSISLQPNFD----- 3020
QY 3009 RGCIKIGIKALGKYVDLKLRLNT-TGISFGCTADLLVGRMTWTFHGHGFLPLALPDVAPITEV 3067
Db 3021 -GCIDNVVINQGWDLTEYVTGGVVEEGCSAKSTVVSYPAPHEYGFLRMNVSSDNNLHV 3079
QY 3068 VYSGFGFRGTQDNNLLYYRTSPD--GPYQVSLREGHTVLRFM-NOEVETQRFVADGAPHY 3124
Db 3080 V---LHFXTTPNGVLFYAANHDSSTIGLSLQDGLKLSNGSGLVIDDRILNDGEDHV 3136
QY 3125 VAFYSNVTGVWLYVDDQLQLVKSHERTT PMLQLQP--EERSLLLLGGLP-----VSG 3174
Db 3137 VTVQHTQGELELTVD--VDNKRLLGSP---QPLILEGGDIFFAGLPDNYRTPRNALA 3188
QY 3175 TFHNFSGCISNVFVQRLRGPQRFVDL---HQNMGSVNVSVGC----- 3213
Db 3189 SLAYFVGCISDVTN-----EEIINFANSAEKKNGNIN---GCPPHVLAYEPSLVPSYYP 3240
QY 3214 -----TPAQL 3218
Db 3241 SGDNEVESPWSNADTLPLPKPDIESTLPPTTPTTTTTTTTTTTTTTTTSTTTTTPSPI 3300
QY 3219 I-----ETSRATAQKVSRRSRQPSQ-----DLACTTPWLPGTIQD---AYQFGGLPSY 3264
Db 3301 VIDEKEKEIEAKTPQKI-LTTRPPAKNLNLPSEDERCKLPEQPNFVDVFTFAGYRFYGLREQR 3359
QY 3265 LQFVGISPSHRNRLHLSMLVRPHASQGLLLSTAPMSGRSPSLVFLNLHGHFVAQTEGPG 3324
Db 3360 LQINSLPVKVRPHHDIGISFRTERPN-GLLI-YAGSKQRDDDFIAVYLLDGRVTYAIR-VG 3416
QY 3325 PRLO--VQSRQHSRAGOWHRVSVRWGMQOIQLVVDGSGTWSQKALHHRVPRAPRPOP--- 3379
Db 3417 AOLQAKITTEAELNDGTWHTVEVVRTQKVSILLIDKLEQPGSGVDLN-----AERSAPVLA 3471
QY 3380 --YTLVSGGL-----PASSYSKLPVSVGSGCLKKQLDKQPLRTPTMVGVVTPC 3428
Db 3472 VELPIYLGGVNKFLESEVKNLTDFKTEVPY---FNGCLKNIKEDAMDLETPEEFVGVVPC 3528
QY 3429 VSGPLEDGLFFPGSEGVVTTLELPKAKMPYVSLELEMRPLAAAGLIF--HLQALA----- 3481
Db 3529 -SEQVERGLFFNNQKAFVKIFDHFVDVGTEMKISDFRPRDPNGLLFSVHGKNSYAILLEV 3587

QY 3482 --TPYMLKVLTEQVLLQANDGAGEFSTWVTP---KLCGRWHRVAVIMGRDITLRLEVD 3536
Db 3588 DNTLYFTVKTDLKNIV-----STNYKLPNNESFCGKTRNVQAIKSKFVINIAVD 3637
QY 3537 -TQSNHTTQRLPESLAGSPALLHLGS-----LPKSSTARPELPAYRGCLRKLKLLNGAPV 3589
Db 3638 FISSNPGVGNESVITRTNRPLFLGHHVAFQAPGIKTKK----SFKGCISKVEVNQRM 3693
QY 3590 NVTASVQIQGAVGMRGCP 3607
Db 3694 NITPNM-VVGDWQGYCP 3710

RESULT 13

ADE09114
ID ADE09114 standard; protein; 1486 AA.

XX AC ADE09114;

XX DT 29-JAN-2004 (first entry)

XX DE Novel protein-related contig polypeptide sequence #180.

XX KW novel gene; novel protein; tissue marker; molecular weight marker;
XX KW chromosome marker; genetic disorder; contig.

XX OS Unidentified.

XX PN WO2003054152-A2.

XX PD 03-JUL-2003.

XX PF 10-DEC-2002; 2002WO-US039555.

XX PR 10-DEC-2001; 2001US-0339739P.
XX PR 11-DEC-2001; 2001US-0339453P.
XX PR 14-MAR-2002; 2002US-0365091P.
XX PR 14-MAR-2002; 2002US-0365384P.
XX PR 12-APR-2002; 2002US-0372381P.
XX PR 12-APR-2002; 2002US-0372615P.
XX PR 22-APR-2002; 2002US-00128558.
XX PR 24-APR-2002; 2002US-0376045P.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
XX PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;
XX PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
XX DR WPI; 2003-569235/53.

XX PT New polynucleotides, useful for expressing recombinant proteins for
XX PT analysis, characterization or therapeutic use, or as markers for tissues
XX PT in which the corresponding protein is preferentially expressed.

XX PS Disclosure; SEQ ID NO 2658; 1177pp; English.

XX CC The invention comprises the amino acid and coding sequences of novel
XX CC proteins. The DNA and protein sequences of the invention are useful as:
XX CC markers for tissues in which the corresponding protein is preferentially
XX CC expressed; as molecular weight markers on gels; as chromosome markers or
XX CC tags; to identify chromosomes or to map related gene positions; and to
XX CC compare with endogenous DNA sequences in patients to identify potential
XX CC genetic disorders. The present amino acid sequence was used in the
XX CC exemplification of the invention.

XX SQ Sequence 1486 AA;

Query Match 20.0%; Score 3968.5; DB 7; Length 1486;
Best Local Similarity 45.4%; Pred. No. 3.8e-218;
Matches 737; Conservative 208; Mismatches 490; Indels 189; Gaps 18;

QY 1 DLYCKLVGGPVAGDPNQTIQGYCDICTAANSNKAHPVSNDAIDGTERWWQSPPLSRGLE 60
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QY 61 YNEVNTLDLGQVHFVAYVLIKFPANSPRDLWLVERSTDFGHTYQPWQFFASSKRDCLER 120
Db 102 YNRVNLTLDLGQLFHVAYILIKFPANSPRDLWLVERSVDFGHTYQPWQFFASSKVDCLKE 161
QY 121 FGPRTLERTQDDDDVICTTEYSRIVPLENGEIVVSLVNGRPGALNFSYSPLLRDFTKATN 180
Db 162 FGREANMAVTRDDDLVLCVTEYSRIVPLENGEIVVSLVNGRPGALNFSYSPLLRDFTKATN 221
QY 181 IRLRFLRTNTLLGLMKGALRDPVTTRRYYSIKDISIGRCVCHGHADVCDAKOPLDPF 240
Db 222 HPLAFLRTNTLLGLHLSKAQDQLSTRRYYSIKDTAIGGCVCNCHGHAEVCNINPEKLF 281
QY 241 RLQACQHNCTGGSCDRCCPGFNQKWPKPATTDSANECQSCNCHGHAYDCYYDPEVDRN 300
Db 282 R--CEQHHTCGETCDRCCTGYNQRRWRPAAWEQSHCEACNCHGHASNCYYDPDVERQQ 339
QY 301 ASQNQDNVYQGGVCLDCQHHTTGINCERCLPGFFRAPDQPLDSPHVCRPCDCESDFTDG 360
Db 340 ASLNTQGIYAGGVCINCQHTAGVNCQCAKGYRPGYVPVADPGCIPCSCDPEHADG 399
QY 361 TCEDLTGRCYCPNFTGELCAACAEGYTDFFPHCYPLPSFPHNDTRQVLPAGQIVNCDN 420
Db 400 -CEQSGRCHCKPNFHGDNCEKCAIGY-NFFPCLRIPFIPVSTPSSDDPVAGDIKGCDCN 457
QY 421 AAGTQGNACRKDPRLGRCVCKPNFRGAHCELCAFGHGPSCHPCQSSPGVANSLCDPES 480
Db 458 L----- 458
QY 481 GQCMCRTGFEGDRCDHCALGYFHFPLCQLCGCSPAGTLPEGCDAGRCQCRPGFDGPHCD 540
Db 459 -----EGVLP EICDAHGRCLCRPGVEGPRCD 484
QY 541 RCLPGYHGYPDCHACADPRGALDQCGGVGGLCHCRPGNTGATCQECSPGYFYPSPICPC 600
Db 485 -----TCRSGFYSFPICQAC 499
QY 601 HCSADGSLHTTCDFTTQGCRCRPRVTGLHCDMVCVPGAYNFPYCEAGS--CHPAGLAPANP 658
Db 500 WCSALGSYQMPCCSVTGQCECRPGVTGQRCDRLSGAYDFPHCQCGSSSACDPAGTINWNL 559
QY 659 ALPETQAPCMCRAHVEGSPCDCKPKGYWGLSASNPEGCTRCSCDPRGTGLGGVTEC-QGNG 717
Db 560 GY-----CQCKLHVEGPTCSRCKLLYNLDKENPSGCSECKHKGTVSGTGECEQGDG 613
QY 718 QCFCKAHVCGKTAACKDGFGLDYADYFGRCRCDVGGALQGQCEBKTGACRCRPNQ 777
Db 614 DCHCKSHVGGSDCTCEDGYFALEKSNYFGCGQCQCDIGGALSMCSPSGVCQCREHV 673
QY 778 GPTCSEPAKDHVLPDLHMRLELEEAATPEGHAVRFGFNPLEFENFSWRGYAHMMAIQPR 837
Db 674 GKVCQRPENNYFFDLHMKYEIEDGSTPNGRDLRFGDPLAFPEFSWRGYAQMVASVQND 733
QY 838 IVARLNV--TSPDLFRLVFRYVNRGSTSVNGQISVREEGKLSCTNCTEQSQPVAFPPST 895
Db 734 VRITLVGKSSGSLFRVILRYVNPGEAVSGHITIYPSWGAA-----QSK EIIFLPSK 786
QY 896 EPAFVTVPQRGFGEFVLNPGIWALLVEAEGVLLDYVLLPSTYYEALLQHRVTEACTY 955
Db 787 EPAFVTLPGNGFADPSITPGMWVACIKAEGLLDYLVLLPRDYEASDLQLPVTEPCAY 846
QY 956 RPSALHSTENCLVYAHLPDLGFPSSAAGTEALCRHD--NSLPRPCPTEQLSPSHPLATCF 1013
Db 847 ---AGPPQENCLLYQHLPVTRFPCTRSCEA--RHFLLDGEPRPVAVRQPTPAHPVMVDLS 901
QY 1014 GSDVDIOLEMAVPQCGYVLVVEYVGEDSHQEMGVAVHTPQAPQCGVNLNHPCPYSSLC 1073
Db 902 GREVELHLRVRIPQVGPVYVVEYSTAAQLFVVDANVKSSGSLAGQVNIYSCNYSVLC 961
QY 1074 RSPARDTOHHLAIFHLDSEASIRLTAEQAHHFLHSVTLVPVEEFSTEFVPRVFCVSSHG 1133

Db 962 RSAVIDHMSRIAMYELLTDADIQLKGHMARFLLHQVCIPIIEEYSAEYVRPQVHCIASYG 1021

QY 1134 TFPSSAACLASRFPKPPQPIILKDCQVLPPLPDLPLTQSQELSPGAPPEGPQRPPTAV 1193

Db 1022 RFVNSATCVSLAHETPPTALILDVLSGRPF-PHLP-----QQSSPSVDV 1065

QY 1194 DPNAPETLLRHHPQGTVFVTTQVPTLGRYAFLLHGYPVHPSPFVEVLINGRIWQGHANA 1253

Db 1066 LPG---VTLKAPQNQVTLRGRVPHLGRYVFIHFYQAAHPTFFPAQVSDGSGWRAGSFHA 1122

QY 1254 SFCPHGYGCRTLVLCGQTMLDVTDNELTVTVRVPEGRWLMDYVLVPEDAYSSSYLQE 1313

Db 1123 SFCPHVLCGRDQVIVXGQIEFDISEPEVAATVKVPEGKSLVLRVLVPAENYDQILHK 1182

QY 1314 EPLDKSYDFISHCATQGYHISPSSSSPFCRNAATSLSLFYNNGALPCGCHEVGAVSPTCE 1373

Db 1183 KSMKSLFEFITNCGKNSFYLDPTASRFCKNSARSLVAFYHKGALPCECHPTGATGPHCS 1242

QY 1374 PFGGQPCRGHVIGRDCSRCATGYWGFPCN--RPCDCGARLCDELGTQCICPPRTVPPDC 1431

Db 1243 PEGSAHASPTSSGGSAPAVQATYGFPRCKPKPCSCGRRLCEEMTGQCRCPRTVRPQC 1302

QY 1432 LVCQPSFGCHPLVGCEECCNSGPFVQBELTDPCTCDMSGQCRCPNVAGRRCDTCAPGFY 1491

Db 1303 EVCETHSFLHPMAGCEGCNCSRGITIEAMPRCDRDSGCGCKPRITGRQCRCASGFY 1362

QY 1492 GYPSRCPCDCHEAGTMASVCDPLTGQCHCKENVQSRCDQCRVGTFSLDAANPKGCTRCF 1551

Db 1363 GFPECVPCNCNRDGTGEPGVCDPGTGACLCKENVEGTECNVCREGSFHLDPANLKGCTSCF 1422

QY 1552 CFGATERCGNSNLARHEFVDMEGVLLSSDRQVVPHEHPBEIELLHADLRSVADTFSELY 1611

Db 1423 CFGVNNQCHSSHKRRTKFVDMLGWHLTADRVDIPVSFNPGSNSMVADLQELPATHSAS 1482

QY 1612 WQAP 1615

Db 1483 WVAP 1486

RESULT 14

AAM50358

ID AAM50358 standard; protein; 953 AA.

XX AC AAM50358;

XX DT 18-FEB-2002 (first entry)

XX DE Human laminin-15 alpha 5 chain.

XX KW Laminin-15; human; retina; eye; therapy; ophthalmological;

XX KW antiinflammatory; rod dystrophy; rod-cone dystrophy;

XX KW retinitis pigmentosa; macular degeneration; retinal detachment.

XX OS Homo sapiens.

XX PN WO200183516-A1.

XX PD 08-NOV-2001.

XX PF 01-MAY-2001; 2001WO-US013943.

XX PR 01-MAY-2000; 2000US-0200863P.

XX PA (MASS-) MASSACHUSETTS GEN HOSPITAL.

XX PI Burgeson RE, Brunken W, Champliand M, Hunter D;

XX DR WPI; 2002-041478/05.

XX DR N-PSDB; AAI70817.

XX PT Novel substantially pure preparation comprising laminin having laminin chain alpha 5, beta 2, and gamma 3, useful for treating retinal disorders

PT such as retinitis pigmentosa, macular degeneration, retinal detachment.

XX Disclosure; Fig 2A; 58pp; English.

CC The present sequence is that of the alpha 5 chain of human laminin-15, a novel member of the laminin family that is produced in the retina. The retina produces 2 novel laminin trimers: laminin-14 (alpha 4, beta 2, gamma 3) and laminin-15 (alpha 5, beta 2, gamma 3). These are expressed within the inter-photoreceptor matrix and in the outer plexiform layer, and may serve to stabilise retinal synapses. The invention provides laminin-15 preparations and cells comprising a nucleic acid encoding the laminin alpha 5, beta 2 and gamma 3 chains, and which are capable of producing laminin-15. The laminin-15 preparation is used in claimed methods of: increasing retinal immunophotoreceptor matrix stability; increasing the stability of retina photoreceptor compounds, especially an outer segment, inner segment or synapse; increasing retina adhesion; treating a disorder associated with retina degeneration, especially rod dystrophy, rod-cone dystrophy, retinitis pigmentosa, macular degeneration and retinal detachment; increasing the stability of synapses of the central nervous system or peripheral nervous system; stimulating neuroregeneration, axon outgrowth or synapse formation; preparing an implant, e.g. a catheter, artificial joint, retinal implant, timed releasing device, neural cell growth guide or artificial tissue, by coating with the laminin-15 preparation; and increasing photosensitivity by implanting a tip coated with the laminin-15 preparation into an eye. The laminin may be recombinant, and the 3 chains co-expressed in the same cell or expressed in different cells

XX SQ Sequence 953 AA;

Query Match 17.6%; Score 3488.5; DB 5; Length 953;

Best Local Similarity 70.9%; Pred. No. 6.6e-191;

Matches 677; Conservative 105; Mismatches 162; Indels 11; Gaps 4;

QY 2662 SGVRLRPPRDLADLAAYTALKFHIQSPVPAPEPGKNTGHPVLYMGSRQATGDMGVSLR 2721

Db 1 SGVQLRTPRDLADLAAYTALKFYLQ--PEPEPGQGTEDRFVMYMGSRQATGDMGVSLR 58

QY 2722 NQKVHVYVRLGKAGPTTSLIDENIGEQAFAVSDRDLTQFGHMSVTVEKQMVHEIKGDTVA 2781

Db 59 DKKVHVYVQLGEAGPAVLSDIDEGEQAFAVSLDRDLTQFGHMSVTVERQMIQETKGDIVA 118

QY 2782 PGSEGLNLHPDDFVYVGGYPSNFTPEPLRFPGLGCIEMETLNEEVVSLYNFEQTFM 2841

Db 119 PGAEGLLNLRPDDFVYVGGYPTFTPPPLLRFPYRGCIEMDTLNEEVVSLYNFERTFQ 178

QY 2842 LDTAVDKPCARSKATGDPWLTDGSLYDGGSGFARISFEKQFNTKRFQELRLVSYNGIIF 2901

Db 179 LDTAVDRPCARSKSTGDPWLTDGSLYDGTGTFARISFDSQISTTKRFEQELRLVSYSGVLF 238

QY 2902 FLKQESQFLCLAVQEGTLVLFYDFGSLGKKADPLQPPQALTAASKAIQVFLLAGNRKRVL 2961

Db 239 FLKQSQFLCLAVQEGSLVLLYDFGAGLKXAVLPQPPPLTSASKAIQVFLLGSRKRVL 298

QY 2962 VRVERATVPSVDQDNMLEMADAYVLGGVPPEQLPLSLRQLFPSSGSGVRCIKIKALGKY 3021

Db 299 VRVERATVYSVEQDNDELEADAYVLGGVPPDQLPPSLRWLFPFGSVRGCVKIKALGKY 358

QY 3022 VDLKRLNTTGISFGCTADLLVGRMTTFHGHGFLPLALPDVAPITEVVYSGFGFRGTQDNN 3081

Db 359 VDLKRLNTTGVSAAGCTADLLVGRAMTFHGHGFLRLALSNAVAPLTGNVYSGFGFHSQAQDSA 418

QY 3082 LLYYRTSPDGPYQVSLRREGHVTILRFMNQVEVETQRFADGAPHYVAFYSNVTGVWLYVDDQ 3141

Db 419 LLYYRASPDCLCQVSLQQGRVSLQLLRTEVKTQAGFADGAPHYVAFYSNATGVWLYVDDQ 478

QY 3142 LQLVKSHERTTPTMLQLQPEEPKRLLLGGLPVSQTFHNFSGCISNVFVQRLRGPQRFVLDH 3201

Db 479 LQQMKPHRGPPELQPPQEGPPRLLGGLPESGTIYFNSGICISNVFVQRLRGPQRFVLDQ 538

QY 3202 QNMGSVNVSVGCTPAQLIETS-----RATAQKVSRRSRQPSQDLACTTPWLPGTIQDA 3254

Db 539 QNLGSVNVSTGCAPALQAOQTPGLGPRGLQATARKASRRSRQPARHPACMLPPHLRTRDS 598

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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:30:58 ; Search time 27.4981 Seconds
(without alignments)
6824.493 Million cell updates/sec

Title: US-10-037-182-4
Perfect score: 19876
Sequence: 1 DLYCKLVGGPVAGGDPNQT.....QKALTQTHAKPSVSPLLWH 3635

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19876	100.0	3635	4	US-09-845-583A-2
2	3488.5	17.6	953	4	US-09-845-583A-4
3	3096	15.6	3084	4	US-09-562-702A-12
4	3096	15.6	3106	4	US-09-562-702A-10
5	3010.5	15.1	3089	4	US-09-562-702A-4
6	3010.5	15.1	3110	4	US-09-562-702A-2
7	3005.5	15.1	3111	2	US-08-460-309-4
8	3005.5	15.1	3111	2	US-08-125-077-4
9	3005	15.1	3088	4	US-09-562-702A-8
10	3005	15.1	3110	4	US-09-562-702A-6
11	3005	15.1	3110	4	US-09-561-709B-7
12	2727	13.7	3075	2	US-08-460-309-5
13	2727	13.7	3075	2	US-08-125-077-5
14	2171.5	10.9	1792	4	US-09-561-818A-4
15	2171.5	10.9	1800	4	US-09-561-818A-8
16	2171.5	10.9	1816	4	US-09-561-818A-2
17	2171.5	10.9	1824	4	US-09-561-818A-6
18	2149.5	10.8	1713	3	US-08-600-982-24
19	2149.5	10.8	1713	5	PCT-US94-10261A-24
20	2112.5	10.6	1792	4	US-09-561-818A-12
21	2112.5	10.6	1816	4	US-09-561-818A-10
22	1668.5	8.4	1799	4	US-09-845-583A-6
23	1612	8.1	1798	4	US-09-561-709B-11
24	1605	8.1	1765	4	US-09-562-702A-16
25	1605	8.1	1765	4	US-09-561-818A-16
26	1605	8.1	1786	4	US-09-562-702A-14
27	1605	8.1	1786	4	US-09-561-818A-14

28	1605	8.1	1786	4	US-09-561-709B-9	Sequence 9, Appli
29	1600	8.0	1798	4	US-09-845-583A-8	Sequence 8, Appli
30	1584	8.0	1725	4	US-09-562-702A-20	Sequence 20, Appl
31	1584	8.0	1725	4	US-09-561-818A-20	Sequence 20, Appl
32	1584	8.0	1786	4	US-09-562-702A-18	Sequence 18, Appl
33	1584	8.0	1786	4	US-09-561-818A-18	Sequence 18, Appl
34	1579.5	7.9	1761	4	US-09-561-709B-1	Sequence 1, Appli
35	1462.5	7.4	1587	4	US-09-845-583A-10	Sequence 10, Appl
36	1462.5	7.4	1587	4	US-09-561-709B-3	Sequence 3, Appli
37	1347.5	6.8	1572	4	US-09-562-702A-32	Sequence 32, Appl
38	1347.5	6.8	1572	4	US-09-561-818A-28	Sequence 28, Appl
39	1347.5	6.8	1605	4	US-09-562-702A-30	Sequence 30, Appl
40	1347.5	6.8	1605	4	US-09-561-818A-26	Sequence 26, Appl
41	1327.5	6.7	1576	4	US-09-562-702A-24	Sequence 24, Appl
42	1327.5	6.7	1576	4	US-09-561-818A-24	Sequence 24, Appl
43	1327.5	6.7	1584	4	US-09-562-702A-28	Sequence 28, Appl
44	1327.5	6.7	1609	4	US-09-562-702A-22	Sequence 22, Appl
45	1327.5	6.7	1609	4	US-09-561-818A-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-09-845-583A-2
; Sequence 2, Application US/09845583A
; Patent No. 6635616
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Brunken, William Joseph
; APPLICANT: Champliand, Marie-France
; APPLICANT: Hunter, Dale
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
; FILE REFERENCE: 10287-056U01
; CURRENT APPLICATION NUMBER: US/09/845,583A
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/200,863
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3635
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-845-583A-2

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Db	61	YNEVNTLDLGQVHFVAYVLIKFANSRPPDLWVLERSTDFGHTYQPWQFFASSKRDCLER	120
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QY 1741 PPASNVELCMCPANRYRGDSQCECAPGYRDTKGLFLGRVCPQCCHGSHDRCLPGSGICVG 1800
Db 1741 PPASNVELCMCPANRYRGDSQCECAPGYRDTKGLFLGRVCPQCCHGSHDRCLPGSGICVG 1800
QY 1801 CQHNTGDCQERCRCRPGFVSSDPSPNPASPCVSCPCPLAVPSNNFADGCVLRNGRTQCLCRP 1860
Db 1801 CQHNTGDCQERCRCRPGFVSSDPSPNPASPCVSCPCPLAVPSNNFADGCVLRNGRTQCLCRP 1860
QY 1861 GYAGASCERCAPGFFGNPLVLGSSCQPCDCSNGDNPNI FSDCDPLTGACRGCLRHTTGP 1920
Db 1861 GYAGASCERCAPGFFGNPLVLGSSCQPCDCSNGDNPNI FSDCDPLTGACRGCLRHTTGP 1920
QY 1921 HCERCAPGFYGNALLPGNCTRCDCSPCGTETCDPQSGRCLCKAGVTGQRCDCRCLEGYFGF 1980
Db 1921 HCERCAPGFYGNALLPGNCTRCDCSPCGTETCDPQSGRCLCKAGVTGQRCDCRCLEGYFGF 1980
QY 1981 EQCQGCRCPCACGPAAGKSECHPQSGQCHCQPGTTPQCLECAPGYWGLPEKGCRRCCQCP 2040
Db 1981 EQCQGCRCPCACGPAAGKSECHPQSGQCHCQPGTTPQCLECAPGYWGLPEKGCRRCCQCP 2040
QY 2041 GHCDPHTGHTCTPPGLSGERCDTCSQHQVVPVPGKPGGHGHIHCEVCDHCWVLLDDDLERA 2100
Db 2041 GHCDPHTGHTCTPPGLSGERCDTCSQHQVVPVPGKPGGHGHIHCEVCDHCWVLLDDDLERA 2100
QY 2101 GALLPAIREQLQGINASSAAWARLHRLNASIADLQSKLRRPPGPRYQAAQLOTLQEQSI 2160
Db 2101 GALLPAIREQLQGINASSAAWARLHRLNASIADLQSKLRRPPGPRYQAAQLOTLQEQSI 2160
QY 2161 SLQODTERLGSQATGVQAGQLLDTTESTLGRAQKLLESVAVGRALNELASRMGQGSP 2220
Db 2161 SLQODTERLGSQATGVQAGQLLDTTESTLGRAQKLLESVAVGRALNELASRMGQGSP 2220
QY 2221 GDALVPSGEQLRWALAEVERLLWDMRTRDLGAQGAVAEAEAEQRLMARVQEOLTSFWE 2280
Db 2221 GDALVPSGEQLRWALAEVERLLWDMRTRDLGAQGAVAEAEAEQRLMARVQEOLTSFWE 2280
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Db 2281 ENQSLATHIRDQLAQYESGLMDLREALNQAVNTTREAEEELNSRNOERVKELQWKQELS 2340
QY 2341 DNATLKATLQAASLILGHVSELLQGIQAKEDLEHLAASLDGAWTPLLKRMQAFSPASSK 2400
Db 2341 DNATLKATLQAASLILGHVSELLQGIQAKEDLEHLAASLDGAWTPLLKRMQAFSPASSK 2400
QY 2401 VDLVEAAEAHAQKLNQALAINLSGIILGINQDRFIQRAVEASNAYSSILQAVQAEDAAG 2460
Db 2401 VDLVEAAEAHAQKLNQALAINLSGIILGINQDRFIQRAVEASNAYSSILQAVQAEDAAG 2460
QY 2461 ALRQASRTWEMVQVRGLAAGARQLLANSALAEETILGHQGRGLGAQGRILQAAGIQLHNW 2520
Db 2461 ALRQASRTWEMVQVRGLAAGARQLLANSALAEETILGHQGRGLGAQGRILQAAGIQLHNW 2520
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Db 2521 ARKNQLAAQIQEAQAMLAMDTSETSEKIAHAKAVAAEALSTATHVQSOLQGMQXNVERWQ 2580
Qy 2581 SQLGGLQGQDLSQVERDASSVSTLEKTLPLLAKLSLENRGVHNASLALSANIGRVRK 2640
Db 2581 SQLGGLQGQDLSQVERDASSVSTLEKTLPLLAKLSLENRGVHNASLALSANIGRVRK 2640
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Db 2641 LIAQARSAASKVKVSMKFNKSGVRLRPPRDLADLAAYTALKFHIQSPVPAPEPGKNTGD 2700
Qy 2701 HFVLYMGSRQATGDYMGVSLRNQKVHVYRLGKAGPTTILSIDENIGEQAFAAVSIDRTLOF 2760
Db 2701 HFVLYMGSRQATGDYMGVSLRNQKVHVYRLGKAGPTTILSIDENIGEQAFAAVSIDRTLOF 2760
Qy 2761 GHMSVTVEKQMVHEIKGDTVAPGSEGLNLNHPDDFVFYVGGYPSNFTPEPLRPPGYLGC 2820
Db 2761 GHMSVTVEKQMVHEIKGDTVAPGSEGLNLNHPDDFVFYVGGYPSNFTPEPLRPPGYLGC 2820
Qy 2821 IEMETLNEEVSVLYNFEQTFMLDTAVDKPCARSKATGDPWLTDGSLDGSGFARISFEKQ 2880
Db 2821 IEMETLNEEVSVLYNFEQTFMLDTAVDKPCARSKATGDPWLTDGSLDGSGFARISFEKQ 2880
Qy 2881 FSNTKRFQDELRLVSYNGIIFFLKQESQFLCLAVQEGTLVLFYDFGSLGKXKADPLOPPQA 2940
Db 2881 FSNTKRFQDELRLVSYNGIIFFLKQESQFLCLAVQEGTLVLFYDFGSLGKXKADPLOPPQA 2940
Qy 2941 LTAASKAIQVFLLAGNRKRVLRVERATVFSVDQDNMLEMADAYYLGVPPEQLPLSLRQ 3000
Db 2941 LTAASKAIQVFLLAGNRKRVLRVERATVFSVDQDNMLEMADAYYLGVPPEQLPLSLRQ 3000
Qy 3001 LFPSCGSGVRCIKGKIKALGXVDLKRLLNTTGISFGCTADLLVGRMTWTFHGGFLPLALPD 3060
Db 3001 LFPSCGSGVRCIKGKIKALGXVDLKRLLNTTGISFGCTADLLVGRMTWTFHGGFLPLALPD 3060
Qy 3061 VAPITEVYSGFGFRGTQDNLLYYRTSPDPGPYQVSLREGHVTLRFMNQEVETQRFVADG 3120
Db 3061 VAPITEVYSGFGFRGTQDNLLYYRTSPDPGPYQVSLREGHVTLRFMNQEVETQRFVADG 3120
Qy 3121 APHYVAFYSNVTGVWLYVDDQLQLVKSHERTTLMQLQPEEPSRLLGLPVSGTFHNFS 3180
Db 3121 APHYVAFYSNVTGVWLYVDDQLQLVKSHERTTLMQLQPEEPSRLLGLPVSGTFHNFS 3180
Qy 3181 GCISNVFVQRLRGPQRFVFDLHQNMGSVNVSVGCTPAQLIETSRATAQKVSRRSRQPSQDL 3240
Db 3181 GCISNVFVQRLRGPQRFVFDLHQNMGSVNVSVGCTPAQLIETSRATAQKVSRRSRQPSQDL 3240
Qy 3241 ACTTPWLPGTIQDAYQFCGGLPSPYLSYQFVGISPSHRNRLHLSMLVRPHAAASQGLLLSTAPM 3300
Db 3241 ACTTPWLPGTIQDAYQFCGGLPSPYLSYQFVGISPSHRNRLHLSMLVRPHAAASQGLLLSTAPM 3300
Qy 3301 SGRSPSLVFLNHHGFVAQTEGPGPRLQVQSRQHSRAGQWHRVSVRWGMQOIQLVVDGSQ 3360
Db 3301 SGRSPSLVFLNHHGFVAQTEGPGPRLQVQSRQHSRAGQWHRVSVRWGMQOIQLVVDGSQ 3360
Qy 3361 TWSQKALHHRVPRAERPQPYTLVSVGGLPASSYSSKLPVSVGFSGLCKKLQDLKQPLRTPT 3420
Db 3361 TWSQKALHHRVPRAERPQPYTLVSVGGLPASSYSSKLPVSVGFSGLCKKLQDLKQPLRTPT 3420
Qy 3421 QMVGVTPCVSGPLEDGLFPFGSEGVTLELPAKMPYVVSLEMRPLAAAGLI FHLGQAL 3480
Db 3421 QMVGVTPCVSGPLEDGLFPFGSEGVTLELPAKMPYVVSLEMRPLAAAGLI FHLGQAL 3480
Qy 3481 ATPYMQLVLTQEVLLQANDGAGEFSTWVTYPKLCDGRWHRVAVIMGRDTRLRLEVDTSQN 3540
Db 3481 ATPYMQLVLTQEVLLQANDGAGEFSTWVTYPKLCDGRWHRVAVIMGRDTRLRLEVDTSQN 3540
Qy 3541 HTTGRLPESLAGSPALLHLGSLPKSSTARPELPAYRGCLRKLLINGAPVNVITASVQIQGA 3600
Db 3541 HTTGRLPESLAGSPALLHLGSLPKSSTARPELPAYRGCLRKLLINGAPVNVITASVQIQGA 3600
Qy 3601 VGMRGCPSGTIALSKQKGKALTQORHAKPSVSPLLWH 3635

Db 3601 VGMRGCPSGTIALSKQKGKALTQORHAKPSVSPLLWH 3635
RESULT 2
US-09-845-583A-4
; Sequence 4, Application US/09845583A
; Patent No. 6635616
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Brunken, William Joseph
; APPLICANT: Champlaud, Marie-France
; APPLICANT: Hunter, Dale
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
; FILE REFERENCE: 10287-056001
; CURRENT APPLICATION NUMBER: US/09/845,583A
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/200,863
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 953
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-583A-4
Query Match 17.6%; Score 3488.5; DB 4; Length 953;
Best Local Similarity 70.9%; Pred. No. 6.2e-206;
Matches 677; Conservative 105; Mismatches 162; Indels 11; Gaps 4;
Qy 2662 SGVRLRPPRDLADLAAYTALKFHIQSPVPAPEPGKNTGDHFVLYMGSRQATGDYMGVSLR 2721
Db 1 SGVQLRTPRDLADLAAYTALKFYLGQ--PEPEPGQGTEDRFVVMYMGSRQATGDYMGVSLR 58
Qy 2722 NQKVHWVYRLGKAGPTTILSIDENIGEQAFAAVSIDRTLOFGHMSVTVEKQMVHEIKGDTVA 2781
Db 59 DKKVHWVYQLGEAGPAVLSDIDEDIGEQAFAAVSLDRTLQFGHMSVTVERQMIQETKGDIVA 118
Qy 2782 PGSEGLNLNHPDDFVFYVGGYPSNFTPEPLRFPFGYLGCIEMETLNEEVSVLYNFEQTFM 2841
Db 119 PGAEGLLNLRPDDFVFYVGGYPSFTFTPPLLRFPFGYLGCIEMDTLNEEVSVLYNFEFTFQ 178
Qy 2842 LDTAVDKPCARSKATGDPWLTDGSLDGSGFARISPEKQFSNTKRFQDELRLVSYNGIIF 2901
Db 179 LDTAVDRPCARSKSTGDPWLTDGSLDGTGTGFARISFDSQISTTKRFEQELRLVSYSGVLF 238
Qy 2902 FLKQESQFLCLAVQEGTLVLFYDFGSLGKXKADPLOPPQALTAASKAIQVFLLAGNRKRVL 2961
Db 239 FLKQOSQFLCLAVQEGSLVLLYDFGAGLKKAVLPLOPPPLTSASKAIQVFLLAGSRKRVL 298
Qy 2962 VRVERATVFSVDQDNMLEMADAYYLGVPPEQLPLSLRQLFPPSGGSGVRCIGIKALGKY 3021
Db 299 VRVERATVYSVEQDNMLEADAYYLGVPDPQLPPLSLRWLFPTGGSGVRCIGIKALGKY 358
Qy 3022 VDLKRLNTTGISFGCTADLLVGRMTWTFHGHGFLPLALPDVAPITEVYSGFGRGTQDNN 3081
Db 359 VDLKRLNTTGVSAAGCTADLLVGRAMTFHGHGFLRLALSNAVPLTGNVYSGFGFHSQAQDSA 418
Qy 3082 LLYYRTSPDGPYQVSLREGHVTLRFMNQEVETQRFVADGAPHYVAFYSNVTGVWLYVDDQ 3141
Db 419 LLYYRASPDGLCQVSLQQGRVSLQLLRTEVKTQAGFADGAPHYVAFYSNATGVWLYVDDQ 478
Qy 3142 LQLVKSHERTTPMLQLQPEEPSRLLGLPVSGTFHNFSGCISNVFVQRLRGPQRFVFDLH 3201
Db 479 LQQMKPHRGPPPELQPEGPPRLLGLLPESGTIYNFSGCISNVFVQRLRGPQRFVFDLQ 538
Qy 3202 QNMGSNVSVGCTPAQLIETS-----RATAKVSRRRSRQPSQDLACTPWLPGTIQDA 3254
Db 539 QNLGSNVSVTGCAPALQAQTPGLGPRGLQATARKASRRSRQPARHPACMLPPHLRTRTDS 598
Qy 3255 YQFGGPLPSYLOFVGISPSHRNRLHLSMLVRPHAAASQGLLLSTAPMSGSRSPSLVFLNHHG 3314
Db 599 YQFGGSLSSHLEFVGILARHNRWPSLSMHVLP-RSSRGLLLFTARLRPGSPSLALFLSNG 657

QY 3315 HFVAQTEGPGRLQVQSRQHSRAGOWHRVSVRWGMQIQIQLVVDGSGTWSQKALHHRVPRA 3374
Db 658 HFVAQMEGLGTRLAQSRQSRGRGRWHKVSVRWEKNRILLVTDGARAMSQEGPHRQOGA 717
QY 3375 ERQPQYTLVGLGVPASSYSSKLPVSVGSGCLKKLQLDKQPLRTPTQMVGVTPCVSGPLE 3434
Db 718 EHPQPHTLVGLGVPASSYSSKLPVTVGSGCVKRLRLHGRPLGAPTRMAGVTPCILGPLE 777
QY 3435 DGLFFPGSGVVTLELPKAKMPYVSYLELEMRPLAAAGLIFHLGOALATPYMQLKVLTEQV 3494
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QY 3495 LLOANDGAGEFSTWVTPK-LCDGRWHRVAVIMGRDTRLLEVDTSQSNHTTGRPLPESLAGS 3553
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QY 3554 PALLHLGSLPKSSTARPELPAYRGCLRLKLLINGAPVNVTVASVQIQAGVGRGCP 3608
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RESULT 3

US-09-562-702A-12
; Sequence 12, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 12
; LENGTH: 3084
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-562-702A-12

Query Match 15.6%; Score 3096; DB 4; Length 3084;
Best Local Similarity 24.1%; Pred. No. 5e-181;
Matches 960; Conservative 470; Mismatches 1208; Indels 1350; Gaps 125;

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Db 38 EMYCKLVEHV-----PGQPVNPPQCRICNQNSSNPYQRPHTNAIDGKNTWWQSPSIKNG 92
QY 59 LEVNEVNTLDLQGVHVAVLKAFNSPRPDLWVLERSTDFGHTYQPVQWQFFASSKRDCL 118
Db 93 VEYHYVTITLDLQGVFQIAVIVVKAANSPPRGNWILERSLD-DVEYKPMQYHVAVTDTECL 151
QY 119 ERFG--PRT-LERITQDDVICTEYSRIVPLENGEIVVSLVNGRPGALNFSYSPLLRDF 175
Db 152 TLNINYPRTGPPSYAKDDEVICTSFYSKIHPLENGEIHISLINGRPSA--DDPSPELLEF 209
QY 176 TKATNIRLRLFRNTLLGLHMGKALR-----DPTVTRRRYYYSIKDISIGGRVCVCHGHADV 230
Db 210 TSARYIRLRFQIRITLNLADLMMFAHKDPREIDPIVTRRRYYYSVKDISVGGMCICYGHARA 269
QY 231 CDAKDLDPDF--RLQACQHNCTGGSCDRCCGFGNQPKWPAATTSANECQSCNCHGHAY 288
Db 270 C-----PLDPATNKRCECHNTCGESCDRCCGFGHQKWPWAGTFLTKSECEACNCHGKAE 325
QY 289 DCYDPEVDRRNASQNDNVYQGGGVCLDCQHHTTGINCERCLPGFRRAPDQPLDSPHVC 348

Db 326 ECIYDETVASRNLSLNHGKIYIGGVGINCTHNTAGINCETCDGFFRPKGVSPNPRPC 385
QY 349 RPDCESDFTDGTCEDLTGRCYCRPNFTGELCAACA--EGYTDFFHCYPLPSFPHNDTRE 406
Db 386 QPCHCDP-----TGSLSVCVDEKY----- 406
QY 407 QVLPAGQIVNCDNAAGTQGNACRKPRLGRVCVKPNFRGAHCELCAFGHG-PSCHPCQ 465
Db 407 -----AQRGLKPGSCHCKTGFGGVNCDRCVRGYHGYPCQPCN 444
QY 466 CSSPGVANSCLDPESGQCMRTGFEGRDCHCALGYFHFPL-----COLGCGSPAGTLPE 520
Db 445 CSGLGSTNE--DPCVGPSCKENVEGEDCSRCKSGFFNLQEDNQKCEECFCSCGVSNRCQ 502
QY 521 G-----CDEAGRCQCRPGFDGPHCDR-----CLPGY----- 546
Db 503 SSYWTYGNIQDMRWYLTDLSGRIEMAPQLDNPDSPOQISINSEARKSLLDGYWWSAPP 562
QY 547 ----- 546
Db 563 PYLGNRLPAVGQQLSFTISYDLEBEEEDDTEKLLQMIIFEGNDLRISTAYKEVYLEPSEE 622
QY 547 -----HG----- 548
Db 623 HVEEVSLEKBAFTIHGNTLPVTRKDFMIVLTNLGEILLIQTNYNLGMDAIFRLSSVNLESP 682
QY 549 --YPDCHACACDPRGALDQCGGVGLCHCRPGNTGATQCECSPG-----FYGPPSCI 598
Db 683 VPYP-----TDRRIATDVE-----VCQPPGYSGSSCETCWRHRRVNGTIFGGI--CE 729
QY 599 PCHCSADGSLHTTCDPTTGQC-RCRPRVTGLHCDMCPGAYNFPYCEAGSCHPAGLAPAN 657
Db 730 PCQCFAHAE--ACDDITGECLNCKDHTGGPYCNECLPGFYGDP--TRGS----- 774
QY 658 PALPETQAPCMCRAHV-----EGPSCDRCKPGYWGLSAS 691
Db 775 --PEDCQFCACPLNIPSNFSPFCHLDRSLGLICDBCPIGYTGPRCERCAEGYFGQPSV 831
QY 692 NPEGCTRCSCDPRGTLGGVTECOG-NGQC-FCKAHVCKTCAACKDGGFGLDYADYFGCR 749
Db 832 PGGSCQPCQCNLDYSIPGSCDLSGSLICKPGTGRYCELCADGYFG-DAVNTKNCQ 890
QY 750 SCRCVGGALGQCEPKTGACRCRPNTOGPTCSEPAKDHVLPDLHMRLELEBAATPEGH 809
Db 891 PCRCIDINGSFSEDCHTRTGQCECRPNVQGRHCDE----- 924
QY 810 AVRFGFNLEFENFESWRGYAHMAIQPRIVARLVNTSPDLFRLVFRVYVNRGSTSVNGQIS 869
Db 925 -----CKPETFGL----- 932
QY 870 VREGLSSCTNCTEQSQPVAFPPSTPEAFVTVPQRFGEFVLPNPGIALLVEAEGVLL 929
Db 933 ----- 932
QY 930 DYVLLPSTVYEALLQHRVTEACTYRPSALHSTENCLVVAHLPLDGFPSAAGTEALCRH 989
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QY 990 DNSLPRPCTEQLSPSHPPPLATCFGSDVDIQLEMAVPPQGYVLVVEYVGEDSHQEMGVA 1049
Db 933 ----- 932
QY 1050 VHTPQAPQGVNLNHPCPYSSLCRSPARDTQHHLAIFHLDSEASIRLTAEQAHHFLHSV 1109
Db 933 ----- 932
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Db 933 ----- 932
QY 1170 LTQSQELSPGAPPEGPPRPTAVDPNAEPTLLRHPQGTVFTTQVPTLGRYAFLLHGYQ 1229

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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:56:24 ; Search time 92.4776 Seconds
(without alignments)
10937.572 Million cell updates/sec

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Perfect score: 19876
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	19876	100.0	3635	9 US-09-845-583-2	Sequence 2, Appli
2	19876	100.0	3635	12 US-10-037-417-47	Sequence 47, Appli
3	19876	100.0	3635	14 US-10-037-182-4	Sequence 4, Appli
4	15842	79.7	3695	12 US-10-312-352-22	Sequence 22, Appli
5	15839	79.7	3695	14 US-10-037-182-2	Sequence 2, Appli
6	15830.5	79.6	3696	15 US-10-312-088-31	Sequence 31, Appli
7	15819.5	79.6	3690	12 US-10-112-944-347	Sequence 347, App
8	15815	79.6	3705	15 US-10-312-088-30	Sequence 30, Appli
9	14771	74.3	3600	12 US-10-037-417-2	Sequence 2, Appli
10	14706.5	74.0	3597	12 US-10-037-417-6	Sequence 6, Appli
11	12354.5	62.2	2743	14 US-10-037-182-36	Sequence 36, Appli
12	6110	30.7	1677	12 US-10-112-944-801	Sequence 801, App
13	6092	30.7	1640	12 US-10-037-417-8	Sequence 8, Appli
14	5495.5	27.6	1634	12 US-10-037-417-49	Sequence 49, Appli
15	5018.5	25.2	3712	12 US-10-037-417-48	Sequence 48, Appli

16	5018.5	25.2	3712	13	US-10-108-605-103	Sequence 103, App
17	5012.5	25.2	3712	12	US-10-037-417-51	Sequence 51, Appl
18	4831.5	24.3	3672	15	US-10-369-493-6146	Sequence 6146, Ap
19	3488.5	17.6	953	9	US-09-845-583-4	Sequence 4, Appli
20	3488.5	17.6	953	12	US-10-037-417-50	Sequence 50, Appl
21	3325	16.7	908	12	US-10-037-417-4	Sequence 4, Appli
22	2970	14.9	3070	10	US-09-961-403-7	Sequence 7, Appli
23	2792	14.0	3084	9	US-09-938-275-4	Sequence 4, Appli
24	2792	14.0	3084	14	US-10-262-670-2	Sequence 2, Appli
25	2729.5	13.7	3075	9	US-09-938-275-5	Sequence 5, Appli
26	2460	12.4	2823	15	US-10-369-493-5220	Sequence 5220, Ap
27	2460	12.4	2823	15	US-10-369-493-5221	Sequence 5221, Ap
28	2185	11.0	1823	12	US-10-363-616-457	Sequence 457, App
29	2184.5	11.0	1816	14	US-10-299-058-4	Sequence 4, Appli
30	2182.5	11.0	1816	14	US-10-299-058-2	Sequence 2, Appli
31	2171.5	10.9	1816	15	US-10-372-683-4	Sequence 4, Appli
32	2149.5	10.8	1693	15	US-10-603-725-4	Sequence 4, Appli
33	2149.5	10.8	1693	15	US-10-603-725-8	Sequence 8, Appli
34	2149.5	10.8	1713	14	US-10-171-311-113	Sequence 113, App
35	2149.5	10.8	1713	15	US-10-372-683-10	Sequence 10, Appl
36	2149.5	10.8	1713	15	US-10-603-725-6	Sequence 6, Appli
37	2149.5	10.8	1724	15	US-10-603-725-2	Sequence 2, Appli
38	2067	10.4	1694	15	US-10-603-725-12	Sequence 12, Appl
39	2067	10.4	1725	15	US-10-603-725-10	Sequence 10, Appl
40	1685	8.5	634	10	US-09-949-029-134	Sequence 134, App
41	1675	8.4	1798	9	US-09-938-275-9	Sequence 9, Appli
42	1672.5	8.4	1801	9	US-09-938-275-8	Sequence 8, Appli
43	1668.5	8.4	1799	9	US-09-845-583-6	Sequence 6, Appli
44	1605	8.1	1765	14	US-10-037-182-8	Sequence 8, Appli
45	1605	8.1	1786	9	US-09-873-676-113	Sequence 113, App

ALIGNMENTS

RESULT 1
US-09-845-583-2
; Sequence 2, Application US/09845583
; Patent No. US20020142954A1
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Brunken, William Joseph
; APPLICANT: Champlaud, Marie-France
; APPLICANT: Hunter, Dale
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
; FILE REFERENCE: 10287-056001
; CURRENT APPLICATION NUMBER: US/09/845,583
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/200,863
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2:
; LENGTH: 3635
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-845-583-2

Query Match	100.0%;	Score	19876;	DB	9;	Length	3635;
Best Local Similarity	100.0%;	Pred. No.	0;				
Matches	3635;	Conservative	0;	Mismatches	0;	Indels	0;
QY	1	DLYCKLVGGPVAGGDPNQT	IQGYCDICTAANSNKAHPVSN	NAIDGTERWWQSPPLSRGLE	60		
Db	1	DLYCKLVGGPVAGGDPNQT	IQGYCDICTAANSNKAHPVSN	NAIDGTERWWQSPPLSRGLE	60		
QY	61	YNEVNTLDLQGVFHVAYVLI	KFANSRPRDLWLVERSTDFGH	YQPWQFFASSKRDCLER	120		
Db	61	YNEVNTLDLQGVFHVAYVLI	KFANSRPRDLWLVERSTDFGH	YQPWQFFASSKRDCLER	120		
QY	121	FGPRTLERITQDDDDVICT	TEYSRIVPLENGEIVVSLVNG	RPGALNFSYSPLLRDTTKATN	180		
Db	121	FGPRTLERITQDDDDVICT	TEYSRIVPLENGEIVVSLVNG	RPGALNFSYSPLLRDTTKATN	180		

181 IRLRFLRNTLLGHLGKALRDPPTVTRRYYSIKDISIGRCVCHGHADVCDAKPLDPF 240 QY
181 IRLRFLRNTLLGHLGKALRDPPTVTRRYYSIKDISIGRCVCHGHADVCDAKPLDPF 240 Db
241 RLOCAQHNTCGGSCDRCCPGFNQKPWKPAATDSANECQSCNCHGHAYDCCYYDPEVDRN 300 QY
241 RLOCAQHNTCGGSCDRCCPGFNQKPWKPAATDSANECQSCNCHGHAYDCCYYDPEVDRN 300 Db
301 ASQNDNVYQGGVCLDCQHHTTGINCERCLPGFFRAPDQLPSPHVCRPCDCESDFTDG 360 QY
301 ASQNDNVYQGGVCLDCQHHTTGINCERCLPGFFRAPDQLPSPHVCRPCDCESDFTDG 360 Db
361 TCEDLTGRCYCRPNFTGELCAACABGYTDPHCHYPLPSFPHNDTREQVLPAGQIVNCDN 420 QY
361 TCEDLTGRCYCRPNFTGELCAACABGYTDPHCHYPLPSFPHNDTREQVLPAGQIVNCDN 420 Db
421 AAGTQGNACRKDPLRGRVCVKNFRGAHCELCAPEGFHGSPCHPCQCSSPGVANSLCDPES 480 QY
421 AAGTQGNACRKDPLRGRVCVKNFRGAHCELCAPEGFHGSPCHPCQCSSPGVANSLCDPES 480 Db
481 GQCMCRTGEGDRCDHICALGYFHFPLCQLCGCSPAGTLPPEGDEAGRCQCRPGFDGPHCD 540 QY
481 GQCMCRTGEGDRCDHICALGYFHFPLCQLCGCSPAGTLPPEGDEAGRCQCRPGFDGPHCD 540 Db
541 RCLPGYHGYPDCHACADPRGALDQCGVGLCHCRPGNTGATCQECSPGFYGFPSICIPC 600 QY
541 RCLPGYHGYPDCHACADPRGALDQCGVGLCHCRPGNTGATCQECSPGFYGFPSICIPC 600 Db
601 HCSADGSLHTTCDPTTGQCRPRVTGLHCDMCPGAYNFPYCEAGSCHPAGLAPANPAL 660 QY
601 HCSADGSLHTTCDPTTGQCRPRVTGLHCDMCPGAYNFPYCEAGSCHPAGLAPANPAL 660 Db
661 PETQAPCMCRHVEGPSCDRCCKPYWGLSASNEPEGTRCSCDPRGTLGGVTECOGNGQCF 720 QY
661 PETQAPCMCRHVEGPSCDRCCKPYWGLSASNEPEGTRCSCDPRGTLGGVTECOGNGQCF 720 Db
721 CKAHVCGKTCACKDGGFFGLDYADYFGCRSCLDVGALQCGCEPKTGACRCRPNTOGPT 780 QY
721 CKAHVCGKTCACKDGGFFGLDYADYFGCRSCLDVGALQCGCEPKTGACRCRPNTOGPT 780 Db
781 CSEPAKHLYLPLDHLHMRLELEEAATPEGHAVRFGFNPLEFENFSWRGYAHMMAIQPRIA 840 QY
781 CSEPAKHLYLPLDHLHMRLELEEAATPEGHAVRFGFNPLEFENFSWRGYAHMMAIQPRIA 840 Db
841 RLNVTSPLFLRFLRYVNRGSTSVMQISVREBGLSSTNCTEQSQPVAFPPSTEPAFV 900 QY
841 RLNVTSPLFLRFLRYVNRGSTSVMQISVREBGLSSTNCTEQSQPVAFPPSTEPAFV 900 Db
901 TVPQRFGEFVFNPGIWAALLVEAGVLLDYVLLPSTYEAALLQHRVTACTYRPSAL 960 QY
901 TVPQRFGEFVFNPGIWAALLVEAGVLLDYVLLPSTYEAALLQHRVTACTYRPSAL 960 Db
961 HSTENCLVYAHPLDGFPSAAGTEALCRHDNSLPRPCPTEQLSPSHPPLATCFGSDVDIQ 1020 QY
961 HSTENCLVYAHPLDGFPSAAGTEALCRHDNSLPRPCPTEQLSPSHPPLATCFGSDVDIQ 1020 Db
1021 LEMAVPQGVYLVVEYVGEDSHQEMGVAVHTPQAPQGVNLNHPCPYSSLCRSPARDT 1080 QY
1021 LEMAVPQGVYLVVEYVGEDSHQEMGVAVHTPQAPQGVNLNHPCPYSSLCRSPARDT 1080 Db
1081 QHHLAIFHLDSEASIRLTAEQAHFFLHVSVTLVPVEEFSTEFVEPRVFCVSSHGTNFPSSA 1140 QY
1081 QHHLAIFHLDSEASIRLTAEQAHFFLHVSVTLVPVEEFSTEFVEPRVFCVSSHGTNFPSSA 1140 Db
1141 ACLASRFPKPPQPIILKDCQVLPPLPDLPLTQSQELSPGAPPEGPQRPPTAVDPNAEPT 1200 QY
1141 ACLASRFPKPPQPIILKDCQVLPPLPDLPLTQSQELSPGAPPEGPQRPPTAVDPNAEPT 1200 Db
1201 LLRHPQGVVFTTQVPTLGRVAFLLHGYQPVHPSFPVEVLINGGRIWQHANASFCPHGY 1260 QY
1201 LLRHPQGVVFTTQVPTLGRVAFLLHGYQPVHPSFPVEVLINGGRIWQHANASFCPHGY 1260 Db

1261 GCRTLVLCEGQTMLDVTDNELTVTVRVPEGRWLWLDYVLIVPEDAYSSSYLQEEPLDKSY 1320 QY
1261 GCRTLVLCEGQTMLDVTDNELTVTVRVPEGRWLWLDYVLIVPEDAYSSSYLQEEPLDKSY 1320 Db
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1321 DFISHCATQGYHISPSSSPFFCRNAATSLSFYNNGALPCGCHEVGAVSPTCEPFGGQCP 1380 Db
1381 CRGHVIGRDCSRCATGYWGFPCNCRPCDCGRLCDELDTGQCICPPRTVPDPDCLVCQPSFG 1440 QY
1381 CRGHVIGRDCSRCATGYWGFPCNCRPCDCGRLCDELDTGQCICPPRTVPDPDCLVCQPSFG 1440 Db
1441 CHPLVGCCEECNCSPGVQBELTDPCTDMDSGQCRPNVAGRRCDTICAPGFYGYPSCRPCD 1500 QY
1441 CHPLVGCCEECNCSPGVQBELTDPCTDMDSGQCRPNVAGRRCDTICAPGFYGYPSCRPCD 1500 Db
1501 CHEAGTMAVSCDPLTGQCHCKENVOGSRCDQCRVGTFSLDAAANPKGCTRCFCFGATERCG 1560 QY
1501 CHEAGTMAVSCDPLTGQCHCKENVOGSRCDQCRVGTFSLDAAANPKGCTRCFCFGATERCG 1560 Db
1561 NSNLARHEFVDMEGWVLLSSDRQVVPHEHPEIELLHADLRVADTFSELYWQAPPSYLG 1620 QY
1561 NSNLARHEFVDMEGWVLLSSDRQVVPHEHPEIELLHADLRVADTFSELYWQAPPSYLG 1620 Db
1621 DRVSSYGGTLHYELHSETQRGDIFIPYESRDPVVLQGNQMSIAFLELAYPPPGQVHRGQL 1680 QY
1621 DRVSSYGGTLHYELHSETQRGDIFIPYESRDPVVLQGNQMSIAFLELAYPPPGQVHRGQL 1680 Db
1681 QLVGEGNFRHLETHNPVSREELMMVLAGLEQLQIRALFSQTSVSLRRVLEVAASEARG 1740 QY
1681 QLVGEGNFRHLETHNPVSREELMMVLAGLEQLQIRALFSQTSVSLRRVLEVAASEARG 1740 Db
1741 PPASNVELCMCPANYRGDSQECAPGYRDTKGLFLGRCVPCQCHGSHDRCLPGSGICVGS 1800 QY
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1801 CQHNTEGDQOCERCPGFVSSDPSNPASPCVSCPCPLAVPSNNFADGCVLRNGRTQCLCRP 1860 QY
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1861 GYAGASCERCAPGFNPLVLGSSCQPCDCSNGDPMNIFSDCDPLTGACRGCLRHTTGP 1920 QY
1861 GYAGASCERCAPGFNPLVLGSSCQPCDCSNGDPMNIFSDCDPLTGACRGCLRHTTGP 1920 Db
1921 HCERCAPGFYGNALLPGNCTRCDCSPCGTETCDPQSGRCLCKAGVTGQRCDCLEGYFQF 1980 QY
1921 HCERCAPGFYGNALLPGNCTRCDCSPCGTETCDPQSGRCLCKAGVTGQRCDCLEGYFQF 1980 Db
1981 EQCQGRPCACGPAKGSCHPQSGQCHCQPGTTGPPQCLECAPYWGGLPEKGCRRCCQCP 2040 QY
1981 EQCQGRPCACGPAKGSCHPQSGQCHCQPGTTGPPQCLECAPYWGGLPEKGCRRCCQCP 2040 Db
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2041 GHCDPHTGHTCTCPPLSGERCDCDTCQHQHVVPVPGKPGGHGJHCEVCDHCVLLDDLLERA 2100 Db
2101 GALLPAIREQLOGINASSAAWARLHRLNASIADLQSKLRPPPGPRYQAAQLOTLQOOSI 2160 QY
2101 GALLPAIREQLOGINASSAAWARLHRLNASIADLQSKLRPPPGPRYQAAQLOTLQOOSI 2160 Db
2161 SLOQDTERLGSOATGVQGOAGQLDTESTLGRAOKLLESVRAVGRALNELASRMGQSP 2220 QY
2161 SLOQDTERLGSOATGVQGOAGQLDTESTLGRAOKLLESVRAVGRALNELASRMGQSP 2220 Db
2221 GDALVPSGEQIRWALAEVERLLWMDTRDILGAQGAFAEAEALQRLMARVQEQLTFSWE 2280 QY
2221 GDALVPSGEQIRWALAEVERLLWMDTRDILGAQGAFAEAEALQRLMARVQEQLTFSWE 2280 Db
2281 ENQSLATHIRDOLAQYESGLMDLREALNQAVENTTREAELNSRQERVKEALQWKQELSQ 2340 QY
2281 ENQSLATHIRDOLAQYESGLMDLREALNQAVENTTREAELNSRQERVKEALQWKQELSQ 2340 Db
2341 DNATLQATLQAASLIILGHVSELIQDQAKEDLEHLEASLDGAWTPLLKRMQAFSPASSK 2400 QY

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QY 3481 ATPYMLKVLTEQVLLQANDGAGEFSTWVTYPKLCGRWHRVAVIMGRDTRLRLEVDTQSN 3540
Db 3481 ATPYMLKVLTEQVLLQANDGAGEFSTWVTYPKLCGRWHRVAVIMGRDTRLRLEVDTQSN 3540
QY 3541 HTTGRLPESLAGSPALLHLGSLPKSSTARPELPAAYRGCLRLKLLINGAPVNVTVASVQIOGA 3600
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Db 3601 VGMGCPSTLALSKQKALTQORHAKPSVSPLLWH 3635

RESULT 2
US-10-037-417-47
; Sequence 47, Application US/10037417
; Publication No. US20040052806A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Eisen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/10/037,417
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 3635
; TYPE: PRT

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QY 2521 ARKNQLAAQIQEAQAMLMDTSETSEKIAHAKAVAAEALSTATHVQSOLQGMQKNVERWQ 2580
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Db 2581 SOLGGLQGDLSQVERDASSSVSTLEKTLFOLLAKLSRLNRGVHNASLALSANIGRVRK 2640
QY 2641 LIAQARSAASKVKVSMKFNCRSGVRLRPPRDLADLAAYTALKFHIQSPVPAPEPGKNTGD 2700
Db 2641 LIAQARSAASKVKVSMKFNCRSGVRLRPPRDLADLAAYTALKFHIQSPVPAPEPGKNTGD 2700
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QY 2761 GHMSVTVKQMVHEIKGDTVAPGSEGLLNLPDDFFVYVGGYPSNFTPEPELRFPGYLGC 2820
Db 2761 GHMSVTVKQMVHEIKGDTVAPGSEGLLNLPDDFFVYVGGYPSNFTPEPELRFPGYLGC 2820
QY 2821 IEMETLNEEVVSLNFEQTFMLDTAVDKPCARSKATGDPWLTGSLDGSFGFARISFEKQ 2880
Db 2821 IEMETLNEEVVSLNFEQTFMLDTAVDKPCARSKATGDPWLTGSLDGSFGFARISFEKQ 2880
QY 2881 FSNTKRFDOELRLVSYNGIIFFLKQESQFLCLAVQEGTLVLFYDFSGSLKKADPLQPPQA 2940
Db 2881 FSNTKRFDOELRLVSYNGIIFFLKQESQFLCLAVQEGTLVLFYDFSGSLKKADPLQPPQA 2940
QY 2941 LTAASKAIQVFLLAGNRKRVLRVERATVFSVDQDNMLEMADAYLGGVPPPEQLPLSLRQ 3000
Db 2941 LTAASKAIQVFLLAGNRKRVLRVERATVFSVDQDNMLEMADAYLGGVPPPEQLPLSLRQ 3000
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Db 3001 LPPSGSVRGCIKIGKALGKYVDLKRLLNTTGISPGCTADLLVGRMTFHHGFLPLALPD 3060
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Db 3121 APHYVAFYSNVTGVWLYVDDQLQLVKSHERTTLMQLQPEEPSRLLLGGLPVSGTFHNFS 3180
QY 3181 GCISNVFVQRLRGPRVFDLHQNMGSVNVSVGCTPAQLIETSRATAQKVSRRSRQPSQDL 3240
Db 3181 GCISNVFVQRLRGPRVFDLHQNMGSVNVSVGCTPAQLIETSRATAQKVSRRSRQPSQDL 3240
QY 3241 ACTTPWLPGTIQDAYQFGGFLPSYLOFVGISPSHRNRLHLSMLVRPHAASQGLLLSTAPM 3300
Db 3241 ACTTPWLPGTIQDAYQFGGFLPSYLOFVGISPSHRNRLHLSMLVRPHAASQGLLLSTAPM 3300
QY 3301 SGRSPSLVFLNHHGHFVAQTEGPGPRLOVQSRQHSRAGQWHRVSVRWGMQIQLVVDGSQ 3360
Db 3301 SGRSPSLVFLNHHGHFVAQTEGPGPRLOVQSRQHSRAGQWHRVSVRWGMQIQLVVDGSQ 3360
QY 3361 TWSQKALHHRVPRAERPQPYTLVSGGLPASSYSSKLPSVGVSGCLKKLQLDKQPLRTP 3420
Db 3361 TWSQKALHHRVPRAERPQPYTLVSGGLPASSYSSKLPSVGVSGCLKKLQLDKQPLRTP 3420
QY 3421 QMVGVTCPVSGPLEDGLFFPGSEGVVTVLELPAKAMPYVSLEMRPLAAAGLIFHLGQAL 3480

; ORGANISM: Mus musculus

US-10-037-417-47

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Query Match      100.0%; Score 19876; DB 12; Length 3635;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3635; Conservative 0; Mismatches 0; Indels 0;
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Db	1	DLYCKLVGGPVAGGDPNQTIQGQYCDICTAANSNKAHPVSNALDGTERRWWQSPPLSRGLE	60
Qy	61	YNEVNVTLDLGQVHFVAYVLIKFANSRPDLWLERSTDFGHTYQPWFPAASSKRDCLER	120
Db	61	YNEVNVTLDLGQVHFVAYVLIKFANSRPDLWLERSTDFGHTYQPWFPAASSKRDCLER	120
Qy	121	FGPRTLRIITQDDDDVICTTEYSRIVPLENGEIVVSLVNGRPGALNFSYSPLLRDFTKATN	180
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Qy	181	IRLRLRTNTLLGHLMGKALRDPVTVTRRRYYYSIKDISIGRCVCHGHADVCDAXDPLDPF	240
Db	181	IRLRLRTNTLLGHLMGKALRDPVTVTRRRYYYSIKDISIGRCVCHGHADVCDAXDPLDPF	240
Qy	241	RLQACAOHNTCGGSCDRCCPGFNQWPKPATTDSANECQSCNCHGHAYDCYYDPEVDRN	300
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Qy	301	ASQNDNVYQGGGVCLDCQHTTGINCERCLPGFFRAPDQPLDSPHVCRPCDCESDFTDG	360
Db	301	ASQNDNVYQGGGVCLDCQHTTGINCERCLPGFFRAPDQPLDSPHVCRPCDCESDFTDG	360
Qy	361	TCEDLTGRCYCRPNFTGELCAACAEGYTDFFHCYPLPSPPHNDTREQVLPAGQIVNDCN	420
Db	361	TCEDLTGRCYCRPNFTGELCAACAEGYTDFFHCYPLPSPPHNDTREQVLPAGQIVNDCN	420
Qy	421	AAGTQGNACRKDPRGLRCVCKPNFRGAHCELAPGFHGPSCHPCQCSSPGVANSLCDPES	480
Db	421	AAGTQGNACRKDPRGLRCVCKPNFRGAHCELAPGFHGPSCHPCQCSSPGVANSLCDPES	480
Qy	481	GQCMCRTGFEGDRCDHCALGYFHFPLCQLCGCSPAGTLPEGDEAGRCQCRPGFDGPHCD	540
Db	481	GQCMCRTGFEGDRCDHCALGYFHFPLCQLCGCSPAGTLPEGDEAGRCQCRPGFDGPHCD	540
Qy	541	RCLPGYHGYPDCHACACDPRGALDQCGVGGLCHCRPGNTGATCQECSPGYFPPSCIPC	600
Db	541	RCLPGYHGYPDCHACACDPRGALDQCGVGGLCHCRPGNTGATCQECSPGYFPPSCIPC	600
Qy	601	HCSADGSLHTTCDPTTGQCRCPRTVTLGHCDMCPGAYNFPYCEAGSCHPAGLAPANPAL	660
Db	601	HCSADGSLHTTCDPTTGQCRCPRTVTLGHCDMCPGAYNFPYCEAGSCHPAGLAPANPAL	660
Qy	661	PETQAPCMCRAHVEGPSCDRCCKPGYWGLSASNPEGCTRCSDPRGTLGGVTECQNGQCF	720
Db	661	PETQAPCMCRAHVEGPSCDRCCKPGYWGLSASNPEGCTRCSDPRGTLGGVTECQNGQCF	720
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Db	781	CSEPAKDHLYPLDLHHMRLELEBAATPEGHAVRFGFNPLEFENFSWRGYAHMMAIQPRIVA	840
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Db	841	RLNVTSPDLFRLVFRYVNRGSTSVNGQISVREEGKLSCTNCTEQSQPVAFPPSTEPAFV	900
Qy	901	TVPQGFGEPPFVLPNGIWALLVEABGVLLDYVLLPSTYYEALLQHRVTEACTYRPSAL	960
Db	901	TVPQGFGEPPFVLPNGIWALLVEABGVLLDYVLLPSTYYEALLQHRVTEACTYRPSAL	960
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Dd	961	HSTENCLVYAHLPDLDFPFAAGTEALCRHNSLPRPCPTQOLSPSHPPPLATCFGSDVDIQ	1021
Qy	1021	LEMAVPQCGQYVLVVEYVGEDSHQEMGVAVHTPQAPQOQGVNLNHPCEYSSLCRSPARDT	1080
Dd	1021	LEMAVPQCGQYVLVVEYVGEDSHQEMGVAVHTPQAPQOQGVNLNHPCEYSSLCRSPARDT	1080
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Dd	1081	QHHLAIFHLDSEASIRLTAEQAHFFLHSVTLPVVEEFSTEFVEPRVFCVSSHGTENPSSA	1140
Qy	1141	ACLASRFKPPQPIILKDCQVLPPLPDLPLTQSQELSFGAPPEGPQRPPTAVDPNAEPT	1200
Dd	1141	ACLASRFKPPQPIILKDCQVLPPLPDLPLTQSQELSFGAPPEGPQRPPTAVDPNAEPT	1200
Qy	1201	LLRHPOGTVVFTTQVPTTLGRYAFLLHGYQPVHPSFPVEVLINGGRIWQHANASFCPHGY	1260
Dd	1201	LLRHPOGTVVFTTQVPTTLGRYAFLLHGYQPVHPSFPVEVLINGGRIWQHANASFCPHGY	1260
Qy	1261	GCRTLVLCEGOTMLDVTDNELTIVRVPEGRWLWLDYVLIVPEDAYSSSYLQEEPLDKSY	1320
Dd	1261	GCRTLVLCEGOTMLDVTDNELTIVRVPEGRWLWLDYVLIVPEDAYSSSYLQEEPLDKSY	1320
Qy	1321	DFISHCATQGYHISPPSSSPFCRNAATSLSLFYNNGALPCGCHEVGAVSPICEPFGGQCP	1380
Dd	1321	DFISHCATQGYHISPPSSSPFCRNAATSLSLFYNNGALPCGCHEVGAVSPICEPFGGQCP	1380
Qy	1381	CRGHVIGRDCSRCATGYWGFPCNRPDCDGCARLCDELGTQCICPPRTVPPDCLVCQPQSFG	1440
Dd	1381	CRGHVIGRDCSRCATGYWGFPCNRPDCDGCARLCDELGTQCICPPRTVPPDCLVCQPQSFG	1440
Qy	1441	CHPLVGCEECNSGPGVQELTDTPTCDMDSGQCRCPNVAGRRCDTCPAGFYGYPSCRPCD	1500
Dd	1441	CHPLVGCEECNSGPGVQELTDTPTCDMDSGQCRCPNVAGRRCDTCPAGFYGYPSCRPCD	1500
Qy	1501	CHEAGTMAVSCDPLTGQCHCKENVOGSRCDQCRVGTFSLDAAKPKGCTRCFCFGATERCG	1560
Dd	1501	CHEAGTMAVSCDPLTGQCHCKENVOGSRCDQCRVGTFSLDAAKPKGCTRCFCFGATERCG	1560
Qy	1561	NSNLARHEFVDMEGWVLLSSDRQVVPHEHRPEIELLHADLRVADTFSELYWQAPPSYLG	1620
Dd	1561	NSNLARHEFVDMEGWVLLSSDRQVVPHEHRPEIELLHADLRVADTFSELYWQAPPSYLG	1620
Qy	1621	DRVSSYGGTLHYELHSETQRGDIPIYESRDPVVLQGNQMSIAFLELAYPPGQVHRGQL	1680
Dd	1621	DRVSSYGGTLHYELHSETQRGDIPIYESRDPVVLQGNQMSIAFLELAYPPGQVHRGQL	1680
Qy	1681	QLVEGNFRHLETHNPVSREELMMVLAGLEQLQIRALFSQTSSSVSLRRVVLEVASEARG	1740
Dd	1681	QLVEGNFRHLETHNPVSREELMMVLAGLEQLQIRALFSQTSSSVSLRRVVLEVASEARG	1740
Qy	1741	PPASNVELCMCPANYRGDSQCECAPGYRDTKGLFLGRCPVCQCHGHSRDLCPGSGICVG	1800
Dd	1741	PPASNVELCMCPANYRGDSQCECAPGYRDTKGLFLGRCPVCQCHGHSRDLCPGSGICVG	1800
Qy	1801	CQHNTGQDQCERCPRPGFVSSDPSNPASPCVPCPLAVPSNNFADGCVLRNGRTQCLCRP	1860
Dd	1801	CQHNTGQDQCERCPRPGFVSSDPSNPASPCVPCPLAVPSNNFADGCVLRNGRTQCLCRP	1860
Qy	1861	GYAGASCERCAPGFFGNPLVLGSSCQPCDCSGNDPNMIFSDCDPLTGACRGLRHTTGP	1920
Dd	1861	GYAGASCERCAPGFFGNPLVLGSSCQPCDCSGNDPNMIFSDCDPLTGACRGLRHTTGP	1920
Qy	1921	HCERCAPGYGNALLPGNCTRCDCSPCGTETCDPQSGRCLCKAGVTGQRCDRCLEGYFGF	1980
Dd	1921	HCERCAPGYGNALLPGNCTRCDCSPCGTETCDPQSGRCLCKAGVTGQRCDRCLEGYFGF	1980
Qy	1981	EQCQGRPCACGPAAGSECHPQSGQCHCQPGTGTGPQCLECAPGYWGLPEKGCRRQCQPR	2040
Dd	1981	EQCQGRPCACGPAAGSECHPQSGQCHCQPGTGTGPQCLECAPGYWGLPEKGCRRQCQPR	2040
Qy	2041	GHCDPHTGHCTCPPGLISGERCDTCSQQHQVPYPGKPGGGHGHCEVCDHCVVLLDDDLERA	2100
Dd	2041	GHCDPHTGHCTCPPGLISGERCDTCSQQHQVPYPGKPGGGHGHCEVCDHCVVLLDDDLERA	2100

	Query Match	100.0%; Score 19876; DB 14; Length 3635;
	Best Local Similarity	100.0%; Pred. No. 0;
	Matches 3635; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	1	DLYCKLVGGPVAGGDPNQTIQGYCDICTAANSNKAHPPVSNADGTERWQSPPLSRGLE 60
Db	1	DLYCKLVGGPVAGGDPNQTIQGYCDICTAANSNKAHPPVSNADGTERWQSPPLSRGLE 60
Qy	61	YNEVNVTLDLGQVFHVAYVLIKFANSPRPDLWLERSTDFGHTYQPQFFASSKRDCLER 120
Db	61	YNEVNVTLDLGQVFHVAYVLIKFANSPRPDLWLERSTDFGHTYQPQFFASSKRDCLER 120
Qy	121	FGRPTLERITQDDVICTEYSRIVPLENGEIVVSLVNGRPGALNFYSPLLRDTFKATN 180
Db	121	FGRPTLERITQDDVICTEYSRIVPLENGEIVVSLVNGRPGALNFYSPLLRDTFKATN 180

QY 181 IRLRFLRNTLLGHLMGKALRDPVTTRYYYSIKDISIGGRVCYCHGHADVCDKOPLDPF 240
Db 181 IRLRFLRNTLLGHLMGKALRDPVTTRYYYSIKDISIGGRVCYCHGHADVCDKOPLDPF 240
QY 241 RLQACQHNTCGSCDRCCPGFNQOPWKPAATDSANECQSCNCHGHAYDCYYDPEVDRN 300
Db 241 RLQACQHNTCGSCDRCCPGFNQOPWKPAATDSANECQSCNCHGHAYDCYYDPEVDRN 300
QY 301 ASQNDNVYQGGVCLDCQHHTTGINCERCLPGFFRAPDQPLDSPHVCRPCDCESDFTDG 360
Db 301 ASQNDNVYQGGVCLDCQHHTTGINCERCLPGFFRAPDQPLDSPHVCRPCDCESDFTDG 360
QY 361 TCEDLTGRCYCRPNFTGELCAACAEGYTDFFHCYPLPSFPFNDTREQVLPAGQIVNCDN 420
Db 361 TCEDLTGRCYCRPNFTGELCAACAEGYTDFFHCYPLPSFPFNDTREQVLPAGQIVNCDN 420
QY 421 AAGTQGNACRKDPRLGRVCVCKPNFRGAHCELCAPGFHGPSCHPCQCSSPGVANSLCDPES 480
Db 421 AAGTQGNACRKDPRLGRVCVCKPNFRGAHCELCAPGFHGPSCHPCQCSSPGVANSLCDPES 480
QY 481 GQCMCRTGFEGDRCDHCALGYFHFPLCQLCCGSPAGTLPPEGCDACRCQCRPGFDGPHCD 540
Db 481 GQCMCRTGFEGDRCDHCALGYFHFPLCQLCCGSPAGTLPPEGCDACRCQCRPGFDGPHCD 540
QY 541 RCLPGYHGYPDCHACADPRGALDQCGVGLCHCRPGNTGATCOECSPGFYGFPPCIPC 600
Db 541 RCLPGYHGYPDCHACADPRGALDQCGVGLCHCRPGNTGATCOECSPGFYGFPPCIPC 600
QY 601 HCSADGSLHTTCDPTTGQCRCRPRVTGLHCDMCVPGAYNFYCEAGSCHPAGLAPANPAL 660
Db 601 HCSADGSLHTTCDPTTGQCRCRPRVTGLHCDMCVPGAYNFYCEAGSCHPAGLAPANPAL 660
QY 661 PETQAPCMRAHVEGSCDRCKPGYWGLSASNPEGCTRCSCDPRGTGGVTECQGNQCF 720
Db 661 PETQAPCMRAHVEGSCDRCKPGYWGLSASNPEGCTRCSCDPRGTGGVTECQGNQCF 720
QY 721 CKAHVCCKTCAACKDGFGLDYADYFGCRSCRCDVGGALQGCGCEPKTGACRCRPNTOGPT 780
Db 721 CKAHVCCKTCAACKDGFGLDYADYFGCRSCRCDVGGALQGCGCEPKTGACRCRPNTOGPT 780
QY 781 CSEPAKDHYPDLHMHMLEEAAATPEGHAVRFGFNPLEFENFSWRGYAHMAIQPRIVA 840
Db 781 CSEPAKDHYPDLHMHMLEEAAATPEGHAVRFGFNPLEFENFSWRGYAHMAIQPRIVA 840
QY 841 RLNVTSPLFRLVFRYVNRGSTSVNGQISVREBGLSSCTNCTEQSQOPVAFPPSTEPAFV 900
Db 841 RLNVTSPLFRLVFRYVNRGSTSVNGQISVREBGLSSCTNCTEQSQOPVAFPPSTEPAFV 900
QY 901 TVPQRGFGEFVLNPGIALLVEAGVLLDYVLLPSTYYEALLQHRVTEACTYRPSAL 960
Db 901 TVPQRGFGEFVLNPGIALLVEAGVLLDYVLLPSTYYEALLQHRVTEACTYRPSAL 960
QY 961 HSTENCLVYAHPLDGFPSAAGTEALCRHDNSLPRPCPTEQLSPSHPLATCFGSDVDIQ 1020
Db 961 HSTENCLVYAHPLDGFPSAAGTEALCRHDNSLPRPCPTEQLSPSHPLATCFGSDVDIQ 1020
QY 1021 LEMAVPQPGQYVLVVEYVGEDSHQEMGVAVHTPQAPQOGVNLNHPCPYSSLCRSPARDT 1080
Db 1021 LEMAVPQPGQYVLVVEYVGEDSHQEMGVAVHTPQAPQOGVNLNHPCPYSSLCRSPARDT 1080
QY 1081 QHHLAIFHLDSEASIRLTAEQAHFLLHSVTLVPVEEFSTEFVEPRVFCVSSHGTENPSSA 1140
Db 1081 QHHLAIFHLDSEASIRLTAEQAHFLLHSVTLVPVEEFSTEFVEPRVFCVSSHGTENPSSA 1140
QY 1141 ACLASRPFPKPPQPIILKDCQVLPPLPDPLTQSQELSPGAPPEGPPQRPPTAVDPNAEPT 1200
Db 1141 ACLASRPFPKPPQPIILKDCQVLPPLPDPLTQSQELSPGAPPEGPPQRPPTAVDPNAEPT 1200
QY 1201 LLRHPQGTVVFTTQVPTLGRYAFLLNGYQPVHPSFPVEVLINGGRIWQHGHANASFCPHGY 1260
Db 1201 LLRHPQGTVVFTTQVPTLGRYAFLLNGYQPVHPSFPVEVLINGGRIWQHGHANASFCPHGY 1260
QY 1261 GCRTLVLCEGQTMLDVTDNELTVTVRVEGRWLWLDVVLIVPEDAYSSSYLQEEPLDKSY 1320

Db 1261 GCRTLVLCEGQTMLDVTDNELTVTVRVEGRWLWLDVVLIVPEDAYSSSYLQEEPLDKSY 1320
QY 1321 DFISHCATQGYHISPSSSSPFCRNAATSLSLFYNNGALPCGCHEVGAVSPTCEPFGGQCP 1380
Db 1321 DFISHCATQGYHISPSSSSPFCRNAATSLSLFYNNGALPCGCHEVGAVSPTCEPFGGQCP 1380
QY 1381 CRGHVIGRDCSRCATGYWGFPPNCRPCDCGARLDELGTGQCICPPRTVPDCLVCQPQSPG 1440
Db 1381 CRGHVIGRDCSRCATGYWGFPPNCRPCDCGARLDELGTGQCICPPRTVPDCLVCQPQSPG 1440
QY 1441 CHPLVGCEECNCSPGVQELTDPTCDMDSGQCRCPNVAGRRCDTCAPGFYGYPSCRPCD 1500
Db 1441 CHPLVGCEECNCSPGVQELTDPTCDMDSGQCRCPNVAGRRCDTCAPGFYGYPSCRPCD 1500
QY 1501 CHEAGTMASVCDPLTGQCHCKENVQSGRCDQCRVGTFSLDAANPKGCTRCFCFGATERCG 1560
Db 1501 CHEAGTMASVCDPLTGQCHCKENVQSGRCDQCRVGTFSLDAANPKGCTRCFCFGATERCG 1560
QY 1561 NSNLARHEFVDMEGWVLLSSDRQVVPHEHRPEIELLHADLRSVADTFSELYWQAPPSYLG 1620
Db 1561 NSNLARHEFVDMEGWVLLSSDRQVVPHEHRPEIELLHADLRSVADTFSELYWQAPPSYLG 1620
QY 1621 DRVSSYGGTLHYELHSETQRGDIPIPYESRPDDVVLQGNQMSIAFLELAYPPPGQVHRGOL 1680
Db 1621 DRVSSYGGTLHYELHSETQRGDIPIPYESRPDDVVLQGNQMSIAFLELAYPPPGQVHRGOL 1680
QY 1681 QLVEGNFRHLETHNPVSREELMMVLAGEQLQIRALFSQTSSSVSLRRVVLEVASEARG 1740
Db 1681 QLVEGNFRHLETHNPVSREELMMVLAGEQLQIRALFSQTSSSVSLRRVVLEVASEARG 1740
QY 1741 PPASNVELCMCPANYRGDSQCECAPGYRYRDTKGLFLGRVPCQCHGSHDRCLPGSGICVG 1800
Db 1741 PPASNVELCMCPANYRGDSQCECAPGYRYRDTKGLFLGRVPCQCHGSHDRCLPGSGICVG 1800
QY 1801 CQHNTGDCQRCRPGFVSSDPSNPASPCVSCPCPLAVPSNNFADGCVLRNGRTQCLCRP 1860
Db 1801 CQHNTGDCQRCRPGFVSSDPSNPASPCVSCPCPLAVPSNNFADGCVLRNGRTQCLCRP 1860
QY 1861 GYAGASCERCAPGFFGNPLVLGSSCQPCDCSGNDPNMIFSDCDPLTGACRGCLRHTTGP 1920
Db 1861 GYAGASCERCAPGFFGNPLVLGSSCQPCDCSGNDPNMIFSDCDPLTGACRGCLRHTTGP 1920
QY 1921 HCERCAPGFYGNALLPGNCTRCDCSPCGTETCDPQSGRCLCKAGVTGQRCDCRCLEGYFGF 1980
Db 1921 HCERCAPGFYGNALLPGNCTRCDCSPCGTETCDPQSGRCLCKAGVTGQRCDCRCLEGYFGF 1980
QY 1981 EQCGCRPCACGPAKSGSECHPQSGQCHCQPGTGPQCLECAPGYWGLPEKGCRRCQCP 2040
Db 1981 EQCGCRPCACGPAKSGSECHPQSGQCHCQPGTGPQCLECAPGYWGLPEKGCRRCQCP 2040
QY 2041 GHCDPHTGHCTCPPGLSGERCDCQSQHQVVPVPGKGGHIGHCEVCHCVVLLDDLERA 2100
Db 2041 GHCDPHTGHCTCPPGLSGERCDCQSQHQVVPVPGKGGHIGHCEVCHCVVLLDDLERA 2100
QY 2101 GALLPAIREQLQGINASSAAWARLHRLNASIADLQSKLRRPPGPRYQAAQQLQTLQCSI 2160
Db 2101 GALLPAIREQLQGINASSAAWARLHRLNASIADLQSKLRRPPGPRYQAAQQLQTLQCSI 2160
QY 2161 SLOQDTERLGSQATGVQAGQLDDTTTESTLGRAQKLLSVRAVGRALNELASRMGQGSP 2220
Db 2161 SLOQDTERLGSQATGVQAGQLDDTTTESTLGRAQKLLSVRAVGRALNELASRMGQGSP 2220
QY 2221 GDALVPSGEQLRWALAEVERLLWDMRTRDLGAQGAFAEAEALAEQRLMARVQELTSFWE 2280
Db 2221 GDALVPSGEQLRWALAEVERLLWDMRTRDLGAQGAFAEAEALAEQRLMARVQELTSFWE 2280
QY 2281 ENQSLATHIRDQLAQYESGLMDLREALNQAVENTTREAELNSRNOERVKEALQWKQELSQ 2340
Db 2281 ENQSLATHIRDQLAQYESGLMDLREALNQAVENTTREAELNSRNOERVKEALQWKQELSQ 2340
QY 2341 DNATLKATLOAASLIILGHVSELLOQIDQAKEDLEHLAASLDGAWTPLLKRMOAFSPASSK 2400

Db 2341 DNATLKATLQAASLILGHVSELLOQIDQAKEDLEHLAASLDGAWTPLLKRMQAFSPASSK 2400

QY 2401 VDLVEAAEAHAQKLNQLAINLSGIILGINQDRFIORAVEASNAYSSILOAVQAAEDAAGQ 2460

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QY 2461 ALRQASRTWEMVQVQRLAAGARQLLANSSALEETILGHQGRGLAQGRLOAAGIQLHNW 2520

Db 2461 ALRQASRTWEMVQVQRLAAGARQLLANSSALEETILGHQGRGLAQGRLOAAGIQLHNW 2520

QY 2521 ARKNQLAAQIQEAQAMLAMDTSETSEKIAHAKAVAAEALSTATHVQSOLQGMQKNVERWQ 2580

Db 2521 ARKNQLAAQIQEAQAMLAMDTSETSEKIAHAKAVAAEALSTATHVQSOLQGMQKNVERWQ 2580

QY 2581 SOLGGLQGQDLSQVERDASSVSTLEKTLPOLLAKLSRLNRGVHNASLALSANIGRVRK 2640

Db 2581 SOLGGLQGQDLSQVERDASSVSTLEKTLPOLLAKLSRLNRGVHNASLALSANIGRVRK 2640

QY 2641 LIAQARSAASKVKVSMKFNRSRGVRLRPPRDLDLAAYTALKFHIQSPVPAPEPGKNTGD 2700

Db 2641 LIAQARSAASKVKVSMKFNRSRGVRLRPPRDLDLAAYTALKFHIQSPVPAPEPGKNTGD 2700

QY 2701 HFVLYMGSRQATGDMGVSLRNQKVHVYRLGKAGPTTLSIDENICEQFAAVSIDRTLQF 2760

Db 2701 HFVLYMGSRQATGDMGVSLRNQKVHVYRLGKAGPTTLSIDENICEQFAAVSIDRTLQF 2760

QY 2761 GHMSVTVEKQMVHEIKGDTVAPGSEGLNLNHPDDDFVYVGGYPSPFTPEPLRFPFGYLCG 2820

Db 2761 GHMSVTVEKQMVHEIKGDTVAPGSEGLNLNHPDDDFVYVGGYPSPFTPEPLRFPFGYLCG 2820

QY 2821 IEMETLNEEVVSLNFEQTFMLDTAVDKPCARSKATGDPWLTGSLDGSFGFARISFEKQ 2880

Db 2821 IEMETLNEEVVSLNFEQTFMLDTAVDKPCARSKATGDPWLTGSLDGSFGFARISFEKQ 2880

QY 2881 FSNTKRFQDELRLVSYNGIIFFLKQESQFLCLAVQEGTLVLFYDFGSLKKADPLQPPQA 2940

Db 2881 FSNTKRFQDELRLVSYNGIIFFLKQESQFLCLAVQEGTLVLFYDFGSLKKADPLQPPQA 2940

QY 2941 LTAASKAIOVFLLAGNRKRVLRVERATVFSVDQDNMLEMADAYILGCVPPPEQLPLSLRQ 3000

Db 2941 LTAASKAIOVFLLAGNRKRVLRVERATVFSVDQDNMLEMADAYILGCVPPPEQLPLSLRQ 3000

QY 3001 LFPSSGSGVRGCIKGKALGKYVDLKRNLNTTGISFGCTADLLVGRMTFHHGHGFLPLALPD 3060

Db 3001 LFPSSGSGVRGCIKGKALGKYVDLKRNLNTTGISFGCTADLLVGRMTFHHGHGFLPLALPD 3060

QY 3061 VAPITEVVYSGFGRGTQDNLLYYRTSPDGPYQVSLREGHVTLRFMNQEVETQRFVADG 3120

Db 3061 VAPITEVVYSGFGRGTQDNLLYYRTSPDGPYQVSLREGHVTLRFMNQEVETQRFVADG 3120

QY 3121 APHYVAFYSNVTGWNLYVDDQLQLVKSHERTPMLQLOPEEPSRLLLGGLPVSGTFHNFS 3180

Db 3121 APHYVAFYSNVTGWNLYVDDQLQLVKSHERTPMLQLOPEEPSRLLLGGLPVSGTFHNFS 3180

QY 3181 GCISNVFVQRLRGPRQVFDLHQNMGSVNVSVGCTPAQLIETSRATAQKVSRRSRQPSQDL 3240

Db 3181 GCISNVFVQRLRGPRQVFDLHQNMGSVNVSVGCTPAQLIETSRATAQKVSRRSRQPSQDL 3240

QY 3241 ACTTPWLPGTIQDAYQFGGGLPSYQLQFVGISPSHRNRLHLSMLVRPHAASQGLLLSTAPM 3300

Db 3241 ACTTPWLPGTIQDAYQFGGGLPSYQLQFVGISPSHRNRLHLSMLVRPHAASQGLLLSTAPM 3300

QY 3301 SGRSPSLVFLNLHGHFVAQTEGPGPRLQVQSRQHSRAGQWHRVSVWGMQMQIQLVVDGSQ 3360

Db 3301 SGRSPSLVFLNLHGHFVAQTEGPGPRLQVQSRQHSRAGQWHRVSVWGMQMQIQLVVDGSQ 3360

QY 3361 TWSQKALHHRVPRAERPQPYTSLVGGLPASSYSSKLPVSVGFSGLKKLQDKQPLRTP 3420

Db 3361 TWSQKALHHRVPRAERPQPYTSLVGGLPASSYSSKLPVSVGFSGLKKLQDKQPLRTP 3420

QY 3421 QMVGVTPCVSGPLEDGLFFPGSEGVTLELPKAKMPYVSLELEMRPLAAAGLIFHLGOAL 3480

Db 3421 QMVGVTPCVSGPLEDGLFFPGSEGVTLELPKAKMPYVSLELEMRPLAAAGLIFHLGOAL 3480

RESULT 4

US-10-312-352-22

; Sequence 22, Application US/10312352

; Publication No. US20040053824A1

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.; TANG, Y. Tom

; APPLICANT: YUE, Henry; AZIMZAI, Yalda

; APPLICANT: HE, Ann; BATRA, Sajeev

; APPLICANT: LO, Terence P.; NGUYEN, Dannie B.

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; APPLICANT: BURFORD, Neil; YAO, Monique G.

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; APPLICANT: ARVIZU, Chandra S.; KHAN, Farrah A.

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; APPLICANT: DELEGEANE, Angelo M.; LEE, Sally

; TITLE OF INVENTION: EXTRACELLULAR MATRIX AND CELL ADHESION MOLECULES

; FILE REFERENCE: PF-0794 USN

; CURRENT APPLICATION NUMBER: US/10/312,352

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; PRIOR FILING DATE: 2000-07-18

; PRIOR APPLICATION NUMBER: US 60/240,111

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; PRIOR APPLICATION NUMBER: US 60/240,106

; PRIOR FILING DATE: 2000-10-12

; PRIOR APPLICATION NUMBER: US 60/244,021

; PRIOR FILING DATE: 2000-10-27

; PRIOR APPLICATION NUMBER: US 60/248,887

; PRIOR FILING DATE: 2000-11-14

; PRIOR APPLICATION NUMBER: US 60/249,570

; PRIOR FILING DATE: 2000-11-16

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: PERL Program

; SEQ ID NO 22

; LENGTH: 3695

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No. US20040053824A1 6382722CD1

US-10-312-352-22

Query Match 79.7%; Score 15842; DB 12; Length 3695;

Best Local Similarity 79.4%; Pred. No. 0;

Matches 2874; Conservative 278; Mismatches 451; Indels 18; Gaps 8;

QY 1 DLYCKLVGSPVAGGDPNQIQQOYCDICTAANSNKAHPVSNADIGTERWQSPPLSRGLE 60
DLYCKLVGSPVAGGDPNQIQQOYCDICTAANSNKAHPVSNADIGTERWQSPPLSRGLE 138
QY 61 YNEVNVTLDLGOVFHVAYVLIKFNPSRPPDLWLERSTDFGHTYQYPWQFFASSKRDCLER 120
DLYCKLVGSPVAGGDPNQIQQOYCDICTAANSNKAHPVSNADIGTERWQSPPLSRGLE 138
QY 139 YNEVNVTLDLGOVFHVAYVLIKFNPSRPPDLWLERSTDFGHTYQYPWQFFASSKRDCLER 198
QY 121 FGPRTLEIRITQDDDDVICTTEYSRIVPLENGEIVVSLVNGRPGALNFSYSPLLRDFTKATN 180
DLYCKLVGSPVAGGDPNQIQQOYCDICTAANSNKAHPVSNADIGTERWQSPPLSRGLE 138
QY 199 FGPQTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRPGAMNFSYSPLLRDFTKATN 258
QY 181 IRLRFLRNTLLGHLMGKALRDPVTTRRRYYYYSIKDISIGRCVCHGHADVCDAXDPLDPF 240
DLYCKLVGSPVAGGDPNQIQQOYCDICTAANSNKAHPVSNADIGTERWQSPPLSRGLE 138
QY 259 VRLRFLRNTLLGHLMGKALRDPVTTRRRYYYYSIKDISIGRCVCHGHADACDAKDPDPP 318
QY 241 RLQACQHNNTCGGSCDRCCPGFNQDPWKPAATDSANECQSNCHGHAYDCYYDPEDDRN 300
DLYCKLVGSPVAGGDPNQIQQOYCDICTAANSNKAHPVSNADIGTERWQSPPLSRGLE 138
QY 319 RLQCTCQHNNTCGGTCDRCCPGFNQDPWKPAATDSANECQSNCHGHAYDCYYDPEDDRR 378
QY 301 ASQNDNVYQGGVCLDCQHHTTGINCERCLPGFFRAPDQPLDSPHVCRCPCDESFTDG 360
DLYCKLVGSPVAGGDPNQIQQOYCDICTAANSNKAHPVSNADIGTERWQSPPLSRGLE 138
QY 379 ASQSLDGTQGGGVCIDCQHHTAGVNCERCLPGFYRSPNHPLDSPHVCRRNCESDFTDG 438
QY 361 TCEDLTGRCYCRPNFTGELCAACAEGYTDFPHCYPLPSFPHNDTREQVLPAGQIVNDCN 420
DLYCKLVGSPVAGGDPNQIQQOYCDICTAANSNKAHPVSNADIGTERWQSPPLSRGLE 138
QY 439 TCEDLTGRCYCRPNFSGERCDCVCAEGTFGFPSCYTPS-SSNDTREQVLPAGQIVNDCS 497
QY 421 AAGTQGNACRDXPRLGRCVCKPNFRGAHCELCPAGFHGSPCHPCQCSSPGVANSLCDPES 480
DLYCKLVGSPVAGGDPNQIQQOYCDICTAANSNKAHPVSNADIGTERWQSPPLSRGLE 138
QY 498 AAGTQGNACRDXPRVGRCLCKPNFQGTGHCCELCPAGFYGPGCQPCQCSSPGVADDRCDPDT 557
QY 481 GQCMCRGTGEGRCDHICALGYFHFPLCQLCGCSPAGTLPPEGDEAGRCQCRPGFDGPHCD 540
DLYCKLVGSPVAGGDPNQIQQOYCDICTAANSNKAHPVSNADIGTERWQSPPLSRGLE 138
QY 558 GQCRVGVFEGATCDRCAPGYFHFPLCQLCGCSPAGTLPPEGDEAGRCCLCQPEFAGPHCD 617
QY 541 RCLPGYHGYPDCHACADPRGALDQCGVGGGLCHCRPGNTGATCQECSPGFYGFPSCTIPC 600
DLYCKLVGSPVAGGDPNQIQQOYCDICTAANSNKAHPVSNADIGTERWQSPPLSRGLE 138
QY 618 RCRPGYHGFPNCACTCDPRGALDQCGAGGLCRCPGYGTGACQECSPGFHGFPSCVPC 677
QY 601 HCSADGSLHTTCDPTTGQCRCPRTVTGLHCDMCPGAYNFYPCBAGSCHPAGLAPANPAL 660
DLYCKLVGSPVAGGDPNQIQQOYCDICTAANSNKAHPVSNADIGTERWQSPPLSRGLE 138
QY 678 HCSAEGSLHAACDPRSGQSCRPRVTGLRCDTCVPGAYNFYPCBAGSCHPAGLAPVDPAL 737
QY 661 PETQAPCMCRAHVEGPSDCRCKPGYWGJLSASNPEGCTRCSCDPRTLGGVTECQ-ENGQC 719
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QY 738 PEAQVPCMCRAHVEGPSDCRCKPGFWGLSPSNPEGCTRCSCDLRGLTGGVAECQPGTGQC 797
QY 720 FCKAHVCGKTCACACKDGFGLDYADYFGCRSCRDVGGALQGQCEPKTGACRCRPNTOGP 779
DLYCKLVGSPVAGGDPNQIQQOYCDICTAANSNKAHPVSNADIGTERWQSPPLSRGLE 138
QY 798 FCKPHVCGQACASCKDGFGLDQADYFGCRSCRDIGGALQSCCEPRTGVCRCPNTOGP 857
QY 780 TCSEPAKDHVLPDLHLMRLELEEAATPEGHAVRFGFNPLEFENFSWRGYAHMMAIQPRIV 839
DLYCKLVGSPVAGGDPNQIQQOYCDICTAANSNKAHPVSNADIGTERWQSPPLSRGLE 138
QY 858 TCSEPARDHYLPDLHLRLELEEAATPEGHAVRFGFNPLEFENFSWRGYAQMAPPVQPRIV 917
QY 840 ARLNVTSPDLFRLVFRYVNRGSTSVNGQISVREEGKLSSTNCTNCTBQSQPVAFPPSTEPAF 899
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QY 918 ARLNLTSPDLFWLFRYVNRGAMSVGRSVREEGRSAAACANCTAQSQPVAFPPSTEPAF 977
QY 900 VTVPQRGFGEFVNLNPGIALLVEAEGVLLDYVLLPSTYYEALLQHRVTEACTYRPSA 959
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QY 978 ITVPQRGFGEFVNLNPGTWARVEAEGVLLDYVLLPWAYEALLQLRVTEACTYRPSA 1037
QY 960 LHSTENCLVYAHPLDGFPSAAGTEALCRHNSLPRPCPTEQLSPSHPPLATCFGSDVDI 1019
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QY 1038 QQSGDNCLLYTHLPDGFPSAAGLEALCRQNSLPRPCPTEQLSPSHPPLITCTGSDVDV 1097
QY 1020 QLEMAVPPQGYVVLVVEYVGEDSHQEMGVAVHTPQRAQQGVNLHPCPYSSLCRSPARD 1079
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QY 1098 QLQVAVPPQGRYALVVEYANEDARQEVGVAVHTPQRAQQGLLSLHPCLYSTLCRGTARD 1157
QY 1080 TQHLAIFHLDSEASIRLTAEQAHHFFLHSLVTLVPVEEFSTEFVEPRVFCVSSHGTFPSS 1139

Db 1158 TQDHLAVPHLDSEASVRLTAEGARFFLHGVTLPVIEEFSEFVEPRVSCISSHGAFGPN 1217
QY 1140 AACLASREPKPPQPIILKDCQVLPPLPDLPLTQSQELSPGAPPEGPQPRPPTAVDPNAEP 1199
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Db 1218 AACLPSREPKPPQPIILRDCQVLPPLPPLGLPLTHAQDLTSPATSPAGPRPPTAVDPDAEP 1277
QY 1200 TLLRHPQGVVFTTQVFTLGRYAFLLHGYQPVHPSFPFVEVLINGGRIWQHANASFCPHG 1259
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QY 1260 YGCRTLVLCGQTMLDVTDNELTVTVRVPPEGRWLWLDYVLPEDAYSSSYLQEEPLDKS 1319
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Db 1338 YGCRTLVVCEGQALLDVTHSELVTVRVPEGRWLWLDYVLPVENYVSFGYLREEPLDKS 1397
QY 1320 YDFISHCATQYHISPSSSPFCRNAATSLSLFYNGALPCGCHEVGAVSPTCEPFGGQC 1379
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Db 1398 YDFISHCAAQYHISPSSSLFCRNAASLSLFYNNGARPCGCHEVGATGPTCEPFGGQC 1457
QY 1380 PCRGHVIGRDCSRCATGYWGFPPNCRPCDCGARLCELTGQCICPPRTVPPDCLVCQPOSF 1439
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QY 1440 GCHPLVGCEECNCSGPGVQELTPTCDMDSGQCRCPNVAGRCDTCAPGYGYPSCRPC 1499
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Db 1518 GCHPLVGCEECNCSGPGIQELTPTCDTDSGQCKRPNVTGRCDTCSPGFHGYPRCRPC 1577
QY 1500 DCHEAGTMASVCDPLTGQCHCKENVOGSRCDQCRVGTFSLDAAKPKGCTRCFCGATERC 1559
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Db 1638 RSSSYTRQEFVDMEGVWLLSTDRQVVPHERQPGTEMLRADLRHVPEAVPEAPPELYWQAP 1697
QY 1616 PSYLGDRVSSYGGTLHYELHSETQRGDIFIPYESRDPVVLOQNMISIAFLELAYPPPGQV 1675
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Db 1698 PSYLGDRVSSYGGTLRYELHSETQRGDVFPVPMESRDPVVLOQNMISITFLEPAYPTPGHV 1757
QY 1676 HRGQLQLVEGNFRHLETHNPVSREELMMVLAGLEQLQIRALFSTSSSVSLRRVVLEVAS 1735
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QY 1736 EAGRPPASNVELCMCPANYRGDSQCECAPGYRDTKGLFLGRVCPQCHGHSDRCLPGS 1795
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Db 1818 PAGQALASNVELCLCPASYRGDSQCECAPGYRDKGLFLGRVCPQCHGHSDRCLPGS 1877
QY 1796 GICVGCQHNTEGDCQRCRCPGFVSSDPSNPASPCVSCPLAVPSNNFADGCVLNRGRTQ 1855
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Db 1878 GVCVDCQHNTEGAHCERCQAGFMSS-RDDPSAPCVSCPCPLSVPSNNFAEGCVLRGGRTQ 1936
QY 1856 CLCRPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSGNGDPNMFSDCDPLTGACRGCLR 1915
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Db 1937 CLCKPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSGNGDPNLLFSDCDPLTGACRGCLR 1996
QY 1916 HTTGPHCERCAPGYGNALLPGNCTRCDCSPCGTETCDPQSGRCCLCKAGVTGQRCDRCL 1975
DLYCKLVGSPVAGGDPNQIQQOYCDICTAANSNKAHPVSNADIGTERWQSPPLSRGLE 138
Db 1997 HTTGPRCEICAPGYGNALLPGNCTRCDCCTPCGTEACDPHSGHCLCKAGVTGRRCDRCQ 2056
QY 1976 GYFGFEQCGCRPCACGPAAGSECHPQSQCHCQPGTTGPPQCLECAPGYWGLPEKGCRR 2035
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Db 2057 GHFGFNGCGGCRPCACGPAAGSECHPQSQCHCQPGTMGPPQCRECAPGYWGLPEQGCRR 2116
QY 2036 CQCPRGHCDPHTGHCTCPPGLSGERCDCSQQHCVVPVPGKPGGHGHCHEVCDHCWVLLD 2095
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Db 2117 CQCPGGRCDPHTGRCNCPPLGSGERCDCSQQHCVVPVPGGPGVHGSINCEVCDHCWVLLD 2176
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Db 2177 DLERAGALLPAIHEQLRGINASSMAWARLHRLNASIADLQSKLRSPLGPRHETAQQL 2236
QY 2156 EOOISISLOQDTERLGSQATGVQAGQLDTESTLGRAQKLLSVRAVGRALNELASRM 2215

Db 2237 EQSTSLGQDARRLGGQAVGTRDQASQLLAGTEATLGHAKTLLAAIRAVDRTLSELSMQT 2296
Qy 2216 GQSGPGDALVPSGEQLRWALAEVERLLWDMRTRDLGACGAVAAEALAEAOIRLWARVQEQ 2275
Db 2297 GHGLANASAPSGEQLLRTLAEBVERLLWEMRARDLGAPQAAAAEALAAQRIARVQEQ 2356
Qy 2276 TSFWEENQSLATHIRDQLAQVESGLMDLREALNQAVNTTREAEEELNSRNOERVKEALQWK 2335
Db 2357 SSLWEENQALATQTRDLRAQHEAGLMDLREALNRAVDATREAQELNSRNOERLBEALQRK 2416
Qy 2336 QELSODNATLKATLQAAASLILGHVSELLOGIDQAKEDLEHLAASLDGAWTPLLKRMQAFS 2395
Db 2417 QELSRDNATLQATLHAARDTLASVFRLLHSLDQAKEELERLAASLDGARTPLLRMQTFS 2476
Qy 2396 PASSKVDLVEAAEAHAQKLNQALNLSGIIILGINQDRFIQRAVEASNAYSSILQAVQAAE 2455
Db 2477 PAGSKRLVEAAEAHAQQLQALNLSIIIDVNQDRLTQRAIEASNAYSRIILQAVQAAE 2536
Qy 2456 DAAGQALRQASRTWEMVQORGLAAGARQOLLANSALLETILGHQGRGLGAGLQAGLQAGIO 2515
Db 2537 DAAGQALQQAADHTWATVVRQGLVDRAQOLLANSSTALEAMLQEQQRGLGVWAALQGARTQ 2596
Qy 2516 LHNWARKNQALAAQIQEAQAMLAMDTSETSEKIAHAKAVAAEALSTATHVQSOLQGMQKN 2575
Db 2597 LRDVRAKKQOLEAHIQAAQAMLAMDTDETSKKIAHAKAVAAEAQDTATRVQSOLQAMQEN 2656
Qy 2576 VERWQSOLGGLQGDLSOVERDASSVSTLEKTLPLLAKLSRLNENRGVHNASIALSANI 2635
Db 2657 VERWQCGYEGLRGQDGLQAVLDAGHSVSTLEKTLPLLAKLSILENRGVHNASIALSASI 2716
Qy 2636 GRVRLIAQARSAAASKVKVSMKFNKGRSGVRLRPPRLDLADLAAAYTALKFTHIQSPVPAPEPG 2695
Db 2717 GRVRELIAQARGAASKVKVPMKFNKGRSGVQLRTPRDLADLAAAYTALKFYLOQ--PEPEPG 2774
Qy 2696 KNTGDHFVLYMGSRQATGDMGVSLRNQKVHVYRLGKAGPTTSLIDENIGEQAFAVSID 2755
Db 2775 QGTEDRFVYMGSRQATGDMGVSLRDKKVHVYQLGEAGPAVLSIDEDIGEQAFAAVSLD 2834
Qy 2756 RTLQFGHMSVTVEKOMVHEIKGDTVAPGSEGLLNHBPDDFVFYVGGYPSNFTPEPLRFP 2815
Db 2835 RTLQFGHMSVTVERQMIQETKGDVAPGAEGLLNLRPDDFVFYVGGYPSFTPPPLLRFP 2894
Qy 2816 GYLGCIEMETLNEEVVSLYNPEQTFMLDТАVDKPCARSKATGDPWLTDGSLDGSGFARI 2875
Db 2895 GYRGCIEMDTLNEEVVSLYNPFRTFQLDТАVDRPCARSKSTGDPWLTDGSLDGTGFARI 2954
Qy 2876 SFEKQFSNTKRFDOELRLVSYNGIIFFLKQESQFLCLAVQEGTLVLFYDFGSLKKADPL 2935
Db 2955 SFDQISTTKRFEQELRLVSYSGVLFLLKQSQFLCLAVQEGSLVLLYDFGAGLKKAVPL 3014
Qy 2936 QPPQALTAASKAIQVFLLAGNRKRVLRVERATVFSVDQDNMLEMADAYILGGVPPEQLP 2995
Db 3015 QPPPLTSASKAIQVFLGGSRKRVLRVERATVVSVEQDNDELEADAYILGGVPPDQLP 3074
Qy 2996 LSLRQLFPPSGGSVRGCIKGIKALGKYVDLKRNLNTTGISFGCTADLLVGRMTFPHGHGFLP 3055
Db 3075 PSURRLFPPTGGSVRGCVKGIKALGKYVDLKRNLNTTGSAGCTADLLVGRAMTFPHGHGFLR 3134
Qy 3056 LALPDVAPITEVYSGFGFRGTQDNLLYYRTSPDGPYQVSLREGHVTILRFMNQEVETOR 3115
Db 3135 LALSNVAPLTGNVYSGFGHSAQDSALLYRASPDGLCQVSLQQRVSLQLLRTEVXTQA 3194
Qy 3116 VFADGAPHYVAFYSNVTGMVLYVDDQLQLVKSHERTTPMLQLQPEEPSRLLLGGLPVSGT 3175
Db 3195 GFADGAPHYVAFYSNATGMVLYVDDQLQOMKPHRGPPPELQPPQEPGPRLLIGGLPESGT 3254
Qy 3176 FHNFSGCISNVFQRLRGPQRFVDLHQNMGSVNVSVGCTPAQLIETS-----RATAQK 3228
Db 3255 IYNFSGCISNVFQRLLPQRFVFDLQQNLGSVNVSTGCAPALQAQTPGLGPRGLQATARK 3314
Qy 3229 VSRRSRQPSQDLACTTPWLPFGTIQDAYQFGGPLPSYLQFVGISPSHRNRLHLSMLVRPHA 3288
Db 3315 ASRRSRQPARHPACMLPPLHRLTTRDSYQFGGSLSSHLEFVGILARHNWPSLSMHVLP- 3373

Qy 3289 ASQGLLLSTAPMSGRSPSLVLFLNHGHFVAQTEGPGRLQVQSRQHSRAGQWHRVSRWG 3348
Db 3374 SSRGLLLFTARLRPGSPSLALFLSNHGHFVAQMEGLGTRLRAQSRQSRPGRWHKVSVRWE 3433
Qy 3349 MQQIQLVVDGSGQTSQKALHHRVPRAERPQPYTTLVSGGLPASSYSKLPVSVGFSGLKK 3408
Db 3434 KNRILLVTDGARAWSQEGPHRQHQAEPHQPHTTLFVGGLPASSHSSKLPVTVGFSGVKR 3493
Qy 3409 LQLDKQPLRTPQMVGVTPCVSGPLEDGLFFPGSGEVVTLELPAKMPYVSLELEMRPLA 3468
Db 3494 LRLHGRPLGAPTRMAGVTPCILGPLEAGLFFPGSGGVITLDLPATLPDVGLELEVRPLA 3553
Qy 3469 AAGLIFHLGQALATPYMQLKVLTEOVLLQANDGAGERSTWVTYPK-LCDGRWHRVAVIMG 3527
Db 3554 VTGLIFHLGQARTPPYLQQLVTEKQVLLRADDDGAGEFSTSVTRPSVLCDGQWHRLAVMKS 3613
Qy 3528 RDTLRELVDTQSNHTTGRLPBESLAGSPALLHLGSLPKSSTARPELPAYRGCLRKLINGA 3587
Db 3614 GNVLRLEVDQAQSNHTVGPLLAAAAGAPAPLYLGLLPEPNAVQPPPAYCGCMRRRLAVNRS 3673
Qy 3588 PVNVTASVQIQAVGMRGCP 3608
Db 3674 PVAMTRSVEVHGAVGASGCPA 3694

RESULT 5
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; Sequence 2, Application US/10037182
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; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Doi, Masayuki
; APPLICANT: Thyboll, Jill
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Best Local Similarity 79.4%; Pred. No. 0;
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Qy 1 DLYCKLVGGPVAGGDPNQTIQGYCDICTAANSKHAHPVSNDAIDGTERWWQSPPLSRGLE 60
Db 79 DLYCKLVGGPVAGGDPNQTIQGYCDICTAANSKHAHPASNAIDGTERWWQSPPLSRGLE 138
Qy 61 YNEVNVTLDLGQVFHVAYVLIKFPANSRPPDLWLBERSTDFGHTYQPWQFFASSKRDCLER 120
Db 139 YNEVNVTLDLGQVFHVAYVLIKFPANSRPPDLWLBERSMDFGRTYQPWQFFASSKRDCLER 198
Qy 121 FGPRTERITQDDDDVICTTEYSRIVPLENGEIVVSLVNGRPPGALNFSYSPLLRDFTKATN 180
Db 199 FGQPTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRPPGAMNFSYSPLLRDFTKATN 258
Qy 181 IRLRFLRTNTLLGHLMGKALRDPPTVTRRYYSIKDISIGGRVCVCHGHADVCDAKDPDLPF 240
Db 259 VRLRFLRTNTLLGHLMGKALRDPPTVTRRYYSIKDISIGGRVCVCHGHADACDAKDPDLPF 318
Qy 241 RLQACQHNHTCGGSCDRCCPGFNQOPKWPATTDANSQCSCNCHGHAYDCYYDPEVDRRN 300
Db 319 RLQCTQHNTCGGTCDCRCPCGPNQOPKWPATANSANCQCSCNCHGHATDCYYDPEVDRRR 378

QY	301	ASQNQDNVYQGGVCLDCQHHTTGINCERCLPGCFRAPPDQPLDSPHVCRPCDCESDFTDG	360
DB	379	ASQSLDGTGYGGGVCLDCQHHTTAGVNCERCLPGFYRSPNHPLDSPHVCRRCNCESDFTDG	438
QY	361	TCEDLTGRCYCPNFTGELCAACAEGYTDPHCYPLPSFPNDTREQVLPAQIVNCDCN	420
DB	439	TCEDLTGRCYCRPNFSGERCDCVCAEGFTGFSPCYTPS-SSNDTREQVLPAQIVNCDCS	497
QY	421	AAGTOGNACRDPRLGRCVCKPNFRGAHCELCAPGEHGPSCHPCQCSPPGVANSLCDPES	480
DB	498	AAGTOGNACRDPVRGRCLCKPNFQGTCHCELCAPGFYGPCCQPCQCSSPGVADDRCDPDT	557
QY	481	GQCMCRTGFEGDRCDHICALGYFHFPLCQLCGCSPAGTLPPEGCDEAGRCQCRPGFDGPHCD	540
DB	558	GQCRCRVGFEGATCDRCAPGYFHFPLCQLCGCSPAGTLPPEGCDEAGRCQLQPEFAGPHCD	617
QY	541	RCLPGYHGYPDCHACADPRGALDQCGVGGLCHCRPGNTGATCQECSPGFYGFPPSCIPC	600
DB	618	RCRPGYHGFPNCACTCDPRGALDQLCAGGLCRCRPGYTGATCQECSPGFHGFPPSCVPC	677
QY	601	HCSADGSLHTTCDDPTTGQRCRPRVTGLHCDMCPGAYNFPYCEAGSCHPAGLAPANPAL	660
DB	678	HCSAEGSLHAACDPRSGQCSRPRVTGLRCDTCVPGAYNFPYCEAGSCHPAGLAPVDPAL	737
QY	661	PETQAPCMCRAHVEGSPCDCKPGYWGLSANPEGCTRCSCDPRGTLGGVTECQ-GNGQC	719
DB	738	PEAQVPCMRAHVEGSPCDCKPGFWGLSPNPEGCTRCSCDLRGLTGGVAECQPGTGQC	797
QY	720	FKAHVCGKTCACCKDGFGLDYADYFGCRSCRDVGALGQGCPEKTCACRCRPNTQGP	779
DB	798	FKPHVCGQACASCKDGFGLDQADYFGCRSCRDIGGALGQSCPEPRTGVCRCRPNTQGP	857
QY	780	TCSEPAKDHLPDLHMRLEEEAATPEGHAVRPGFNPLEFENFSWRGYAHMMAIQPRIV	839
DB	858	TCSEPARDHYLPDLHLRLLEEEAATPEGHAVRPGFNPLEFENFSWRGYAQMAPPVQPRIV	917
QY	840	ARLNVTSPLFRLVFRVYNRGSTSVNGQISVREBGLSSCTNCTEQSQPVAFPPSTEPAF	899
DB	918	ARLNLTSPLFWLVFRVYNRGAMSVSGRVSVREGRSAACANCTAQSQPVAFPPSTEPAF	977
QY	900	VTVPQRGFGEFVLNPGIHWALLVEAEGVLLDYVLLPSTYYEALLQHRVTEACTYRPSA	959
DB	978	ITVPQRGFGEFVLNPGTWALRVEAEGVLLDYVLLPSAYYEALLQLRVTEACTYRPSA	1037
QY	960	LHSTENCLVYAHLPDLGFPSSAAGTEALCRHDNSLPRPCPTQQLSPSHPPPLATCFGSDVDI	1019
DB	1038	QQSGDNCLLYTHLPDLGFPSSAAGLEALCRQDNSLPRPCPTQQLSPSHPPPLITCTGSDVDV	1097
QY	1020	QLEMAVPPQGYVLVVEYVGEDSHQEMGVAVHTPQAPQQGVNLNHPCPYSSLCRSPARD	1079
DB	1098	QLQVAVPPGRYALVVEYANEDARQEVGVAVHTPQAPQQGLLSLHPCLYSTLCRGTARD	1157
QY	1080	TQHHLAIFHLDSIASRLTAEQAHFFLHSHVTLVPVEEFSTEFVEPRVFCVSSHGTNFPSS	1139
DB	1158	TQDHLAVFHLDSIASVRLTAEQARFFLHGVTLPVEEFSPFVEPRVSCISSHGAFGPNS	1217
QY	1140	AACLASRFPKPPQPIILKDCQVLPPLPDLPLTQSOELSPGAPPEGQPRPPTAVDPNAEP	1199
DB	1218	AACLPSRFPKPPQPIILRDCQVPLPPGLPLTHAODLTATSPAGPRPRPPTAVDPDAEP	1277
QY	1200	TLLRHPQGTWFTTQVPTLGRYAFLLHGYQPVHPSPFVEVLINGGRIWQGHANASFCPHG	1259
DB	1278	TLLREPOATVFTTHVPTLGRYAFLLHGYQPAHPPTFVEVLINAGRVMQGHANASFCPHG	1337
QY	1260	YGCRTLVLCEQTMLDVTDNELTTVVRVPEGRWLMDYVLVPEDAYSSSYLOEPEPLDKS	1319
DB	1338	YGCRTLVCCEQALLDVTHSLTTVVRVPEGRWLMDYVLVVPENVYSFGYLREPEPLDKS	1397
QY	1320	YDFISHCATQGYHISPSSSSPFCRNAATSLSLFYNNGALPCGCHEVGAVSPTCEPFGGQC	1379
DB	1398	YDFISHCAAQGYHISPSSSSPFCRNAASLSLFYNNGARPCGCHEVGATGTCPEPFGGQC	1457

QY	1380	PCF	GHVIGRDCSR	CATGYWGF	PNCRPCD	CGARL	CDEL	TGQCIC	PPRTVP	PPDCLV	CQPSF	1439																																			
DB	1458	PCH	AVIGRDCSR	CATGYWGF	PNCRPCD	CGARL	CDEL	TGQCIC	PPRTIP	PPDCLL	CQPTF	1517																																			
QY	1440	GCH	PLVGC	EECNCS	GGPGVQ	ELTPT	CTDMD	SGQCR	CPNV	AGRRCD	TCAP	GFYGYPS	CRPC	1499																																	
DB	1518	GCH	PLVGC	EECNCS	GGPGVQ	ELTPT	CTD	DSGQ	CKRNV	TGRRCD	TCSP	GFHGYPR	CRPC	1577																																	
QY	1500	DCH	EAGT	MASV	CDPL	TGQCH	CKENV	QSGR	CDQCR	VGTFT	SLDA	ANPK	GCTRC	FCFGATERC	1559																																
DB	1578	DCH	EAGT	APGV	CDPL	TGQCY	CKENV	QPKD	QCSL	GTFT	SLDA	ANPK	GCTRC	FCFGATERC	1637																																
QY	1560	GNS	NLAR	HEFV	DMEG	VLLSS	DQWV	PHEH	RPEI	ELLHAD	LR--	--SV	ADT	FESELY	WQAP	1615																															
DB	1638	RSS	YTRQ	EFV	DMEG	VLLSS	DQWV	PHER	QPGT	EMLRAD	LHRV	PEAV	PEAF	PELY	WQAP	1697																															
QY	1616	PSY	LDRV	SSYGG	TLLHY	ELHSET	ORGDI	FIPY	ESRP	DDVVL	QGNQ	MSIA	AFLE	LAYPP	PGQV	1675																															
DB	1698	PSY	LDRV	SSYGG	TLLRY	ELHSET	ORGDV	FVP	MESR	DDVVL	QGNQ	MSIT	TFLE	PAYPT	PGHV	1757																															
QY	1676	HRQ	LOL	VEGN	FRHLE	THNP	VSRE	ELMM	VLAG	LEQL	QIRAL	FSQT	SSSV	SLRRV	VALEVAS	1735																															
DB	1758	HRQ	LOL	VEGN	FRHLE	THNP	VSRE	ELMM	VLAG	LEQL	QIRAL	FSQI	SSAV	SLRRV	VALEVAS	1817																															
QY	1736	EAG	RPP	PAS	NVEL	CMCP	ANVR	GDSC	QECAP	GYIRD	TKGL	FLGR	CVPC	QCHG	SHDR	CLPGS	1795																														
DB	1818	PAG	GALA	S	NVEL	CLCP	ASVR	GDSC	QECAP	GYIRD	VKG	FLGR	CVPC	QCHG	SHDR	CLPGS	1877																														
QY	1796	GIC	V	COH	NT	EGDQ	CERC	RC	PGFV	SSDP	SNPAS	PCVSC	PCPL	AVPS	NNFAD	GCVL	RNGRTQ	1855																													
DB	1878	GVC	V	COH	NT	EGAH	CERC	CO	QAF	MSR-R	DDP	SAPCV	SC	PLSV	PSNN	FAEG	CVLR	GGRTQ	1936																												
QY	1856	CLC	RPGY	AG	AS	CERC	AP	FFGN	PLVL	GSSC	QPCD	CSG	NGD	PNMI	FSDC	DLT	GTAC	RGC	CLR	1915																											
DB	1937	CLC	RPGY	AG	AS	CERC	AP	FFGN	PLVL	GSSC	QPCD	CSG	NGD	PNMI	FSDC	DLT	GTAC	RGC	CLR	1996																											
QY	1916	HTT	GP	H	CERC	AP	GFY	GNAL	PLGN	CTRC	DC	SC	PGT	ETCD	PSGR	CLCK	AGVT	QORC	DR	CLLE	1975																										
DB	1997	HTT	GP	RCEI	CAP	GFY	GNAL	PLGN	CTRC	DC	TPC	GTEA	CD	PHSG	HC	CLCK	AGVT	GRR	CD	R	COE	2056																									
QY	1976	GYF	GE	Q	CG	RPC	CAC	GA	KG	SECH	PQSG	QCHQ	CPGT	TGP	QCLE	CAP	GYW	GL	PEK	G	CRR	2035																									
DB	2057	GHF	GEN	CGG	CRPC	CAC	GA	AE	GE	SECH	PQSG	QCHC	RP	GT	MGP	QCRE	CAP	GYW	GL	PEQ	G	CRR	2116																								
QY	2036	CQC	PRGH	CD	PHT	GHCT	CP	PG	L	S	GER	CDT	CS	QHQV	VP	PGK	PGG	GH	I	H	CEV	CD	HC	CV	VLLLD	2095																					
DB	2117	CQC	PRGH	CD	PHT	GR	CN	CP	PG	L	S	GER	CDT	CS	QHQV	VP	PGK	PGG	GH	I	H	CEV	CD	HC	CV	VLLLD	2176																				
QY	2096	DLR	AG	ALL	PAI	RE	Q	LOG	IN	ASA	AWAR	LH	R	LN	ASIA	D	LSK	L	R	R	P	P	P	P	P	P	RY	QAA	QLO	T	L	2155															
DB	2177	DLR	AG	ALL	PAI	HEQ	L	R	GIN	ASS	MAW	AR	LH	R	LN	ASIA	D	LSK	L	R	S	P	L	G	P	R	H	ETA	Q	Q	LE	V	L	2236													
QY	2156	EQS	I	S	I	Q	D	T	ER	L	G	S	QAT	V	G	QAG	Q	L	D	T	T	E	S	T	L	G	R	A	Q	L	L	E	S	V	R	AV	G	R	AL	N	E	L	A	S	R	M	2215
DB	2237	EQS	T	S	L	Q	D	A	R	R	L	G	G	Q	AV																																

QY 421 AAGTOGNACKDPRLGRVCVKPNFRGAHCELCAPGFHGSPCHPCQCSSPGVANSLCDPES 480
Dd 498 AAGTOGNACKDPRLGRVCVKPNFRGAHCELCAPGFHGSPCHPCQCSSPGVANSLCDPES 480
QY 481 GQCMCRTEGDRCDHCHALGYFHFPLCQLCGCSPAGTLPPEGDEAGRCQCRPGDFGPHCD 540
Dd 558 GQCRVGFEGATCDRCAPGYFHFPLCQLCGCSPAGTLPPEGDEAGRCQLCQPEFAGPHCD 617
QY 541 RCLPGYHGPDDCHACADPRGALDQCGVGGGLCHCRPGNTGATCQECSPGFYGFPPSCIPC 600
Dd 618 RCRPGYHGFNCQACTCDPRGALDQCGAGGLCRCPGYTGATCQECSPGFHGFPPSCVPC 677
QY 601 HCSADGSLHTTCDPTTGQCRCPRTVTLGHCDMCPGAYNFPFYCEAGSCHPAGLAPANPAL 660
Dd 678 HCSAEGSLHAACDPRSGQCSRPRVTGLRCDTCVPGAYNFPFYCEAGSCHPAGLAPVDPAL 737
QY 661 PETQAPCMCAHVEGSPCDRCCKPGYWGLSASNPEGCTRCSDBRGTLGGVTECQ-GNGQC 719
Dd 738 PEAQVPCMAHVEGSPCDRCCKPGFGLSPSNPEGCTRCSDBRGTLGGVAECQPGTGQC 797
QY 720 FCKAHVCGKTCACACKDGFGLDYADYFGCRSCRDVGALGQCGEPTKGACRCRPNTOGP 779
Dd 798 FCKPHVCGQACASCKDGFGLDQADYFGCRSCRDIGGALGQSCPEPTGVCRCRPNTOGP 857
QY 780 TCSEPAKDHVLPDLHMHRLLELEAATPEGHAVRFGFNPLEFENFNSWRGYAHMMAIQPRIV 839
Dd 858 TCSEPARDHVLPDLHHLRLELEAATPEGHAVRFGFNPLEFENFNSWRGYAQAQMAPVQPRIV 917
QY 840 ARLNVTSPDLFRLVRYVNRGSTSVNGQISVREEGKLSLSCNTNCTEQSQSPVAFPPSTEPAF 899
Dd 918 ARLNLTSPDLFWLVRYVNRGAMSVSGRVSREGRSATCANCTAQSQPVAFPPSTEPAF 977
QY 900 VTPVQRFGEFPVLPNGIALLVEAEGVLLDYVLLPSTYYEARALLQHRVTEACTYRPSA 959
Dd 978 ITVPQRFGEFPVLPNGTALRVEAEGVLLDYVLLPWAYEARALLQLRVTEACTYRPSA 1037
QY 960 LHSTENCLVYAHLPDGPFPASAAGTEALCRHNSLPRPCPTQEQISPSHPPLATCFGSDVDI 1019
Dd 1038 QQSGDNCLLYTHLPDGPFPASAAGLEALCRQDNSLPRPCPTQEQISPSHPPLITCTGSDVDV 1097
QY 1020 QLEMAVPQPGQYVLYVEYVGEDSHQEMGVAVHTPQAPQOGVNLHPCPYSSSLCRSPARD 1079
Dd 1098 QLQVAVPQPGRYALVVEYANEDARQEVGVAVHTPQAPQOGVNLHPCPYSSSLCRGTARD 1157
QY 1080 TQHHLAIFHLDSEASIRLTAEQAFFLHSHVTLVPVEEFSTFVEPRVFCVSSHGTENPSS 1139
Dd 1158 TQDHLAVFHLDSSEASVRLTAEQARFFLHGVTLPVPIEEFSPEFVEPRVSCISSHGAFGPNS 1217
QY 1140 AACLASRFPKPPQPIILKDCQVLPPLPDLPTQSQELSPGAPPEGQPRPPTAVDPNAEP 1199
Dd 1218 AACLPSRFPKPPQPIILRDCQVILPPLPGLPLTHAQDLTPAMSPAGPRPPTAVDPPDAEP 1277
QY 1200 TLLRHPQGTVFTTQVPTLGRYAFLLHGYQVHPSPFPVEVLINGGIWQHGHANASFCPHG 1259
Dd 1278 TLLREPQATVFTTHTVPTLGRYAFLLHGYQVPAHPTFPVEVLINAGRVWQGHANASFCPHG 1337
QY 1260 YGCRTLVLCGQTMLDVTDNELTVTVRVEGRWLWLDYVLIVPEDAYSSSYLQEEPLDKS 1319
Dd 1338 YGCRTLVVCQGALLDVTHSELTVTVRVPKGRWLWLDYVLVVPENVYSFGYLREEPLDKS 1397
QY 1320 YDFISHCATQGYHISPSSSSPFCRNAATSLFYNNGALPCGCHEVGAVSPTCEPFGGQC 1379
Dd 1398 YDFISHCAAQGYHISPSSSSLFCRNAAASLIFYNNGARPCGCHEVGATGPTCEPFGGQC 1457
QY 1380 PCRGHVIGRDCSRCATGYWGFNCRPCDCGARLDCDELTGQICPPRTVPPDCLVCQPSF 1439
Dd 1458 PCHAHVIGRDCSRCATGYWGFNCRPCDCGARLDCDELTGQICPPRTIPPPDCLLCQPQTF 1517
QY 1440 GCHPLVGCEECNSGPGVQBELTDPCTCDMSDGGQCRCPNVAGRRCDTCAPGFYGYPSCRPC 1499
Dd 1518 GCHPLVGCEECNSGPGVQBELTDPCTDSDGGQCKRPNVTGRRCDTCSPGFHGYPRCRPC 1577
QY 1500 DCHEAGTMASVCDPLTGTQCHCKENVOGSRCDQCRVGTFSLDAANPKGCTRCFCFGATERC 1559

Dd 1578 DCHEAGTAPGVCDDPLTGTQCYCKENVQGPKCDQCCLSGTFSLDAANPKGCTRCFCFGATERC 1637
QY 1560 GNSNLARHEFVDMEGVWLLSSDRQVVPHEHRPEIELLHADLR---SVADTFSELYWOAP 1615
Dd 1638 RSSSYTRQEFVDMEGVWLLSTDRQVVPHERQPGTEMLRADLRHVPEAVPEAPPELYWOAP 1697
QY 1616 PSYLGDRVSSYGGTLLHYELHSETQRGDIPIFYESRPDVVLOGNMSIAFLELAYPPPGQV 1675
Dd 1698 PSYLGDRVSSYGGTLLRYELHSETQRGDVFPVPMESRPDVVLOGNMSITFLEPAYPTPGHV 1757
QY 1676 HRGQLQLVEGNFRHLETHNPVSREELMMVLAGLEQLQIRALFESQTSSSVSLRRVVLEVAS 1735
Dd 1758 HRGQLQLVEGNFRHTETRTNTVSREELMMVLASLEQLQIRALFQISSAVFLRRVALEVAS 1817
QY 1736 EAGRGPPASNVELCMCPANYRGDSQCBAPGYRDTKGLFLGCVPCQCHGSHDRCLPGS 1795
Dd 1818 PAGQALASNVELCLCPASYRGDSQCBAPGYRDTKGLFLGRCVPCQCHGSHDRCLPGS 1877
QY 1796 GICVGCQHNTEGDQCERCPRPGFVSSDPSPNPASPCVSCPCPLAVPSNNFADGCVLRNGRTQ 1855
Dd 1878 GVCVDCQHNTEGAHCERCQAGFVSS-RDDPSAPCVSCPCPLSVPSNNFAEGCVLRGGRTQ 1936
QY 1856 CLCRPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSNGNDPMIFSDCDPLTGACRGCLR 1915
Dd 1937 CLCKPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSNGNDPNLLFSDCDPLTGACRGCLR 1996
QY 1916 HTTGPHCERCAPGFYGNALLPGNCTRCDCSPCGTETCDPQSGRCCLCKAGVTGQRCDCRCL 1975
Dd 1997 HTTGPRCEICAPGFYGNALLPGNCTRCDCCTPCGTEACDPHSGHCLCKAGVTGRRCDRCQ 2056
QY 1976 GYFGFECQCGCRPCACGPAKSGSECHPQSGQCHCQPGTTGPOCLECAPGYWGLPEKGCRR 2035
Dd 2057 GHFGFDGCGCRPCACGPAEAGSECHPQSGQCHCQPGTMGMPQCECAPGYWGLPEQGCRR 2116
QY 2036 CQCPRGHCDPHTGHTCTPPGLSGERCDCSQOQHOVPVPGKPGGHHCEVCDHCVVLLLD 2095
Dd 2117 CQCPGRCDDPHTGRCNCPPLSGERCDCSQOQHOVPVPGGVPVHCEVCDHCVVLLLD 2176
QY 2096 DLERAGALLPAIREQLQGINASSAAWALHRLNASIADLQSKLRRPPGPRYQAAQLOTL 2155
Dd 2177 DLERAGALLPAIHEQLRGINASSMAWALHRLNASIADLQSKLRRPLGPRHETAQOLEVL 2236
QY 2156 EQQSISLQDTERLGSQ-ATGVQGAQQLDTESTLGRAQKLLSVRAVGRALNELASR 2214
Dd 2237 EQQSTSLGQDARLGGQAAVGT RDQASQLLAGTEATLGHAKTLLAAIRAVDRTLSELMSQ 2296
QY 2215 MGQSGPDALVPSGEQLRWALAEVERLLWDMTRDLDGAQGAVAEAEAEAEAEAEAEAEAE 2274
Dd 2297 TGHGLANASAPSGEQLRTLAEVERLLWEMRRARDLGAPOAAAEAEAEAEAEAEAEAEAE 2356
QY 2275 LTSFWEENQSLATHIRDQLAQYESGLMDLREALNQAVNTTREAEEELNSRNQERVKEALQW 2334
Dd 2357 LSSLWEENQALATQTRDLRAQHEAGLMDLREALNRAVDATREAQELNSRNQERLEELQOR 2416
QY 2335 KQELSDNATLKATIQAASLILGHVSELIQCIDQAKEDLEHLAASLDGAWTPLLKRMQAF 2394
Dd 2417 KQELSRDNATLQATLHAARDTLASVFRLLHSLDQAKEELERLAASLDGARTPLLQRMQTF 2476
QY 2395 SPASSKVDLVEAAEAHAQKLNQLAINLSGILGINQDRFIQRAVEASNAYSILQAVQAA 2454
Dd 2477 SPAGSKLRLVEAAEAHAQQLGQLALNLSSILDVNQDRLLTQRAIEASNAYSRILQAVQAA 2536
QY 2455 EDAAGQALRQASRTWEMVVRGLAAGARQLLANSSALEETILGHQGRIGLAQGRLOAAGI 2514
Dd 2537 EDAAGQALQQADHTWATVVRQGLVDRQQQLLANSTALEEAMLQEQORLGLVWAAALQGART 2596
QY 2515 QLHNWARKNQALAAQIEAQAMAMTDSETSEKIAHAKAVAAEALSTATHVQSLOQMOK 2574
Dd 2597 QLQDVRAKQDQLEAHTQAAQAMAMTDSETSEKIAHAKAVAAEAOQDTRVQSLOQAMQE 2656
QY 2575 NVWRWQSLGGLOQDLSQVERDASSSVSTLEKTLPLQLAKLSRLENRGVHNASLALSAN 2634

Db 2657 NVERWQGYEGLRGQDLGQAVLDAGHSVSTLEKTLPLLAKLSILENRGVHNASLAS 2716

QY 2635 IGRVRKLIQAARSASKVKVSMKFNKNGRSGVRLRPPRDLADLAAYTALKPHIQSPVPAPEP 2694

Db 2717 IGRVRELIAQARGAASKVKVPMKFNKNGRSGVQLRTPRDLADLAAYTALKFYLQG--PEPEP 2774

QY 2695 GKNTGDHFVLYMGSRQATGDMGVSLRNQKVHWYRLGKAGPTTSLIDENIGEQAFAAVSI 2754

Db 2775 GQGTEDRFVVMYMGSRQATGDMGVSLRDKKVHWYQLGEAGPAVLSDIDEDGEQAFAAVSL 2834

QY 2755 DRTLQFGHMSVTVEKQMVHEIKGDTVAPGSEGLNLNLPDDDFVYVGGVPSNFTPPPELRF 2814

Db 2835 DRTLQFGHMSVTVERQMIQETKGDTPAPGAEGLLNLRPDDDFVYVGGVPSFTTPPLLR 2894

QY 2815 PGYLGCIEMETLNEEVVSLYNFEQTFMLDTAVDKPCARSKATGDPWLTGDSYLDGSGFAR 2874

Db 2895 PGYRGCIEMDTLNEEVVSLYNFERTFQDLDTAVDRPCARSKSTGDPWLTGDSYLDGTFAR 2954

QY 2875 ISPEKQFSNTKRFQDLRLVSYNGIIFFLKQESQFLCLAVQEGTLVLFDFGSLKKADP 2934

Db 2955 ISFDSQISTTKRFEQELRLVSYSGVLFFLKQSQSFLCLAVQEGSLVLLYDFGAGLKKAVP 3014

QY 2935 LQPPQALTAASKAIQVFLLAGNRKRVLRVERATVFSVDQDNMLEMADAYILGCVPEQL 2994

Db 3015 LQPPPLTSASKAIQVFLGGSRKRVLRVERATVYSVEQDNLDLEADAYILGCVPPDQL 3074

QY 2995 PLSLRQLFPSSGSGVRCIGIKIKALGKYVDLKRNTTGISFGCTADLLVGRMTTFHGHGFL 3054

Db 3075 PPSLRRLFTGGSVRCIGIKIKALGKYVDLKRNTTGVSACTADLLVGRAMTFHGHGFL 3134

QY 3055 PLALPDVAPITEVVYSGFGRGTQDNLLYRTSPDGPYQVSLREGHVTLRFMNOEVETQ 3114

Db 3135 RLALSNVAPLTGNVYSGFGFHSAQDSALLYIRASPDGLCQVLSQQGRVSLQLLRTEVKTQ 3194

QY 3115 RVFADGAPHYVAFYSNVGTGVMLYVDDQLQLVKSHERTTQMLQLQPEESRLLGLPVSG 3174

Db 3195 AGFADGAPHYVAFYSNATGVMLYVDDQLQMKPHRGPPELQPEGPPRLLLGLPESG 3254

QY 3175 TPFNFSGCISNVFQRLRGPQRVFDLHQNMGSVNVSVGCTPAQLIETS-----RATAQ 3227

Db 3255 TIYFNSGICISNVFQRLRGPQRVFDLQNLGSVNVSTGCAPALQATPGLGPRGLQATAR 3314

QY 3228 KVSRRSRQPSQDLACTPWLPGTIQDAYQFGGPLPSYLFQVFGISPSHRNRLHLSMLVRPH 3287

Db 3315 KASRRSRQPARHPACMLPPLRLTRDSYQFGGSLSSHLEFVGILARHRNWPFLSMHVLPR 3374

QY 3288 AASQGLLLSTAPMSGRSPSLVFLFNHGHFVAQTEGPGPRLQVQSRQHSRAGQWHRVSVRW 3347

Db 3375 -SSRGLLLFTARLRPGSPSLALFLSNHGFVAQMEGLTRLRAQSRQSRPGRWHKVSVRW 3433

QY 3348 GMQIQILVVDGQTSQKALHHRVPRAERPQPYTLVSGGLPASSYSSKLPVSVGFSGLK 3407

Db 3434 EKNRILLVTDGARAWSQEGPHRQHQAEPHQPHTLVFGGLPASSHSSKLPVTVGFSGCVK 3493

QY 3408 KLQLDKQPLRTPQTQMVGVTPCVSGPLEDGLFFPGSEGVVTLPLPKAMPVYVLSLEMRPL 3467

Db 3494 RLRLHGRPLGAPTRMAGVTPCILGPLEAGLFFPGSGGVITLDLPGATLPDVGLELEVRPL 3553

QY 3468 AAAGLIFHLGOALATPYMQLKVLTEQVLLQANDGAGEFSTWVTYPK-LCDGRWHRVAVIM 3526

Db 3554 AVTGLIFHLGOARTPPYIQLQVTEKQVLLRADGAGEFSTVTRPSVLCDGQWHLAVMK 3613

QY 3527 GRDTLRLEVDTSQNHHTGRLPESLAGSPALLHLGSLPKSSTARPELPAVRCGLRKLING 3586

Db 3614 SGNVLRLEVDAQSNHTVGPLAAAGAPAPLYLGLPEPMAVQPPWPPAYCGCMRRLAVNR 3673

QY 3587 APVNVTVASQIQGAVGMGECPS 3608

Db 3674 SPVAMTRSVVEVHGAVGASGCPA 3695

RESULT 7

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; GENERAL INFORMATION:

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; APPLICANT: Yang, Yonghong

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; TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and

; TITLE OF INVENTION: Secreted Polypeptides

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; CURRENT APPLICATION NUMBER: US/10/112,944

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; SOFTWARE: pt_FL_genes Version 5.0

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; LENGTH: 3690

; TYPE: PRT

; ORGANISM: Homo sapiens

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Query Match 79.6%; Score 15819.5; DB 12; Length 3690;

Best Local Similarity 79.4%; Pred. No. 0;

Matches 2870; Conservative 279; Mismatches 454; Indels 13; Gaps 8;

QY 1 DLYCKLVGGPVAGDPNQITQGOYCDICTAANSNKAHPVSNADIGTERWWQSPPLSRGLE 60

Db 79 DLYCKLVGGPVAGDPNQITRGOYCDICTAANSNKAHPASNAIDIGTERWWQSPPLSRGLE 138

QY 61 YNEVNTLDLGQVFHVAYVLIKFNANSPRDLWLVERSTDFGHTYQPWQFFASSKRDCLER 120

Db 139 YNEVNTLDLGQVFHVAYVLIKFNANSPRDLWLVERSMDFGRTYQPWQFFASSKRDCLER 198

QY 121 FGPRTLERITQDDDDVICTTEYSRIVPLENGEIVVSLVNGRPGALNFSYSPLLRDTKATN 180

Db 199 FGPQTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRPGAMNFSYSPLLRDTKATN 258

QY 181 IRLRFLRTNTLLGLHMGKALRDPVTVTRRYYYSIKDISIGGRVCVCHGHADVCDAKDPDPF 240

Db 259 VRLRFLRTNTLLGLHMGKALRDPVTVTRRYYYSIKDISIGGRVCVCHGHADACDAKDPDPF 318

QY 241 RLQACQHNTCGGSCDRCCPGFNQPKPATTDSANECQSCNCHGHAYDCYYDPEVDRRN 300

Db 319 RLQCTCQHNTCGGTCDCRCPGFNQPKPATANSANECQSCNCHGHATDCYYDPEVDRRR 378

QY 301 ASQNDNVYQGGGVCLDCQHTTGTINCERCLPGFPRAPDQLDSPHVCRCPCESDFTDG 360

Db 379 ASQSLDGTYYQGGGVCLDCQHTTGTINCERCLPGFVRSNPHLDSPHVRCRCNCESDFTDG 438

QY 361 TCBDLTGRCYCRPNFTGELCAACAEGYTDFPHCYPLPFPFHNDTREQVLPAGIIVNCDN 420

Db 439 TCEDLTGRCYCRPNFSGERCDVCAEGFTGFSPCYTPS-SSNDTREQVLPAGQIVNCDCS 497
QY 421 AAGTQGNACKRDPRLGRCVCKNFRGAHCELCAPEGHGPSCHPCQCSSPGVANSLCDPES 480
Db 498 AAGTQGNACKRDPRLGRCVCKNFRGAHCELCAPEGHGPSCHPCQCSSPGVANSLCDPES 557
QY 481 GQCMCRTEGEGDRCDHCAFGYFHPPLCQCGCSPAGTLPPEGDEAGRCQCRPGFDPGPHCD 540
Db 558 GQCRCRVGEFATCDRCAPGYFHPPLCQCGCSPAGTLPPEGDEAGRCQCRPGFDPGPHCD 617
QY 541 RCLPGYHGVDPDCHACADPRGALDQCCGVGLCHCRPGNTGATCOECSPGFYGFPPSCIPC 600
Db 618 RCRPGYHGVDPDCHACADPRGALDQCCGVGLCHCRPGNTGATCOECSPGFYGFPPSCIPC 677
QY 601 HCSADGSLHTTCDPTTGQCRRCRPRVTGLHCDMCPVPGAYNFPYCEAGSCHPAGLAPANPAL 660
Db 678 HCSAEGSLHAACDPRSGQCSRPRVTGLRCDTCVPGAYNFPYCEAGSCHPAGLAPVDPAL 737
QY 661 PETQAPCMRAHVEGSPCDRCCKPGYVWGLSASNPEGCTRCSCDPRGTGLGVTECO-GNGQC 719
Db 738 PEAQVPCMRHVEGSPCDRCCKPGYVWGLSASNPEGCTRCSCDPRGTGLGVTECO-GNGQC 797
QY 720 FCKAHVCGKTAACAKDGFGLDYADYFGCRSCRCDVGGALGQCEPKTGACRCRPNTOGP 779
Db 798 FCKPHVCGQACASCKDGFGLDQADYFGCRSCRCDIGGALGQCEPKTGACRCRPNTOGP 857
QY 780 TCSEPAKHVLPDLHLMRLLEEEAATPEGHAVRFGFNPLEFENFWSRWGYAHMAIQRIIV 839
Db 858 TCSEPARDHVLPDLHLMRLLEEEAATPEGHAVRFGFNPLEFENFWSRWGYAHMAIQRIIV 917
QY 840 ARNLNVTSPDLFRLVFRYVNRGTSVNGQISVREBGLSSCTNCTEQQSQOPVAFPPSTEPAF 899
Db 918 ARNLNVTSPDLFRLVFRYVNRGTSVNGQISVREBGLSSCTNCTEQQSQOPVAFPPSTEPAF 977
QY 900 VTVPQRGFGEPFVLPNGIALLVEAEGVLLDYVLLPSTYYEALLQHRVTEACTYRPSA 959
Db 978 ITVPQRGFGEPFVLPNGIALLVEAEGVLLDYVLLPSTYYEALLQHRVTEACTYRPSA 1037
QY 960 LHSTENCLVYAHLPDGFPSAAGTEALCRHDSNLPRLPCPTQELSPSHPPPLATCFGSDVDI 1019
Db 1038 QQSGDNCLLYTHLPDGFPSAAGTEALCRHDSNLPRLPCPTQELSPSHPPPLATCFGSDVDI 1097
QY 1020 QLEMAVPPQGVYVLYVEYVEDSHQEMGVAVHTPQAPQGVNLHPCPYSSLCRSPARD 1079
Db 1098 QLVAVPPQGVYVLYVEYVEDSHQEMGVAVHTPQAPQGVNLHPCPYSSLCRSPARD 1157
QY 1080 TOHHLAIFHLDSSEIRLTAEQAHFFLHSHVTLVPVEEFSTEFVEPRVFCVSSHGFENPSS 1139
Db 1158 TQDHLAVFHLDSSEIRLTAEQAHFFLHSHVTLVPVEEFSTEFVEPRVFCVSSHGFENPSS 1217
QY 1140 AACLASFPPKPPQIILKDCQVLPPLDPLTQSQELSPGAPPEGPQRPPTAVDPNAEP 1199
Db 1218 AACLSPFPKPPQIILKDCQVLPPLDPLTQSQELSPGAPPEGPQRPPTAVDPNAEP 1277
QY 1200 TLLRHPQGTVFTTQVTLGRYAFLLHGYQVHPSPFPVEVLINGGRWQHGHANASFCPHG 1259
Db 1278 TLLRHPQGTVFTTQVTLGRYAFLLHGYQVHPSPFPVEVLINGGRWQHGHANASFCPHG 1337
QY 1260 YGCRTLVLCGQTMLDVTDNELTIVTVRVPGRWLDYVLIVPEDAYSSSYLQEEPLDKS 1319
Db 1338 YGCRTLVLCGQTMLDVTDNELTIVTVRVPGRWLDYVLIVPEDAYSSSYLQEEPLDKS 1397
QY 1320 YDFISHCATQGYHISPSSSSPFCRNAATSLSPYNNALPCGCHEVGAVSPTCEPFGGQC 1379
Db 1398 YDFISHCATQGYHISPSSSSPFCRNAATSLSPYNNALPCGCHEVGAVSPTCEPFGGQC 1457
QY 1380 PCRGHVIGRDCSRCATGYWGFPPNCRPCDGCARLDELGTQCICPPRTVPPDCLVCQPQSF 1439
Db 1458 PCRGHVIGRDCSRCATGYWGFPPNCRPCDGCARLDELGTQCICPPRTVPPDCLVCQPQSF 1517
QY 1440 GCHPLVGCCECNCSGPGVQELTDPDTCMDMSGQCRCPNVAGRRCDTCAPGYGYPSCRPC 1499

Db 1518 GCHPLVGCCECNCSGPGIQLTDPDTCMDMSGQCKRPNVTGRRCDTCSPGFHGYPRCRPC 1577
QY 1500 DCHEAGTMASVCDPLTGQCHCKENVOGSRCDQCRVGTGTFSLDAANPKGCTRCFCFGATERC 1559
Db 1578 DCHEAGTMASVCDPLTGQCHCKENVOGSRCDQCRVGTGTFSLDAANPKGCTRCFCFGATERC 1637
QY 1560 GNSNLARHEFVDMEGWVLLSSDRQVVPHEHRPEIELLHADLR---SVADTFSELYWQAP 1615
Db 1638 RSSSYTRQEFVDMEGWVLLSSDRQVVPHEHRPEIELLHADLR---SVADTFSELYWQAP 1697
QY 1616 PSYLGDRVSSYGGTLLHYELHSETQGRDIFIPYESRPDPVVLQGNQMSIAFLELAYPPPGQV 1675
Db 1698 PSYLGDRVSSYGGTLLHYELHSETQGRDIFIPYESRPDPVVLQGNQMSIAFLELAYPPPGQV 1757
QY 1676 HRGQLQVVEGNFRHLETHNVPVSREELMMVLAGLEQLQIRALFSQTSSSSVSLRRVLEVAS 1735
Db 1758 HRGQLQVVEGNFRHLETHNVPVSREELMMVLAGLEQLQIRALFSQTSSSSVSLRRVLEVAS 1817
QY 1736 EAGRGPPASNVELCMCPANYRGDSQCECAPGYRDTKGLFLGRCPVPCQCHGSHDRCLPGS 1795
Db 1818 PAGQALASNVELCLCPASYRGDSQCECAPGYRDTKGLFLGRCPVPCQCHGSHDRCLPGS 1877
QY 1796 GICVGCQHNTGEGDQCCRCRPGFVSSDPSPNPASPCVSCPCPLAVPSNNFADGCVLRNGRTQ 1855
Db 1878 GVCVDCQHNTGEGDQCCRCRPGFVSSDPSPNPASPCVSCPCPLAVPSNNFADGCVLRNGRTQ 1936
QY 1856 CLCRPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSNGNDPNNMFSDCDPLTGACRGCLR 1915
Db 1937 CLCRPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSNGNDPNNMFSDCDPLTGACRGCLR 1996
QY 1916 HTTGPHCERCAPGYGNALLPGNCTRCDCSPCGTETCDPQSGRCLCKAGVTGQRCDCRCL 1975
Db 1997 HTTGPHCERCAPGYGNALLPGNCTRCDCSPCGTETCDPQSGRCLCKAGVTGQRCDCRCL 2056
QY 1976 GYFGFEQCCGCRPCACGPAAGSECHPSQSGQCHCQPGTTGPPQCLECAPGYWGLPEKGCR 2035
Db 2057 GHFGDGGCGCRPCACGPAAGSECHPSQSGQCHCQPGTTGPPQCLECAPGYWGLPEKGCR 2116
QY 2036 CQCPRGHCDPHTGHTCPTPGLSGERCDCSCQHQHVVPVPGKPGHGHICEVCDHCVVLLLD 2095
Db 2117 CQCPRGHCDPHTGHTCPTPGLSGERCDCSCQHQHVVPVPGKPGHGHICEVCDHCVVLLLD 2176
QY 2096 DLERAGALLPAIREQLQGINASSAAWARIHLRNASIALDQSKLRRPPGPRYQAQLOTL 2155
Db 2177 DLERAGALLPAIREQLQGINASSAAWARIHLRNASIALDQSKLRRPPGPRYQAQLOTL 2236
QY 2156 EQQSISLQDTERIGSQATGVQAGQLDTESTLGRAQKLLSVRAVGRALNELASRM 2215
Db 2237 EQQSISLQDTERIGSQATGVQAGQLDTESTLGRAQKLLSVRAVGRALNELASRM 2296
QY 2216 GQSGPGDALVPSGQLRWALAEVERLLWNRTRDLGAQGAFAEAEAEAEAEAEAEAEAEAEAE 2275
Db 2297 GQSGPGDALVPSGQLRWALAEVERLLWNRTRDLGAQGAFAEAEAEAEAEAEAEAEAEAEAE 2356
QY 2276 TSFWEENQSLATHIRDQLAQYESGLMDLREALNQAVNTTREAEEELNSNRNQERVKEALQWK 2335
Db 2357 TSFWEENQSLATHIRDQLAQYESGLMDLREALNQAVNTTREAEEELNSNRNQERVKEALQWK 2416
QY 2336 QELSODNATLKATLQAAASLIIGHVSELLQGIQDQAKEDLEHLAASLDGAWTPLLKRMQAFS 2395
Db 2417 QELSODNATLKATLQAAASLIIGHVSELLQGIQDQAKEDLEHLAASLDGAWTPLLKRMQAFS 2476
QY 2396 PASSKVDLVEAAEAHAQKLNQLAINLSGIILGINQDRFIQRAVEASNAYSSILQAVQAAE 2455
Db 2477 PASSKVDLVEAAEAHAQKLNQLAINLSGIILGINQDRFIQRAVEASNAYSSILQAVQAAE 2536
QY 2456 DAAGQALROASRTWEMVVRGLAAGARQILLANSALLETILGHQRLGLAQGLQAAGIQ 2515
Db 2537 DAAGQALROASRTWEMVVRGLAAGARQILLANSALLETILGHQRLGLAQGLQAAGIQ 2596
QY 2516 LHNVWARKNQLAAQIQEAAQAMLMDTSETSEKIAHAKAVAAEALSTATHVQSOLQGMQKN 2575
Db 2597 LHNVWARKNQLAAQIQEAAQAMLMDTSETSEKIAHAKAVAAEALSTATHVQSOLQGMQKN 2656

QY 2576 VERWQSLGGLQGDLSQVERDASSVSTLEKTLPLLAKLSRLNRRGVHNASIALSANI 2635
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 2657 VERWQSQYEGLRGQDLGQAVLDAGHSVSTLEKTLPLLAKLSILNRRGVHNASIALSASI 2716
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 2636 GRVRKLIQAARSAASKVKVSMKFNKGRSGVRLRPPRDLADLAAYTALKFHIQSPVPAPEPG 2695
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 2717 GRVRELIAQARGAASKVKVPMKFNKGRSGVQLRTPRDLADLAAYTALKFYLG--PEPEPG 2774
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 2696 KNTGDHFVLYMGSRQATGDYMGVSLRNQKVHWYRLGKAGTTLSDENIGEQFAAVID 2755
: | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 2775 QGTEDRFVYMGSRQATGDYMGVSLRDKKVHWYQLGEAGPAVLSIDEDIGEQAFAVSLD 2834
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 2756 RTLQFGHMSVTVEKQMVHEIKGDTVAPGSEGLNLHPDDFFVYGGYPSNFTPTPEPLRFP 2815
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 2835 RTLQFGHMSVTVERQMIQETKGDIVAPGAEGLLNLRPDDFFVYGGYPSFTPTPPPLRFP 2894
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 2816 GYLGCIENTLNEEVVSLYNFEQTFMLDTAVDKPCARSKATGDPWLTDGSLDGSFARI 2875
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 2895 GYRGCIEMDTLNEEVVSLYNFERTFQDPTAVDRPCARSKSTGDPWLTDGSLDGTGFARI 2954
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 2876 SFEKQFNTKRFQDELRLVSYNGIIFFLKQESQFLCLAVQECTLVLFYDFSGSLKKADPL 2935
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 2955 SFDSQISTTKRFEQELRLVSYSGVLFELKQSQFLCLAVQESLVLLYDFGAGLKKAVPL 3014
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 2936 OPPQALTAASKAIQVFLLAGNRKRLVVRVERATVFSVDQDNMLEMADAYLGGVPEQLP 2995
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 3015 QPPPLTSASKAIQVFLGGSRKRLVVRVERATVYSVEQDNLELADAYLGGVPPDQLP 3074
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 2996 LSLRQLFPSSGVRGCIKGIKALGKYVDLKLRLNTTGISFGCTADLLVGRMTFHHGFLP 3055
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 3075 PSLRRLFTGSGVRGCVKGIKALGKYVDLKLRLNTTGVSACTADLLVGRAMTFHHGFLR 3134
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 3056 LALPDVAPITEVTVYSGFGFRGTQDNNLLYRTSPDGPYQVSLREGHVTLRFMNQEVETQR 3115
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 3135 LALSNVAPLTGNVYSGFGFHSQAQDSALLYRASPDGLCQVSLQGRVSLQLLRTEVKTA 3194
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 3116 VFADGAPHYVAFYSNVTGWLYVDQQLVKSHERTTPMLQLOPEEPSRLLGLGLPVSGT 3175
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 3195 GFADGAPHYVAFYSNATGWLYVDQLOQMKPHRGPPPELQPEGPPRLLGLGLPVSGT 3254
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 3176 FHNFGCISNVFVQRLRGPQRVFDLHONMGSVNVSVGCTPAQLIETSRATAQ--KVSRRS 3233
: | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 3255 IYNFSGCISNVFVQRLRGPQRVFDLQNLGSVNVSTGCPALQAQTPGLPRGLQASRRS 3314
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 3234 RQPSQDLACTPWLPGTIQDAYQFGGELPSYLQFVGISPSHRNRLHLSMLVRPHAAOGL 3293
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 3315 RQPARHPACMLPPLHRTTRDSYQFGGSLSSHLEFVGILARHNWPSLSMHVLP--SRGL 3373
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 3294 LLSTAPMSGRSPSLVFLNHHGFVAQTEGPPRLQVQSRQHSRAGQWHRVSVRWGMQIQ 3353
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 3374 LLFTARLRPGSPSLALFLSNGHFVAQMEGLTRLRQSRQSRPPGRWHKVSVRWEXNRL 3433
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 3354 LVVDGSGQTSQKALHHRVPRAPERPQPYTLVSGGLPASSYSSKLPVSVGFGCLKKQLDK 3413
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 3434 LVTDGARAWSQEGPHRQHQAEHPQHTLVGGLPASSHSSKLPVTVGFGCVKRLRHG 3493
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 3414 QPLRTPQMGVTPCVSGPLEDGLFFPGSEGVVTLLELPKAKMPYVSLELEMRPLAAAGLI 3473
: | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 3494 RPLGAPTRNAGVTPCILGPLEAGLFFPGSGGVITLDPGATLDPVGLLEVRPLAVTGLI 3553
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 3474 FHLGOALATPYMQLKVLTEQVLLQANDGAGEFSTWVTPK--LCDGRWHRVAVIMGRDILR 3532
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 3554 FHLGOARTPPYLQLOVTEKQVLLRADDDGAGEFSTSVTRPSVLCDGQWHRRLAVMKSGNVLR 3613
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 3533 LEVDTSNHTTGRLLPESLAGSPALLHLGSLPKSSTARPELPAVRCGLRKLINGAPVNT 3592
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 3614 LEVDAQSNHTVGPLLAAAAGAPAPLYLGLPEPMAVQWPFPAYCGCMRRRLAVNRSVPVMT 3673
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 3593 ASVQIQGAVGMREGCPS 3608
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 3674 RSVEVHGAVGASGCPA 3689
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

RESULT 8
US-10-312-088-30
; Sequence 30, Application US/10312088
; Publication No. US20030219862A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Cogswell, John P.
; APPLICANT: Kabnic, Karen S.
; APPLICANT: Lai, Ying-Ta
; APPLICANT: Martensen, Shelby A.
; APPLICANT: Murdock, Paul R.
; APPLICANT: Smith, Randall F.
; APPLICANT: Strum, Jay C.
; APPLICANT: Xiang, Zhacaying
; APPLICANT: Xie, Qing
; APPLICANT: Rizni, Safia K.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50029
; CURRENT APPLICATION NUMBER: US/10/312,088
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/19929
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,161
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/213,156
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 3705
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-312-088-30

Query Match 79.6%; Score 15815; DB 15; Length 3705;
Best Local Similarity 79.1%; Pred. No. 0;
Matches 2873; Conservative 279; Mismatches 451; Indels 28; Gaps 9;

QY 1 DLYCKLVGGPVAGGDPNQTIQGYCDICTAANSNKAHPVSNALDGTERRWQSPPLSRGLE 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 79 DLYCKLVGGPVAGGDPNQTIQGYCDICTAANSNKAHPASNAIDGTERWQSPPLSRGLE 138
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 61 YNEVNVTLDLGOVHFVAYVLKIFANSRPDLWVLERSTDFGHTYQWQFFASSKRDCLER 120
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 139 YNEVNVTLDLGOVHFVAYVLKIFANSRPDLWVLESMDFGRTYQWQFFASSKRDCLER 198
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 121 FGPRTLERITQDDDVICTEYSRIVPLENGEIVWSLVNRPALNFSYSPLLRDTKATN 180
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 199 FGPQTLERITRDAACICTEYSRIVPLENGEIVWSLVNRPALNFSYSPLLRDTKATN 258
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 181 IRLRFLRNTLLGLHLMGKALRDPVTTRYYYSIKDISIGRCVCHGHADVCDAKPLDPF 240
: | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 259 VRLRFLRNTLLGLHLMGKALRDPVTTRYYYSIKDISIGRCVCHGHADVCDAKPLDPF 318
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 241 RLQACQHNCTCGSCDCRCCPGFNQCPWKPAATDSANECQSCNCHGHAYDCYDPEVDRRN 300
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 319 RLQCTCQHNCTCGTCDRCPCPGFNQCPWKPAATANSANECQSCNCHGHAYDCYDPEVDRRR 378
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 301 ASQNDNVYQGGSVCLDCQHTTGINCERCLPGFFRAPDQPLDSPHVCRCPCDCESDFTDG 360
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 379 ASQSLDGTYYQGGVCLDCQHTTGINCERCLPGFYRSPNHPDLSPHVCRRCNCESDFTDG 438
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 361 TCEDLTGRCYCPNFTGELCAACAEGYTDFFHCYPLPSFPHNDTREQVLPAGQIVNCDN 420
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 439 TCEDLTGRCYCRPNFSGERCDCVCAEGTFPSCYPTPS--SSNDTREQVLPAGQIVNCDN 497
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 421 AAGTQGNACRDKPRLGRVCVCKPNFRGAHCELCAFGHGPSCHPCQCSSPGVANSLCDPES 480
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 498 AAGTQGNACRDKPRLGRVCVCKPNFQGTCELCAFGFYGPGCQCCQCSSPGVADDRCDPDT 557
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 481 GQCMCRTGFEGDRCDHICALGYFHFPLCQLCGCSPAGTLPPEGCEAGRCQCRPGFDGPHCD 540
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

Db 558 GQCRVRVGFEGATCDRCAPGYFHFPLCOLCGCSPAGTLPPEGCD EAGRCLCQPEFAGPHCD 617

QY 541 RCLPGYHGYPDCHACACDPRGALDQQCGVGGGLCHCRPGNTGATCQECSPGYFGFPSCIPPC 600

Db 618 RCRPGYHGFPCNCACTCDPRGALDQLCGAGGLCRCPGYTGTAQCQECSPGFHGFPPSCVPC 677

QY 601 HCSADGSLHTTCDPTTGQCRRCRPRVTGLHCDMCPVGAYNFFPYCEAGSCHPAGLAPANPAL 660

Db 678 HCSAEGSLHAACDPRSGQCSRPRVTGLRCDTCVPGAYNFFPYCEAGSCHPAGLAPVDPAL 737

QY 661 PETQAPCMCRAHVEGPSCDRCCKPGYWGLSASNPEGCTRCSCDRPGTLGGVTECQ-GNGQC 719

Db 738 PEAQVPCMCRAHVEGPSCDRCCKPGFWGLSPNPEGCTRCSCDLRGTGLGVAECQPGTGQC 797

QY 720 FCKAHVCGKTAACKDGGFFGLDYADYFGCRSCRCVDGGALGQCGEPKTGACRCRPNTOGP 779

Db 798 FCKPHVCGQACASCKDGGFFGLDQADYFGCRSCRCDIGGALGQSCBPRGTGVCRCRPNTOGP 857

QY 780 TCSEPAKDHVLPDLHHRMLELEEAATPEGHAVRFGFNPLEFENFSWRGYAHMMAIQPRIV 839

Db 858 TCSEPARDHVLPDLHHLRLELEEAATPEGHAVRFGFNPLEFENFSWRGYAQMAPPVQPRIV 917

QY 840 ARLNVTSPDLFLVRYVNRGSTSVNGQISVREEGKLSCTNCTEQSQPVAFPPSTEPAPF 899

Db 918 ARLNLTSPDLFLVRYVNRGAMSVSGRVSVREEGRSATCANCATAQSQPVAFPPSTEPAPF 977

QY 900 VTVPORGFGEFVLPNGIALLVEAEGVLLDYVLLPSTYYEALLCHRVTEACTYRPSA 959

Db 978 ITVPORGFGEFVLPNGTVALRVEAEGVLLDYVLLPSAYYEALLQLRVTEACTYRPSA 1037

QY 960 LHSTENCLVYAHLELDGFPSSAAGTEALCRHNSLPRPCPTQOLSHPPLATCFGSDVDI 1019

Db 1038 QQSGDNCLLYTHLELDGFPSSAAGLEALCRQNSLPRPCPTQOLSHPPLITCTGSDVDV 1097

QY 1020 QLEMAVPOPGQYVLVVEYVEDSHQEMGVAVHTPQAPQOQVNLNHPCPYSSLCRSPARD 1079

Db 1098 QLOQAVPOPGRYALVVEYANEDARQEVGVAVHTPQAPQOGLLSLHPCLYSTLCRGITARD 1157

QY 1080 TOHHLAIFHLDSEASIRLTAEQAHFFLHSVTLVPVEEFSTEFVERVEFCVSSHGTENPSS 1139

Db 1158 TQDHLAVFHLDSSEASVRLTAEQARFFLHGVTLPVPIEEFSPFVEPRVSCISSHGAFGPN 1217

QY 1140 AACLASRFPKPPQPIILKDCQVLPPLPDLPLTQSQELSPGAPPEGPQPRPPTAVDPNAEP 1199

Db 1218 AACLPSRFPKPPQPIILRDCQVILPPLPGLPLTHAQDLTPAMSPAGPRPPTAVDPDAEP 1277

QY 1200 TLLRHPQGTVFTTQVPTLGRYAFLLHGYQPVHPSPPVEVLINGGRVWQHGHANASFCPHG 1259

Db 1278 TLLREPOATVFTTHVPTLGRYAFLLHGYQPAHPTFPVEVLINAGRVWQHGHANASFCPHG 1337

QY 1260 YGCRTLVLCGQTMLDVTDNELTVTVRVPEGRWLWDYVLIVPEDAYSSSYLQEEPLDKS 1319

Db 1338 YGCRTLVCEGQALLDVTHSELVTVRVPKGRWLWDYVLVVPENVYSFGYLREEPDKS 1397

QY 1320 YDFISHCATQGYHISPSSSSPFCRNAATSLSFYNNGALPCGCHVEGAVSPTCEPFGGQC 1379

Db 1398 YDFISHCAAQGYHISPSSSSLFCRNAASLSLFYNNGARPCGCHVEGATGPTCEPFGGQC 1457

QY 1380 PCRGHVIGRDCSRCATGYWGFPPNCRPCDCGARLDELGTQCICPPRTVPPDCLVCQPQSF 1439

Db 1458 PCHAHVIGRDCSRCATGYWGFPPNCRPCDCGARLDELGTQCICPPRTIPPDCLLCQPQTF 1517

QY 1440 GCHPLVGCEEENCSGPGVQBELTDPCTCDMDSGQCRCPNVAGRRCDTCAPGFYGYPSCRPC 1499

Db 1518 GCHPLVGCEEENCSGPGIQBELTDPCTDSDGQCRPNVTGRRCDTCSPGFHGYPRCRPC 1577

QY 1500 DCHAEAGTMASVCDPLTGQCHCKENVQSRCDQCRVGTFFSLDAANPKGCTRCFCFGATERC 1559

Db 1578 DCHAEAGTAPGVCDPLTGQCYCKENVQPKDCQSLGTFFSLDAANPKGCTRCFCFGATERC 1637

QY 1560 GNSNLARHEFVDMEGWVLLSSDRQVWPHEHRPETELLHADLR---SVADTFSELYWQAP 1615

Db 1638 RSSSYTRQEFVDMEGWVLLSTDQVWPHERQPGTEMLRADLRHVPEAVPEAFPELYWQAP 1697

QY 1616 PSYLGDRVSSYGGTLYHELHSETQRGDIFIPYESRDPVVLOGNQMSIAFLELAYPPPGQV 1675

Db 1698 PSYLGDRVSSYGGTLYHELHSETQRGDVFPVPMESRDPVVLOGNQMSITFLEPAYPTPGHV 1757

QY 1676 HRGQLQLVEGNFRHLETHNPVSREELMMVLAGLEQLQIRALFSQTSSSVSLRRVVLEVAS 1735

Db 1758 HRGQLQLVEGNFRHTETRTNTVSREELMMVLASLEQLQIRALFSQISSAVFLRRVALEVAS 1817

QY 1736 EAGRPPASNVELCMCPANYRGDSQCECAPGYRYDTKGLFLGRVCPCQCHGSHDRCLPGS 1795

Db 1818 PAQOGALASNVELCLCPASYRGDSQCECAPGFYRDVKGLFLGRVCPCQCHGSHDRCLPGS 1877

QY 1796 GICVGCQHNTGEOCERCPRPGFVSSDPSPNPASPCVSCPCPLAVPSNNFADGCVLRNGRTQ 1855

Db 1878 GVCVDCQHNTGAEHCERCQAGFVSS-RDPSAPCVSCPCPLSPVSPNNFAEGCVLRGGRTQ 1936

QY 1856 CLCRPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSNGNDPNMIFSDCDPLTGACRGCLR 1915

Db 1937 CLCRPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSNGNDPNLFSDDCDPLTGACRGCLR 1996

QY 1916 HTTGPHCERCAPGYGNALLPGNCTRCDCSPCGTETCDPQSGRCCLCKAGVTGQRCDCRCL 1975

Db 1997 HTTGPRCEICAPGYGNALLPGNCTRCDCTPCGTEACDPHSGHCLCKAGVTGRRCDRCQE 2056

QY 1976 GYFGPEQQCGCRPCACGPAKGSCHPQSGQCHCQPGTTGPPQCCECAPGYWGLPEKGCRR 2035

Db 2057 GHFGDGGCGCRPCACGPAAGSECHPQSGQCHCRPGTGMGPQCRECAPGYWGLPEQGCRR 2116

QY 2036 CQCPRGHCDPHGHTCTCPPGLSGERCDCSCQHQVVPVPGKPGGHGTHCEVCDHCVVLLLD 2095

Db 2117 CQCPRGCRDPTHGRCNCPPGLSGERCDCSCQHQVVPVPGGPGVHSHCEVCDHCVVLLLD 2176

QY 2096 DLERAGALLPAIREQLOGINASSAAWALHRLNASIADLQSKLRPPGPPRYQAAQOQLTL 2155

Db 2177 DLERAGALLPAIHEQLRGINASSMAWALHRLNASIADLQSKLRSPGLPRHETAQOQLEVL 2236

QY 2156 EQQSISLQQDTERLGSQATGVQ-----QAGQLDTESTILGRAQKLLSVRAVG 2205

Db 2237 EQQSTSLGQDARRLGGQAGAPRPPRAPGCGFHLIYQASQLLAGTEATLGHAKTLLAAIRA 2296

QY 2206 RALNELASRMGQSGPDALVPSGEQLRWALAEVERLLWDMRTRDLGAQGAVAEAEALAEQ 2265

Db 2297 RTLSELSMQTHGLGLANASAPSGEQLRTLAEVERLLWEMRARDLGAPOAAAEEALAAQ 2356

QY 2266 RLMARVQEQLTSFWEENQSLATHIRDQLAQYESGLMDLREALNOAVNTTREAEBELNSRNQ 2325

Db 2357 RLLARVQEQLSSLWEENQALATQTRDLAQHEAGLMDLREALNRAVDATREAQELNSRNQ 2416

QY 2326 ERVKEALQWKQELSODNATLKATLQAASLILGHVSELQIGIDQAKEDLEHLAASLDGAWT 2385

Db 2417 ERLEEALQRKQELSRDNATLQATLHAARDTLASVFRLLHSLDQAKEELERLAAASLDGART 2476

QY 2386 PLLKRMQAFSPASSKVDLVEAAEAHAQKLNQLAINLSGIIILGINQDRFIQRAVEASNAYS 2445

Db 2477 PLLQRMQTFSPAGSKLRLVEAAEAHAQQLGQALNLSIIILDVNQDRLTQRAIEASNAYS 2536

QY 2446 SILQAVQAAEDAAGQALRQASRTWEMVVQGLAAGARQLLANSSALEETILGHQGRGLA 2505

Db 2537 RILQAVQAAEDAAGQALQQADHTWATVVRQGLVDRAQQLLANSTALEEAMLQEQQRGLV 2596

QY 2506 QGRLOAAGIQLHNVMARKNQLAAQIQEAQAMLAMDTSETSEKIAHAKAVAAEALSTATHV 2565

Db 2597 WAALQAGARTQLRDVRAKDKQLEAHIQAAQAMLAMDTDETSKIAHAKAVAAEAQDTATRV 2656

QY 2566 QSOLQGMQKNVERWQSLGGLQGDLSQVERDASSSVSTLEKTLPLQILAKLSRLENRGVH 2625

Db 2657 QSOLQAMQENVERWQGYEGLRGQDLGQAVLDAGHSVSTLEKTLPLQILAKLSILENRGVH 2716

QY 2626 NASIALSANIGRVRKLIQAARSAASKVKVSMKFNGRSGVRLRPPRDLADLAAYTALKFHI 2685

Db 2717 NASIALSASIGRVRRELIAQARGAASKVKVPMKFNGRSGVQLRTPRDLADLAAYTALKFYL 2776

Qy 2686 QSPVPAPEPGKNTGDHFLVLMGSRQATGDMGVSLRNQKVHVYRLGKAGPTTISIDENI 2745
Db 2777 QG--PEPEPGQGTEDRFVVMGSRQATGDMGVSLRDKKVHVYQLGEAGPAVLSIDEDI 2834
Qy 2746 GEQFAAVSIDRTLQFGHMSVTVVEKQMVHEIKGDTVAPSGEGLNLNHPDDFVFYVGGYPSN 2805
Db 2835 GEQFAAVSLDRTLQFGHMSVTVVERQMIQETKGDTVAFGAEGLLNLRPDDFVFYVGGYPST 2894
Qy 2806 FTPEPLRPPGYLGCIEMETLNEEVVSLYNFEQTFMLDTAVDKPCARSKATGDPWLTDGS 2865
Db 2895 FTPEPLRPPGYRGCIEMDTLNEEVVSLYNFERTFQLDTAVDRPCARSKSTGDPWLTDGS 2954
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Db 2955 YLDGTFARISFDSQISTTKRFEQELRLVSYSGVFLFKQQSQFLCLAVQEGSLVLLYDF 3014
Qy 2926 GSGLKKADPLQPPQALTAASKAIQVFLLAGNRKRVLRVERATVFSVDQDNMLEMADAYY 2985
Db 3015 GAGLKAAPLQPPPLTSASKAIQVFLLAGNRKRVLRVERATVFSVEQDNMLEMADAYY 3074
Qy 2986 LGVPEPEQLPLSLRQLFPSPGSGVRGCIKIGIKALGYVDLKRLLNTTGISFGCTADLLVGR 3045
Db 3075 LGVPPDQLPPSLRRLFPPTGSGVRGCVKIGIKALGYVDLKRLLNTTGVSAGCTADLLVGR 3134
Qy 3046 MTFHGGFLPLALPDVAPITEVYVSGFGFRGTQDNLLYRTSPDGPYQVSLRREGHVTLR 3105
Db 3135 MTFHGGFLRLALSNAVPLTGNVYSGFGFHSQAQDSALLYRASPDGLCQVSLQGRVSLQ 3194
Qy 3106 FMNQEVETQRFADGAPHYVAFYSNVTVWLVYDDQLQVKSHERTTTLMQLQPEEPSRL 3165
Db 3195 LLRTEVKTQAGFADGAPHYVAFYSNATGVWLVYDDQLQVKSHERTTTLMQLQPEEPSRL 3254
Qy 3166 LLGGIPVSGTFHNFSGCISNVFQRLRGPQRVFDLHQMGSVNVSVGCTPAQLIETS-- 3222
Db 3255 LLGGIPESGTIYNFSGCISNVFQRLRGPQRVFDLHQMGSVNVSVGCTPAQLIETS-- 3314
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Db 3315 PRGLQATARKASRRSRQPARHPACMLPPHLRTTRDSYQFGGSLSSHLEFVGLARHNWP 3374
Qy 3279 HLSMLVRPAAASQGLLLSTAPMSGRSPSLVLFLNHGHFVAQTEGPGPRQLVQSRQHSRAG 3338
Db 3375 SLSMHVLP--SSRGLLLFTARLRPGSPSLALFLSNGHFVAQMEGLGTRLRQSRQSRPG 3433
Qy 3339 QWHRVSVRWGMQIQLVVDGSGTWSQKALHHRVPRARPPQPYTLVSGGLPASSYSSKLPV 3398
Db 3434 RWHKVSVRWEKNRILLVTDGARAWSQEGPHRQHQGAHPQPHTLFVGGGLPASSHSSKLPV 3493
Qy 3399 SVGFSGCLKQLQDKQPLRPTQMVGVTVCVSGPLEDGLFFPGSEGVVTLLELPKAKMPYV 3458
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Qy 3459 SLELEMRPLAAAGLIFHLGOALATPYMQLKVLTEQVLLQANDGAGEFSTWVTPK-LCDG 3517
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Qy 3518 RWHRVAVIMGRDTRLREVDQSNHTTGRLPESLAGSPALLHLGSLPKSSTARPELPAYRG 3577
Db 3614 QWRLAVMKSGNVLRLEVDQSNHTVGPLLAAAGAPAPLYLGGLPERPMAVQPPWPAYCG 3673
Qy 3578 CLRKLLINGAPNVNTASVQIQGAVGMRGCP 3608
Db 3674 CMERLAVNRSPVAMTRSVVEHGAVGASGCPA 3704

RESULT 9
US-10-037-417-2
; Sequence 2, Application US/10037417
; Publication No. US20040052806A1
; GENERAL INFORMATION:
; APPLICANT: Kexuda, Ramesh
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T

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; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Eisen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/10/037,417
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
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; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 3600
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-037-417-2

Query Match 74.3%; Score 14771; DB 12; Length 3600;
Best Local Similarity 74.8%; Pred. No. 0;
Matches 2739; Conservative 275; Mismatches 472; Indels 178; Gaps 26;

QY 1 DLYCKLVGGPVAGGDPNQTIQGOYCDICTAANSNKAHPVSNADGTERWQSPPLSRGLE 60
Db 58 DLYCKLVGGPVAGGDPNQTIQGOYCDICTAANSNKAHPASNAIDGTERWQSPPLSRGLE 117
QY 61 YNEVNTLDLGQVHFVAYVLIKFPANSRPDLWVLERSTDFGHTYQPWQFFASSKRDCLER 120
Db 118 YNEVNTLDLGQVHFVAYVLIKFPANSRPDLWVLERSMDFGRTYQPWQFFAASKRDCLER 177
QY 121 FGPRTLERITQDDVICITTEYSRIVPLENGEIVVSLVNGRPGALNFSYSPLLRDFTKATN 180
Db 178 FGPQTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRPGAMNFSYSPLLREFTKATN 237
QY 181 IRLRFLRTNTLLGHLMGKALRDPPTVTRRRYYYSIKDISIGRCVCHGADVCDKADLPDPF 240
Db 238 VRLRFLRTNTLLGHLMGKALRDPPTVTRRRYYYSIKDISIGRCVCHGADACDAKADPTDPF 297

QY	241	RLQACQHTTCGGSCDRCCPGFNQOPWKPATTDSANECQSCNCHGAYDCYDPEVDRN	300
Db	298	RLQCTQHNTCGGTCDRCPCPGFNQOPWKPATANSANECQ-CECYGHATDCYDPEVDRR	356
QY	301	ASQNDNVYQGGVCLDCQHHTTGINCERCLPGFFRAPDQPLDSPHVCRCDCESDFTDG	360
Db	357	ASQSLDGTQGGGVCLDCQHHTTGINCERCLPGFYRSPNHPDPSHVCRGCNCESDFTDG	416
QY	361	TCEDLTGRCYCRPNFTGELCAACAEGYTDFFPHCYPLSPFPHNDTREQVLPAGQIVNCDCN	420
Db	417	TCEDLTGRCYCRPNFSGERCDCVCAEGFTGPPSCY-REHLPNGNDTREQVLPAGQIVSCDCS	475
QY	421	AAGTQGNACRKDPRLGRCVCKPNFRGAHCALCAPGHGSPCHPCQCSS---PGVANSLCD	477
Db	476	AAGTQGNACRKDPVRGRLCKPNFQTHCELCAPGFYGPC-PASVPALWPMATAVTLTQ	534
QY	478	PESGQCMCRGT-----FEGDRCDHCALGYFHFPL-CQLCGGSPAGTLPPEGCDEAG	526
Db	535	ASAGAENASRGPHVIAVPPATFTLSASH-----PLRSAVCGGSPAGTLPPEGCDEAG	586
QY	527	RCQCRPGFDPHCDRCLPGYHGYPDCHACADPRGALDQOCGVGGGLCHCRPGNTGATCQE	586
Db	587	RCLCOPEFAGPHCDRCRPGYHGFNCACTCDPRGALDQLCGAGGLCERCPGYTGATCQE	646
QY	587	CSPGFYGFPSICIPCHCSADGSLHTTC-----DPTTGQCRCP-RVTGL-H-CDMCVPGAYN	639
Db	647	CSPGFHGFPS-----CPATALLKAPCTQPTVPGVSAAGPVRGCGVTHVCPVPTTSPTA	701
QY	640	FPYCEAGSCHPAGLAPANPALPETQAPCMCRAHVEGSPCDRCCKPGYWGLSASNPEGCTRC	699
Db	702	KPLFTAGSCHPAGLAPVDPALPEVSPPCMCAHVEGSPCDRCCKPGFWGLSNPEGCTRC	761
QY	700	SCDPRGTLGGVTECGNGQCFCKAHVCGKTCAAACKDGFGLDYADYFGCRSCRCDVGGAL	759
Db	762	SCDLRGTLGGVAECQGTQCFCKPHVCGQACASCKDGFGLDQADYFGCRSCRCDIGGAL	821
QY	760	GQCEPKTAGRCRPNTOGPTCSEPAKDHVLPDLHHMRLELEEAATPEGHVRFGFNPLE	819
Db	822	GQCEPRITGVCRPNTOGPTCSEPARDHYLPDLHLRLLELEEAATPEGHVRFGFNPLE	881
QY	820	FENFSWRYGAHNMAIQPRIVARLNVTSPDLFELVFRYVNRGSTSVNGQISVREEGKLSSC	879
Db	882	FENFSWRYGAQMAPVQPRIVARLNLTSPDLFWLFRYVNRGAMSVSGRVSVREEGRSATC	941
QY	880	TNCTEQSQPVAFPPSTEPAFVTVPQRGFGEPPVFNPGIWallVEAEGVLLDYVVLPPSTY	939
Db	942	ANCTAQSQPVAFPPSTEPAFITVPQRGFGEPPVFNPGTWalRVEAEGVLLDYVVLPPSAY	1001
QY	940	YEAALLQHRVTEACTYRPSALHSTENCLVYAHLPDGFPPSAAGTEALCRHNSLPRPCPT	999
Db	1002	YEAALLQLRVTEACTYRPSAQSPSCLLYTHLPDGFPPSAAGLEALCRQDNLPRPCPT	1061
QY	1000	EQLSPSHPPPLATCGSDVDIQLEMAVPPQGVYLVVEYVGEDSHQEMGVAVHTPQRAPOQ	1059
Db	1062	EQLSPSHPPPLITCTGSDVDVQLQVAVPQPGRYALVVEYANEDARQEVGVAVHTPQRAPOQ	1121
QY	1060	GVNLNHPCPYSSLCESPARDTOHHLAI FHLDSBASIRLTAEQAHFHLHSVTLVPVEEFST	1119
Db	1122	GLLSLHPCLYSTLCRTGRTARDTDHLAVFHLDSBASVRLTAEQARFFLHGVTLPVPIEFSP	1181
QY	1120	EFVEPRVFCVSSHGTFNPSSAACLASRFKPPPIILKDCQVLPPLDPLTQSQELSPG	1179
Db	1182	EFVEPRVSCISSHGAFGNPNSAACLPSPRFKPPPIILRDCQVILPPLGLPLTHAQDLTPA	1241
QY	1180	APPEGQPRPPTAVDPNAEPTLLRHPQGTVVFTTQVPTLGRYAFLLHGYQPVHPSFPVEV	1239
Db	1242	MSPAGPRPRPPTAVDPAEPTLLREPQATVVFTTHVPTLGRYAFLLHGYQPAHPTFPVEV	1301
QY	1240	LINGGRIWQGHANASCPHGYGCRTLVLCEGQTMLDVTDNELTIVTVRVPGRWLWLDYVL	1299
Db	1302	LINAGRIVWQGHANASCPHGYGCRTLVVCQEQALLDVTHSELTVTVRVPKGRWLWLDYVL	1361
QY	1300	IVPEDAYSSSYLQEEPLDKSYDFISHCATQGYHISPSSSSPPFCRNAATSLSPFYNNGALP	1359

Db	1362	VVPENVYSGYLREEPLDKSYDFISHCAAQGYHISPSSSSLFCRNAASLSLFYNNGARP	1421
Qy	1360	CGCHEVGAVSPTCEPFGQPCRGHVIGRDCSRCATGYWGFPPNCRPCDCGARLCDELGTGQ	1419
Db	1422	CGCHEVGATGPTCEPFGQPCCHAHVIGRDCSRCATGYWGFPPNCRACDCGARLCDELGTGQ	1481
Qy	1420	CICPPRTVPPDCLVCQPOSFGCHPLVGCCECNCSGPGVQELTDPCTCDMDSGQCRCPNVA	1479
Db	1482	CICPPRTIPPDCLLCQPTFGCHPLVGCCECNCSGPGTQELTDPCTCDTDSGQCRCPNVT	1541
Qy	1480	GRRCDTCAPGYGYPSCPCDCHAEAGTMASVCDPLTGOCHCKENVQGSRCQDQCRVGTFSL	1539
Db	1542	GRRCDTCSPGFHGYPRCPDCHAEAGTAPGVCDPLTGOCYCKENVQGPCKDCQCSLGTFSL	1601
Qy	1540	DAANPKGCTRCFCGATERCGNSNLARHEFFVDMEGWVLLSSDRQVWPHEHRPEIELLHAD	1599
Db	1602	DAANPKGCTRCFCGATERCRSSSYTRQEFFVDMEGWVLLSTDQVWPHERQPGTEMLRAD	1661
Qy	1600	LR----SVADTFESELWQAPPSYLGDRVSSYGGTTLHYELHSETQGDIFIPYESRPDVVL	1655
Db	1662	LFRHVEAVPEAFPELYWQAPPSYLGDRVSSYGGTTLRYELHSETQRGDVFVPMESRPDVVL	1721
Qy	1656	QGNQMSIAFLELAYPPGQVHRGQLQLVEGNFRHLETHNPVSREELMMVLAGLEQLOIRA	1715
Db	1722	QGNQMSITFLEPAYPTPGHVHRGQLQLVEGNFRHTETRNTVVSREELMMVLASLEQLOIRA	1781
Qy	1716	LFSQSSSVSLRRVVLEVASBAGRPPASNVELCMCPANYRGDSCQECAPGYRDTKGLF	1775
Db	1782	LFSQISSAVFLRRVALEVASPAGQALASNVELCLCPASYRGDSCQECAPGFYRDVKGLF	1841
Qy	1776	LGRVPCQCHGHSRCLPGSGTCVGCQHNTGDCQERCPRPGFVSSDPSNPASPCVSCPCP	1835
Db	1842	LGRVPCQCHGHSRCLPGSGVCV-CQHNTGEGAHCECAQAGFVSS-RDDPSAPCVSCPCP	1899
Qy	1836	LAVPSNNFADGCVLRNGRTQCLCRPGYAGASCERCAPGFGFNPLVLGSSCQPCDCSNGD	1895
Db	1900	LSVPSN-----RCAPGFGFNPLVLGSSCQPCDCSNGD	1932
Qy	1896	PNMIFSDCDPLTGACRGCLRHTTGPHCERCAPGFYGNALLPGNCTRCDCSPCGTETCDPQ	1955
Db	1933	PNLLFSDCDPLTGACRGCLRHTTGPRCCEICAPGFYGNALLPGNCTRCDCPTCGTEACDPH	1992
Qy	1956	SGRCLCKAGVTGQRCDRCLEGYGFEQCGCRPCACGPAAGSECHPQSGQCHCQPGTTG	2015
Db	1993	SGHCLCKAGVTGRRCDRCQEGHFGFDGCGGRPCACGPAAGSECHPQSGQCHCQPGTMG	2052
Qy	2016	PQLECAPGYWGLPEKGCRRQCQPRGHCDPHTGHCTCPPGLSGERCDCSCQHQVQVPQK	2075
Db	2053	PQRCBAPGYWGLPEQGCRRQCQPGGRCDPHTGRNCNCPGLSGERCDCSCQHQVQVPGG	2112
Qy	2076	PGHGIHCEVCDHCVVLLDDLERAGALLPAIREQLOGINASSAAWARLHRLNASIADL-	2134
Db	2113	PVGHSIHCEVCDHCVVLLDDLERAGALLPAIHEQLRGINASSMAWARLHRLNASIADLQ	2172
Qy	2135	-----QSKLRRPPGPYQAAQQLTLEQQSISLQQDTERLGSQ	2172
Db	2173	VLSVLAFPPQPGPVQAFTRFLPQSLRSPGPRHETAQQLVLEQQSTSLP-----PQ	2225
Qy	2173	ATGVQOQAGQLDTTTESTLGRAQKILLESVRAGRALNELASRMGQSGPDALVPSGEQLR	2232
Db	2226	AVGTRDQASQLLAGTEATLGHAKTLLAAIRAVIDRTLSELMSQTGHLGLANASAPSGEQLL	2285
Qy	2233	WALAEVERLLWDMRTRDLGAQGAVAEAEALAEAOQLMARVQEQLTSFWEENQSLATHIRDQ	2292
Db	2286	RTLAEVERLLWEMRRARDLGAPQAAAEAEALAAQORVLARVQEQLSSLWEENQALATQTRDR	2345
Qy	2293	LAQYESGIMDLREALNQAVNTTREAEEELNSRNOERVKEALQWKQELSQDNATLKATLOAA	2352
Db	2346	LAQHEAGIMDLREALNRAVDATREAQELNSRNOERLEEALQRQELSRDNATLOATLHAA	2405
Qy	2353	SLILGHVSELLOQIDQAK-EDLEHLAASLDGAWTPLLKRMQAFSPASSKVDLVEAAEAHA	2411

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Db 2466 QQLQCLALNLS-IILDVNQDRLTQRAIEASNAYSRIQAVQAEDAAGQALQADHTWQT 2524
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Db 2525 VVQRLVDRAQOLLANSTALEEAMLOEQORLGLGECWAPMGALRPAGTQLRDVRAKKDQL 2584
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Db 2585 EAHIQAAQAMLAMDTGETSKIAHAKAVAAEAQDTATRVQSLOQAMQENVERWQCYEGL 2644
Qy 2587 QGQLSQVERDASSVSTLEKTLPLLAKLSRLNRGVHNASLALSANIGRVKRLIAQAR 2646
Db 2645 RGQDLGQAVLDAGSAVSTLEKTLPLLAKLSILENRGVHNASLALSASIGRVRELIQAR 2704
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Db 2705 GAASKVYVPMKFNRSRQVLRTRPRDLADLAAAYTALKFVLQG--PEPEPGQGTEDRFVMY 2762
Qy 2706 MGSROATGDMGVSLRNQKVHVVYRLGKAGPTTSLIDENIGEQAFAVSDIRTLQFGHMSV 2765
Db 2763 MGSROATGDMGVSLRDKKVHVVYQLGEAGPAVLSIDEDIGEQAFAVSLDRTLQFGHMSV 2822
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Db 2823 TVERQMTQETKGDTVAPGAEGLLNLRPDDFVYVGGYPSFTTPEPLLRFPYGRYCIEMDT 2882
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Qy 2886 RFDQELRLVSYNGIIFFLKQESQFLCLAVQEGTLVLFYDFSGSLKADPLQPPQALTAAS 2945
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Qy 3186 VFVQRLGPRQVFDLHQNMGSVNVSVGCTPAQLIETSRATAQKVSRRSRQPSQDLACTTP 3245
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Qy 3246 WLPGTIQDAYQFGGPLPSYLOFVGISPSHRNRLHLSMLVRPHAAASQGLLLSTAPMSGRSP 3305
Db 3302 PHLRTTRDSYQFGGSLSSHLEFVGILARHN----- 3332
Qy 3306 SLVFLNHGHFVAQTEGPGPRLQVQSRQHSRAGQWHRVSVRWGMQQLVVDGSGQTSQK 3365
Db 3333 -----VSVWEKNRILLVTDGARAWSQE 3355
Qy 3366 ALHHRVPRAERPQPYTLVSGGLPASSYSKLPVSVGFGSLKQLDQKPLRTPPTOMGVV 3425
Db 3356 GPHRQHQGAEPHPQHTLFFVGGLPASSHSSKLPVTVGSGCVKRLRLHGRPLGAPTRMAGV 3415
Qy 3426 TPCVSGPLEDGLFFPGSEGVVTELEPKAKMPYVSLELEMRPLAAAGLIFHLGOALATPYM 3485
Db 3416 TPCILGPLEAGLFFPGSGGVITLGLPGATLPDVGLELEVRPLAVTGLIFHLGOARTPPYL 3475

Qy 3486 QLKVLTEQVLLQANDGAGEFSTWVTPK-LCDGRWHRVAVIMGRDTRLRLVDTQSNHTTG 3544
Db 3476 QLOVLPFRQVLLRADDGAGEFSTVTRPSVLCDGQWHR LAVMKSGNVLRLLEVDAQSNHTVG 3535
Qy 3545 RLPESLAGSPALLHLGSLPKSSTARPELPAYRGCRLKLLINGAPVNVVTASVQIQGAVGMR 3604
Db 3536 PLLAAAGAPAPLYLGLPEPNAVQPPPAYCGCMRRLAVNRSPVAMTRSVVEVHGAUGAS 3595
Qy 3605 GCPS 3608
Db 3596 GCPA 3599
RESULT 10
US-10-037-417-6
; Sequence 6, Application US/10037417
; Publication No. US20040052806A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
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; APPLICANT: Patturajan, Meera
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; APPLICANT: Lepley, Denise M
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; APPLICANT: Ellerman, Karen
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; APPLICANT: Rothenberg, Mark
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; APPLICANT: Boldog, Ferenc L
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; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Eisen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/10/037,417
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 3597
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-037-417-6									
Query Match		74.0%;	Score 14706.5;	DB 12;	Length 3597;				
Best Local Similarity		74.5%;	Pred. No. 0;						
Matches 2729;		Conservative 274;	Mismatches 482;	Indels 177;	Gaps 25;				
Qy	1	DLYCKLVGGPVAGGDPNQTIOGOYCDICTAANSNKAHPVSNDAIDGTERWWQSPPLSRGLE	60						
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Qy	61	YNEVNVTLDLGQVHVAYVLIKFA NSPRPDLWVLERSTDFGHTYQYPWQFFAASKRDCLE	120						
Db	118	YNEVNVTLDLGQVHVAYVLIKFA NSPRPDLWVLERSTDFGHTYQYPWQFFAASKRDCLE	177						
Qy	121	FGPRTLERITQDDDDVICTTEYSRIVPLENGEIVVSLVNGRPGALNFSYSPLLRDTTKATN	180						
Db	178	FGPRTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRPGAMNFSYSPLLRDTTKATN	237						
Qy	181	IRLRFRLRTNLLGHLMGKALRDPVTTRYYYSIKDISIGGRVCVCHGHADVCDAKDPDPF	240						
Db	238	VRLRFRLRTNLLGHLMGKALRDPVTTRYYYSIKDISIGGRVCVCHGHADVCDAKDPDPF	297						
Qy	241	RLQACQHNTCGGSCDRCCPGFNQOPWKPAATDTSANECQSCNCHGHAYDCYDPEVDRRN	300						
Db	298	RLQCTQHNTCGGTCDRCCPGFNQOPWKPATANSANECQ-CECYGHATDCYDPEVDERR	356						
Qy	301	ASQNQDNVYQGGVCLDCQHHTTGINCERCLPGFFRAPDQPLDSPHVCRCPCDESDFDTG	360						
Db	357	ASQSLDGTYYQGGVCIDCQHHTTGVNCERCLPGFYRSPNHPDLSPHVCRGCNCESEDFTG	416						
Qy	361	TCEDLTGRCYCRNFTGELCAACAEGYTDPPHCYPLPSFPFNDTREQVLPAGQIVNCDN	420						
Db	417	TCEDLTGRCYCRNFSGERCDVCAEGFTGFPSY-REHLPNGNDTREQVLPAGQIVSCDCS	475						
Qy	421	AAGTQGNACRDXPRLGRVCVCKPNFRGAHCELCAPGFHGSPCHPCQCSS--PGVANSLCD	477						
Db	476	AAGTQGNACRDXPRVGRCLCKPNFQGTGHCCLCAPGFYGPGC-PASVFALEWPMATAVLTQ	534						
Qy	478	PESGQCMRTG-----FEGDRCDHCALGYFHFPL-CQLCGSPAGTLPFGCDEAG	526						
Db	535	ASAGAEWASRGPHVIAVPPATFTLSASH-----PLRSVCGSPAGTLPFGCDEAG	586						
Qy	527	RCQCRPGFDGPHCDRCLPGYHGYPDCHACADPRGALDQCGVGLCHCRPGNTGATCQE	586						
Db	587	RCLCQPEFAGPHCDRCRPGYHGFNCAACTCDPRGALDQLCGAGGLCRCPGYGTACQE	646						
Qy	587	CSPGFYGFPPCIPCHCSADGSLHTTC---DPTTGQCRCPRTVTLGHCDMCPVGAYNFPY	642						
Db	647	CSPGFHGFPS----CPATALLKAPCTQPTFVGVSAAAGP-VRGCGVTRVCPVPTTSPT	700						
Qy	643	CEAGSCHPAGLAPANPALPETOAPCMCRAHVEGSPSCDRCKPGYWGILSASNPEGCTRCSCD	702						
Db	701	AKLALATLPVWPVPDLPALPEAQVPCMCRAHVEGSPSCDRCKPGFWGLSPSNPEGCTRCSCD	760						
Qy	703	PRGTLGGVTECQ-GNGQCFCKAHVCGKTCACAKDGFFGLDYADYFGCRSCRCDVGGALGQ	761						
Db	761	LRGTLGGVAECQPGTGQCFCKPHVCGQACASCADGFFGLDQADYFGCRSCRCDIGGALGQ	820						
Qy	762	GCEPKTGACRCRPNTOGPTCSEPAKDHLYPLDLHMLRLELEEAATPEGHAVRFGFNPLEFE	821						
Db	821	SCEPRTGVCRCRPNTOGPTCSEPARDHYLPDLHLRLLELEEAATPEGHAVRFGFNPLEFE	880						
Qy	822	NFSWRGYAHMMAIQPRIVARLNVTSPDLFRLVFRYVNRGSTSVNGQISVREEGKLSSCTN	881						
Db	881	NFSWRGYAQMAMAPVQPRIVARLNLTSPDLFWLFRYVNRGAMSVSGRVSVREEGRSAACAN	940						
Qy	882	CTEQSQPVAFPPSTEPAFVTVQRFGEFVLPNGIALLVEAGVLLDYVLLPSTYYE	941						
Db	941	CTAQSQPVAFPPSTEPAFITVQRFGEFVLPNGTVALRVEAGVLLDYVLLPSAYYE	1000						
Qy	942	AALLQHRVTEACTYRPSALHSTENCLVYAHLPDGFPPSAAGTEALCRHNSLPRPCPTEQ	1001						
Db	1001	AALLQLRVTEACTYRPSAQSPSPSCLLYTHLPDGFPPSAAGLEALCRQDNSLPRPCPTEQ	1060						

Qy	1002	LSPSHPPPLATCFGSDVDIOLEMAVPOPGQYVLVVEYVGEDSHQEMGVAVHTPQAPQQGV	1061
Db	1061	LSPSHPPPLITCTGSDVDVQLQVAVPOPGRYALVVEYANEDARQEVGVAVHTPQAPQQGL	1120
Qy	1062	LNLHPCPYSSLCRSPARDTQHHLAIFHLHDSEASIRLTAEQAHFHLHSVTLVPVEERSTEF	1121
Db	1121	LSLHPCLYSTLCRTARTDQDHLAVFHLHDSEASVRLTAEQARFHLHGVTLVPPIEFSPEF	1180
Qy	1122	VEPRVFCVSSHGTENPSSAACLASREPFPPOPIILKDCQVLPPLPDLPLTQSQEELSPGAP	1181
Db	1181	VEPRVSCISHGAFGPNSSAACLPSPFPPOPIILRDCQVLPPLPDLPLTHAODLTPAMS	1240
Qy	1182	PEGQPRPPTAVDPNAEPTLLRHPQGTIVFTTQVPTLGRYAFLLHGYQPVHPSFPVEVLI	1241
Db	1241	PAGPRPRPPTAVDPDAEPTLLRHPQGTIVFTTQVPTLGRYAFLLHGYQPAHPTFPVEVLI	1300
Qy	1242	NGGRIWQGHANASFCPHGYGCRITLVCBQTMLDVTDNELTIVTVRPEGRWLWLDYVLIV	1301
Db	1301	NAGRVWQGHANASFCPHGYGCRITLVCEGQALLDVTHSELITVTVRVPKGRWLWLDYVLIV	1360
Qy	1302	PEDAYSSSYLOEPELDKSYDFISHCATQGYHISPSSSSPFCRNPATSLSLFYNNGALPCG	1361
Db	1361	PENVISFYLRPEELDKSYDFISHCAAGYHISPSSSSLFCRNPAAASLSLFYNNGARPCG	1420
Qy	1362	CHEVGAVSPTCEPFGGQCPGRHVIGRDCSRCATGYWGFNCRPCDCCGARLDELGTGQCI	1421
Db	1421	CHEVGATGPTCEPFGGQCPCHAHVIGRDCSRCATGYWGFNCRACDCCGARLDELGTGQCI	1480
Qy	1422	CPRTVPPDCLVCQPSFGCHPLVGCCECNCSPGVQELTDPCTCDMDSGQCRCPNVAGR	1481
Db	1481	CPRTTIPDCLLCQPTFGCHPLVGCCECNCSPGQIELTDPCTDTSQCRCPNVAGR	1540
Qy	1482	RCDTCAPGYGYPSRCPCDCHEAGTMASVCDPLTGQCHCKENVOGSRCDQCRVGTFSLDA	1541
Db	1541	RCDTCSPGFHGYPRCPCDCHEAGTAGVCDPLTGQCYCKENVOGPKCDQCSLGTFSLDA	1600
Qy	1542	ANPKGCTRCFCFGATERCGNSNLARHEFVDMEGWLLSSDRQVVPHEHRPEIELLHADLR	1601
Db	1601	ANPKGCTRCFCFGATERCRSSSYTRQEFVDMEGWLLSTDRQVVPHERQPGTEMLRADLR	1660
Qy	1602	---SVADTFSELYWQAPPSYLGDRVSSYGGTTHYELHSETQRGDIPIPYESRPDVVLQ	1657
Db	1661	HVPEAVPEAFPELYWQAPPSYLGDRVSSYGGTTHYELHSETQRGDFVPMESRPDVVLQ	1720
Qy	1658	NQMSIAFLELAYPPGQVHRGQLQVVEGNFRHLETHNPVSREELMMVLASLEQLQIRALF	1717
Db	1721	NQMSITFLEPAYPTGQVHRGQLQVVEGNFRHLETHNPVSREELMMVLASLEQLQIRALF	1780
Qy	1718	SQSSSVSLRRVLEVASEAGRPASNVELCMCPANYRGSDCECAPGYRDTKGLFLG	1777
Db	1781	SQISSAVFLRRVLEVASPAGQALASNVELCLCPASYRGSDCECAPGYRDTKGLFLG	1840
Qy	1778	RCVPCQCHGHSRCLPGSGICVGCQHNTEGQCRCPGFVSSDPSPNAPSPCVSCPCPLA	1837
Db	1841	RCVPCQCHGHSRCLPGSGVCV-CQHNTGHAHCERCQAGFVSS-RDDPSAPCVSCPCPLS	1898
Qy	1838	VPSNNFADGCVLRNRTQCLCRPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSGNGDPN	1897
Db	1899	VPSN-----RCAPGFFGNPLVLGSSCQPCDCSGNGDPN	1931
Qy	1898	MFSDCDPLTGACRGLRHTTTPHCERCAPGYGNALLPGNCTRCDCSPCGTETCDPQSG	1957
Db	1932	LLFSDCDPLTGACRGLRHTTTPRCCEICAPGYGNALLPGNCTRCDCPCGTEACDPHSG	1991
Qy	1958	RCLCKAGVTGQRCRCLGEGYFGEQCGQCRPCACGPAAGSECHPQSGQCHCQPGTTGPQ	2017
Db	1992	HCLCKAGVTGRRCDRCQEGHFGFDGCGGCRPCACGPAAGSECHPQSGQCHCQPGTMGPQ	2051
Qy	2018	CLECAPGYWGLPEKGCRRCCQPRGHCDPHTGHTCTPPGLSGERCDTCSQHQHVVPKPG	2077
Db	2052	CRECAPGYWGLPEQGCRRCCQPGGRCDPHTGRCNCPPLSGLSGERCDTCSQHQHVVPKPG	2111

QY 2078 GHGIHCEVCDHCVLLDDLERAGALLPAIREIQOGINASSAAWARLHRLNASIADL--- 2134
Db 2112 GHSIHCEVCDHCVLLDDLERAGALLPAIHEIQRGINASSMAWARLHRLNASIADLQVL 2171
QY 2135 -----QSKLRPPGPVQAQOLOTLEBOQSIISLOQDTERLGSQAT 2174
Db 2172 SVLAPPPQPGVQAFTRLPQSLRSPGPRHETAQOQLEVLQOQSTSLP-----PQAV 2224
QY 2175 QVQQAQQLLDTTESTLGRAQKLLSVRAVGRALNELASRMGQSPGPDALVPSGEQLRWA 2234
Db 2225 GTRDQASQLLAGTEATLGHAKTLLAAIRAVDRITLSELMSTQHLGLANASAPSGEQLLRT 2284
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Db 2285 LAEVERLLWEMRRARDLGAPQAAAEALAAQAVLARVQEOQLSSLWEEENQALATQTRDLA 2344
QY 2295 QYESGLMDLREALNQAVNTTREAEBELNSRNOERVKBALQWKQELSQDNATLKATLQAAASL 2354
Db 2345 QHEAGLMDLREALNRAVDATREAQELNSRNOERLEEALQKQELSQRDNATLQATLHAARD 2404
QY 2355 ILGHVSELQIDQAK-EDLEHLAASLDGAWTPLLKRMQAFSPASSKVDLVEAAEAHAQK 2413
Db 2405 TLASVFRLLLEGLSPLKFQELERLAASLDGARTPLLQRMQTFSPAGSKLRLVEAAEAHAQ 2464
QY 2414 LNQLAINLSGIILGINQDRFIQRAVEASNAYSSILQAVQAAEDAAGQALRQASRTWEMVV 2473
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Db 2524 RQGLVDRAQQLLANSTALEEAMLQEQRLGLGECWAPMGALRPAGTQLRDVRAKQDQLEA 2583
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Db 2584 HIQAQAMLAMDTGETSKKIAHAKAVAAEAQDTATRVQSQLQAMQENVERWQSQYEGLRG 2643
QY 2589 QDLSQVERDASSSVSTLEKTLPLLAKLSRLNENGVNASLALSANIGRVKRLIAQARSA 2648
Db 2644 QDLQCAVLDAQSAVSTLEKTLPLLAKLSILENRGVNASLALSASIGRVRELIQAARGA 2703
QY 2649 ASK-VKVMKFNKGRSGVRLRPRDLADLAAYTALKFHIQSPVPAPEPGKNTGDHFFVLYMG 2707
Db 2704 ASKVVKVPMKFNKGRSGVQLRTPRDLADLAAYTALKFVLQG--PEPEPGQGTEDRFVVMYG 2761
QY 2708 SRQATGDMGVSLRNQKVHVYRLGKAGPTTLSIDENIGEQAFAVSDIRTLQFGHMSVTV 2767
Db 2762 SRQATGDMGVSLRDKKVHVYQLGEAGPAVLSDIDIGEQAFAVSLDRTLQFGHMSVTV 2821
QY 2768 EKQMVHEIKGDTVAPGSEGLNLHPDDFVYVGGYPSNFTPPPELRFPFGYLGCIEMETLN 2827
Db 2822 ERQMIQETKGDTVAPGAEGLLNLRPDDFVYVGGYPSFTTPPLLRFPFGYRGCIEMDTLN 2881
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Db 3002 IQVFLGSGSRKRVLRVERATVYSVEQDNLDLEADAYILGGVPPDQLP-SLRLRFPFTGGS 3060
QY 3008 VRGCIKGIKALGYVDLKRNLNTGISFGCTADLLVGRMTTFHGHGFLPLALPDVAPITEV 3067
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QY 3068 VYSGFGRGTQDNLLYYRTSPDGPYQVSLREGHVTLRFMNQEVETQRVFADGAPHYVAF 3127
Db 3121 VYSGFGFSAQDSALLYRASVPVRPHQVSLQOQGRVSLQLLRTEVKTQAGFADGAPHYVAF 3180
QY 3128 YSNVTGWLYVDDQLQLVKSHERTTQMLQLOPEEPSRLLLGLPVSQVSGTFHNFSGCISNVF 3187

Db 3181 YSNATGWLYVDDQLQMKPHRGPPPELOQPOQEPGPRLLGLLGGLPESGTIYNFSGCISNVF 3240
QY 3188 VQRLRGPQRFVFDLHONMGSVNVSVGCTPAQLIETSRATAQKVSRRSRQPSQDLACTTPEWL 3247
Db 3241 VQRLRGPQRFVFDLQONLGSVNVSTGCAPALQAOQTPGLGPRQASRRSRQPARHPACMLPPH 3300
QY 3248 PGTIQDAYQFGGPLPSYLOFVGISPSHRNRLHLSMLVRPHAAASQGLLLSTAPMSGRSPSL 3307
Db 3301 LRTRDSYQFGGSLSSHLEFVGILARHN----- 3329
QY 3308 VLFNLHGHFVAQTEGPGPRLOVQSRQHSRAGQWHRVSVRWGMQOQIQLVVDGSGQVTSQKAL 3367
Db 3330 -----VSVRWEKNRILLVTDGARAWSQEGP 3354
QY 3368 HHRVPRAEERPQPYTTLVSGGLPASSYSSKLPVSVGFSGCLKKLQDKQPLRTPPTQMVGVTP 3427
Db 3355 HRQHQAEHPQPHITLFGGLPASSHSSKLPVTVGFGCVKRLRLHGRPLGAPTRMAGVTP 3414
QY 3428 CVSGPLEDGLFFPGSEGVVTLPLKAKMPYVSLELEMRPLAAAGLIFHLGQALATPYMQL 3487
Db 3415 CILGPLEAGLFFPGSGGVITLGLPGATLPDVGLELEVRPLAVTGLIFHLGQARTPPYIQL 3474
QY 3488 KVLTEQVLLQANDGAGEFSTVWTPK-LCDGRWHRVAVIMGRDTRLLEVDTSQSNHTTGR 3546
Db 3475 QVLRQVLLRADDDGAGEFSTVTRPSVLCGQWHLAVMKSNGVLRLEVDQAQSNHTVGPL 3534
QY 3547 PESLAGSPALLHLGSLPKSSTARPELPAYRGCLRLKLLINGAPVNVTVASVQIQGAVGMRGC 3606
Db 3535 LAAAGAPAPLYLGLPEPMAVQPPWPAYCGCMRRLAVNRSVPVAMTRSVVEHGVGASGC 3594
QY 3607 PS 3608
Db 3595 PA 3596

RESULT 11
US-10-037-182-36
; Sequence 36, Application US/10037182
; Publication No. US20030044899A1
; GENERAL INFORMATION:
; APPLICANT: Trygsvason, Karl
; APPLICANT: Doi, Masayuki
; APPLICANT: Thyboll, Jill
; TITLE OF INVENTION: Recombinant Laminin 10
; FILE REFERENCE: 99-274-F
; CURRENT APPLICATION NUMBER: US/10/037,182
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,449
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/279,282
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 2743
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-037-182-36

Query Match 62.2%; Score 12354.5; DB 14; Length 2743;
Best Local Similarity 82.4%; Pred. No. 0;
Matches 2198; Conservative 172; Mismatches 290; Indels 7; Gaps 4;

QY 1 DLYCKLVGGPVAGGDPNQITQOQYCDICTAANSNKAHPVSNADIGTERWWQSPPLSRGLE 60
Db 79 DLYCKLVGGPVAGGDPNQITQOQYCDICTAANSNKAHPASNAIDGTERWWQSPPLSRGLE 138
QY 61 YNEVNVTLDLGQVHFVAYVLKFNANSPRDLWLERSTDFGHTYQPWQFFASSKRDCLER 120
Db 139 YNEVNVTLDLGQVHFVAYVLKFNANSPRDLWLERSMDFGRTYQPWQFFASSKRDCLER 198
QY 121 FGPRTIERITQDDDDVICTTEYSRIVPLENGEIVVSLVNCRPGALNFSYSPLLRDTKATN 180

Db 199 FGPOTLERITRDAACITTEYSRIVPLENGEIVVSLVNGRPGAMNFSYSPLLREFTKATN 258
Qy 181 IRLRFLRTNTLLGHLMGKALRDPPTVTRRYYSIKDISIGGRVCVCHGADVCDKOPDPF 240
Db 259 VRLRFLRTNTLLGHLMGKALRDPPTVTRRYYSIKDISIGGRVCVCHGADACDAKDPDPF 318
Qy 241 RLQACQHNTCGSGCDRCPCPGFNQOPWKPAITDSANECQSCNCHGHAYDCYDPEVDRRN 300
Db 319 RLQCTCQHNTCGGTCDRCPCPGFNQOPWKPATANSANECQSCNCHGHAYDCYDPEVDRR 378
Qy 301 ASQNDNVYQGGVCLDCQHHTTGINCERCLPGFFRAPDQPLDSHVHCRPCDCESDFTDG 360
Db 379 ASQSLDGTYYQGGVCLDCQHHTTAGVNCERCLPGFYRSPNHPDLSHVHCRRCNCESDFTDG 438
Qy 361 TCEDLTGRYCRNFTGELCAACAEYTDFFHCYPLSPFPHNDTRBQVLPAGQIVNCDN 420
Db 439 TCEDLTGRYCRNFSGERCDVCAEGFTGFPSCYTPS-SSNDTREQVLPAGQIVNCDCS 497
Qy 421 AAGTQGNACRKPRLGRVCVKNFRGAHCELCAPFGHGPSCHPCQSSSPGVANSLCDPES 480
Db 498 AAGTQGNACRKPVRGRCLCKPNFQGTGHCCLCAPFGYGPQCPCQSSSPGVADDRCDPDT 557
Qy 481 GQCMCRITGEGDRCDHCAALGYFHFPLCQLCGGSPAGTLPPEGCDAGRCQCRPGDFGPHCD 540
Db 558 GQCRVGVFEGATCDRCAPGYFHFPLCQLCGGSPAGTLPPEGCDAGRCCLCQPEFAGPHCD 617
Qy 541 RCLPGYHGYPDCHACADPRGALDQCGVGGLCHCRPGNTGATCQECSPGFYGFPPCIPC 600
Db 618 RCRPGYHGFPCQACTCDPRGALDQCGAGGLCRCPGYGTGTACQECSPGFHGFPPSCVPC 677
Qy 601 HCSADGSLHTTCDPTTGQCRCRPRVTGLHCDMCPVGAYNFPYCEAGSCHPAGLAPANPAL 660
Db 678 HCSAEGSLHAACDPRSGQSCRPRVTGLRCDTCTVPGAYNFPYCEAGSCHPAGLAPVDPAL 737
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Db 798 FCKPHVCGQACASCKDGFGLDQADYFGCRSCRDIGGALQGSCEPRTGVCRCRPNTQGP 857
Qy 780 TCSEPAKHLYLPDLHMLRLELEAATPEGHAVRFGFNPLEFENFWSRGYAHMMAIQPRIV 839
Db 858 TCSEPARDHYLPDLHLRLLELEAATPEGHAVRFGFNPLEFENFWSRGYAHMMAIQPRIV 917
Qy 840 ARLNVTSDDLRLVFRYVNRGSTSUNGQISVREEGLSSCTNCTEQSQPVAFPPSTEPAF 899
Db 918 ARLNLTSDDLFWLVFRYVNRGAMSVSRGVSVREGRSAACANCTAQSQPVAFPPSTEPAF 977
Qy 900 VTVPQRGFGEPFVLPNGIALLVEAGVLLDYVLLPSTYYEALLQHRVTEACTYRPSA 959
Db 978 ITVPQRGFGEPFVLPNGIALLVEAGVLLDYVLLPSTYYEALLQHRVTEACTYRPSA 1037
Qy 960 LHSTENCLVYAHLPDLGFPAAAGTEALCRHDNSLRPCPTQQLSPSHPPPLATCFGSDVDI 1019
Db 1038 QQSGDNCLLYTHLPDLGFPAAAGTEALCRQDNSLRPCPTQQLSPSHPPPLITCTGSDVDV 1097
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Db 1098 QLQVAVPQPGRYALVVEYANEDARQEVGVAVHTPQAPQCGLLSLHPCLYSTLCRGTARD 1157
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Db 1158 TQDHLAVEHLDSEASVRLTAEQARFFLHGVTLPVEEFSPFEVPRVSCISSHGAFGPNS 1217
Qy 1140 AACLASRFPKPPQPIILKDCQVLPPLPDLPLTQSQELSPGAPPEGQPRPPTAVDPNAEP 1199
Db 1218 AACLPSPKPPQPIILRDCQVLPPLPGLPLTHAQDLTPATSPAGPRPRPPTAVDPDAEP 1277
Qy 1200 TLLRHPOQTWVFTTQVPTLGRYAFLLHGYQPVHPSFPFVVEVLINGGRIWQGHANASFCPHG 1259

Db 1278 TLLREPQATVVTTHVPTLGRYAFLLHGYQPAHPTFPVEVLINAGRVMQGHANASFCPHG 1337
Qy 1260 YGCRTLVLCEQTMLDVTDNELTTVRVPEGRWLWLDYVLVPEDAYSSSYLQEEPLDKS 1319
Db 1338 YGCRTLVLCEQQALDDVTHSELTVTVRVPEGRWLWLDYVLVPEVNTVSFGYLREEPLDKS 1397
Qy 1320 YDFISHCATQGYHISPSSSPFCRNAATSLSYFNNGALPCGCGHEVGAVSPTCEPFGQC 1379
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Qy 1380 PCRGHVIGRDCSRCATGYWGFPCNCRPCDCGARLDELGTGQCICPPRTVPPDDCLVCQPSF 1439
Db 1458 PCHAHVIGRDCSRCATGYWGFPCNCRPCDCGARLDELGTGQCICPPRTIIPDDCLLCQPTF 1517
Qy 1440 GCHPLVGECECNCSPGVQBELTDPCTCDMSGQCRCPNVAGRRCDTCAFGFYGYPSCRPC 1499
Db 1518 GCHPLVGECECNCSPGIGELTDPCTDTSGQCKRPNVTGRRCDTCSFGFHYPRCRPC 1577
Qy 1500 DCHEAGTMASVCDPLTGQCHCKENVQSRCDQCRVGTFSLDAANPKGCTRCFCFGATERC 1559
Db 1578 DCHEAGTAPGVCDPLTGQCYCKENVQGPCKDQCSLGTFSLDAANPKGCTRCFCFGATERC 1637
Qy 1560 GNSNLARHEFVDMEGWVLLSSDRQVVPHEHRPEIELLHADLR---SVADTFSELYWQAP 1615
Db 1638 RSSSYTRQEFVDMEGWVLLSTDRQVVPHERQGTETMLRADLRHVPEAVPEAPPELYWQAP 1697
Qy 1616 PSYLGDRVSSYGGTILYELHSETQRGDIFIPYESRDPDVVLQGNQMSIAFLELAYPPPGQV 1675
Db 1698 PSYLGDRVSSYGGTILYELHSETQRGDVVFVMESSRPDVVLQGNQMSITFLEPAYPTPGHV 1757
Qy 1676 HRGQLQLVEGNFRHLETHNPVSREELMMVLASLEQLQIRALFSQTSSSVSLRRVVLEVAS 1735
Db 1758 HRGQLQLVEGNFRHTETRTNTVSRREELMMVLASLEQLQIRALFSQISSAVSLRRVALEVAS 1817
Qy 1736 BAGRGPPASNVELCMCPANYRGDSQCECAPGYRDTKGLFLGRVCPCQCHGSHDRCLPGS 1795
Db 1818 PAQQALASNVELCLCPASRYGDSQCECAPGYRDKGLFLGRVCPCQCHGSHDRCLPGS 1877
Qy 1796 GTCVGCQHNTGDCQERCRPGFVSSDPSPASPCVSCPCPLAVPSNNFADGCVLRNGRTQ 1855
Db 1878 GVCVDCQHNTGEGAHCECQAGFMSS-RDDPSAPCVSCPCPLSVPSNNFAEGCVLRGGRTQ 1936
Qy 1856 CLCRPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSGNGDPNMFSDCDPLTGACRGCLR 1915
Db 1937 CLCKPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSGNGDPNLLFSDCDPLTGACRGCLR 1996
Qy 1916 HTTGPHCERCAPGYGNALLPGNCTRCDCSPCGTETCDPQSGRCLCKAGVTGQRCDRCLE 1975
Db 1997 HTTGPRCETCAPGYGNALLPGNCTRCDCPTCGTEACDPHSGHCLCKAGVTGRRCDRCQE 2056
Qy 1976 GYFGEQCGCRPCACGPAAGSECHPQSGQCHQCPGTTGPQCLECAPGYWGLPEKGCRR 2035
Db 2057 GHFGNGCGGCRPCACGPAAGSECHPQSGQCHQCHCPGTGMPQCRECAPGYWGLPEQGCRR 2116
Qy 2036 CQCPRGHCDPHTGHCTCPPLSGERCDCSCQHQVVPVPGKPGGHHIHCCEVCDHCVVLLLD 2095
Db 2117 CQCPGRCDDPHTGRCNCPPLSGERCDCSCQHQVVPVPGGPGVHSHIHCCEVCDHCVVLLLD 2176
Qy 2096 DLERAGALLPAIREQLQGINASSAAWARLHRLNASIADLQSKLRRPPPGPRYQAAQQLQTL 2155
Db 2177 DLERAGALLPAIHEQLRGINASSMAWARLHRLNASIADLQSKLRSPLGPRHETAQQLQTL 2236
Qy 2156 EQQSISLQDTERLGSQATGVQAGQLDTESTLGRAQKLLSVRAVGRALNELASRM 2215
Db 2237 EQQSTSLGQDARRLGGQAVTRDQASQLLAGTEATLGHAKTLLAAIRAVDRILSELMSQT 2296
Qy 2216 GQSGPDALVPSGEQLRWALAEVERLLWDMRTRDLCAGQAVAEAEAEAEAEAEAEAEAEAEAE 2275
Db 2297 GHGLANASAPSGEQLLRLTAEVERLLWEMRARDLJGAPQAAAEAEAEAEAEAEAEAEAEAE 2356
Qy 2276 TSFWEENQSLATHIRDQLAQYESGLMDLREALNQAVNTTREAELNSRNOERVKEALQWK 2335
Db 2357 SSLWEENQALATQTRDLAQHEAGLMDLREALNRAVDATREAQELNSRNOERLEBALQRK 2416

	Best Local Similarity	72.0%; Pred. No. 0;	Matches 1205; Conservative	159; Mismatches	295; Indels	14; Gaps	6;
Qy	1970	CDRCLEGYFGEQCCQCRPCACGPAAGKSECHPQSGQCHCQPGTTGPOCLECAPGYWGLP	2029				
Db	1	CDRCQEGHFGNGCGGCRPCACGPAAGSECHPQSGQCHCQPGTMGPPQCRECAPGYWGLP	60				
Qy	2030	EKGRRRCQPRGHCDPTHGCHCTCPPGLSGERCDCSQQHQVVPVGKPGGGHGIHCEVCDHC	2089				
Db	61	EQGRRRCQCPGGRCDPTHGRCNCPPGLSGERCDCSQQHQVVPVGPGPVGHSIHCEVCDHC	120				
Qy	2090	VVLLDDLERAGALLPAIREQLQGINASSAAWARLHRLNASIADLQSKLRRPPGPRYQAA	2149				
Db	121	VVLLDDLERAGALLPAIHEQLRGINASSMAWARLHRLNASIADLQSKLRSPLGPRHETA	180				
Qy	2150	QQLQTLQEQQSISLQQDTERLGSQATGVQGGQAGQLDDTTTESTLGRAQKLLESVRAVGRALN	2209				
Db	181	QQLLEVLQEQQSTSLGQDARRLGGQAVGTRDQASQLLACTEATLGHAKTLLAAIRAVDRTLS	240				
Qy	2210	ELASRMGQGS PGDALVPSGEQLRWALAEVERLLWDMRTRDGLGAQGAVAEAEALAEQRILMA	2269				
Db	241	ELMSQTGHLGLANASAPSGEQLLRTLAEVERLLWEMRARDLGAQPAAAEAEALAAQRLLA	300				
Qy	2270	RVQEQLTSFWEEANSIATHIRDQLAQYESGLMDLREALNQAVNTTREAEEELNSRNGQERVK	2329				
Db	301	RVQEOQLSSLWEEANQATQTRDLAQHEAGLMDLREALNRAVDATREAQOELNSRNGQERLE	360				

QY	2330	EALQWKQELSQDNATLKATLQAASLIILGHVSELLQIGIDQAKEDLEHLAASLDGAWTPLLK	2389
Db	361	EALQWKQELSRDNATLQATLHAARDTLASVFRLLHSLDQAKEELERLAASLDGARTPLIQ	420
QY	2390	RMQAFSPASSKVDLVEAAEAHAQKLNQLAINLSGIIILGINQDRFIQRAVEASNAYSSILQ	2449
Db	421	RMQTFSPAGSKRLRVEAAEAHAQQLGQLALNLSSIIILDVNQDRILTQRAIEASNAYSRIQ	480
QY	2450	AVQAAEDAAGQALRQASRTWEMVVRGLAAGARQLLANSSALEETILGHQRLGLAQGRL	2509
Db	481	AVQAAEDAAGQALQQADHTWATVVRQGLVDRACQLLANSTALEEAMLEQQRLGLVWAAL	540
QY	2510	QAAGIQLHNVWARKNLAAQIQEAQAMLAMDTSETSEKIAHAKAVAAEALSTATHVQSOL	2569
Db	541	QGARTQLRDVRAKKDQLEAHIQAAQAMLAMDTDETSEKIAHAKAVAAEAQDTATRVQSOL	600
QY	2570	QGMQKNVERWQSQLGGIQQGDLSQVERDASSSVSTLEKTLPLLAKLSRLNRCGVHNASL	2629
Db	601	QAMQENVERWQGYEGJRGQDLGQAVLDAGHSVSTLEKTLPLLAKLSILENRCGVHNASL	660

QY	2630	ALSANIGRVKLIQAARSAASKVKVSMKFNGRSGVRLRPDRDLADLAAAYTALKFHIQSPV	2689
Dd	661	ALSASIGRVRELIAQARGAASKVKVPMKFNGRSGVQLRTPRDLADLAAAYTALKFYLG--	718
QY	2690	PAPEPGKNTGDHFVLVMGSRQATGDYMGVSLRNOKVHVYRLKGAGPTTLSIDENIGEQQF	2749
Dd	719	PEPEPGQGTEDRFVVMGSRQATGDYMGVSLRDKKVHVYQLGEAGPAVLSDIEDIGEQQF	778
QY	2750	AAVSIDRTLQFGHMSVTVEKQMVHEIKGDTVAPSEGLNLNHPDDFVFYVGYPSPNFSTPP	2809
Dd	779	AAVSLDRTLQFGHMSVTVERQMIQETKGDTVAPCAEGLLNLRPDDFVFYVGYPSTFTPP	838
QY	2810	EPLRFPGYLGCIENTLINEEVVSLYNFEQTFLMDTAVDKPCARSKATGDPWLTGDSYLDG	2869
Dd	839	PLLRFPGYRGCIEMDTLINEEVVSLYNFERTFOLDTAVDRPCARSKSTGDPWLTGDSYLDG	898
QY	2870	SGFARISFEKQFSNTRKFRDQELRLVSYNGIIFFLKQESQFLCLAVQEGTLVLPDFDGSGL	2929
Dd	899	TGFARISFDSQISITKRFEQELRLVSYSGLVFLKQSQFLCLAVQEGSLVLLYDFGAGL	958
QY	2930	KKADPLOPPQALTAASKAIQVFLLAGNRKXRLVRVERATVFSVDQDNMLEMADAYYLGCV	2989
Dd	959	KKAVPLOPPPPLTSASKAIQVFLLGGRKXRLVRVERATVYSVEQDNDELEADAYYLGCV	1018

[illegible]

Db 1019 PPQPLPRLPFTGGVRCVKGIKALGKYVDLKRLLNTTGVSAAGCTADLLVGRAMTFH 1078
QY 3050 GHGFLPALPDVAPITEVYSGFGRGTQDNLLYYRTSPDQYQVSLRGHVTIRFMNQ 3109
Db 1079 GHGFLRLALSNAVPLTGNVYSGFGRHSAQDSALLYRASPDGLCQVSLQGRVSLQLRT 1138
QY 3110 EVETQRFADGAPHYVAFYSNVTGVWLVYDDQLVLKSHERTPMLQLQPEEPRLLLG 3169
Db 1139 EVKTOAGFADGAPHYVAFYSNATGVWLVYDDQLQMKPHRGPPPELQPEGPRLLLG 1198
QY 3170 LPVSGTFHNFSGISNFFVQRLRGPQRFVDFLHQNMGSVNVSVGCTPAQLIETS----- 3222
Db 1199 LPESGTIYNFSGISNFFVQRLRGPQRFVDFLHQNMGSVNVSVGCTPAQLIETS----- 3222
QY 3223 RATAQKVSRRSRQPSQDLACTTPWLPDGTIQDAYQFGGPLESYLQFVGISPSHRNRLHLSM 3282
Db 1259 QATARKASRRSRQPARHPACMLPPHLRTRDSYQFGGSLSSHLEFVGILARHNWPSLSM 1318
QY 3283 LVRPHAASQGLLLSTAPMSGRSPSLVFLNHHGFVAQTEGEPRLQVQSRQSRAGQWHR 3342
Db 1319 HVLPFR-SSRGLLLFTARLRPGSPSLALFLSNHGFVAQMEGLGRLRAQSRQSRPRGRWHK 1377
QY 3343 VSVRWGMQIQLVVDGSGTWSQKALHHRVPRAPRPPQYTLVSGGLPASPSSYSSKLPVSVGF 3402
Db 1378 VSVRWKRNRIILLVTDGARAWSQEGPHRQGAHPQPHLTFVGGPLPASHSSKLPVTVGF 1437
QY 3403 SGCLKLQLDKQPLRTPQTMGVTPCVSGPLEDGLFFPGSEGVVTLPLPKAMPYVLSLEL 3462
Db 1438 SGCVKRLRLHGRPLGAPTRMAGVTPCILGPLEAGLFFPGSGGVITLPLPGATLPDVGLEL 1497
QY 3463 EMRPLAAAGLIFHLGQALATPYMQLKVLTEQVLLQANDGAGEFSTWVTPK-LCDGRWHR 3521
Db 1498 EVRPLAVTGLIFHLGQARTPPYLQVTEKQVLLRADDGAGEFSTVTRPSVLCDDGQWHR 1557
QY 3522 VAVIMGRDTRLEVDTSQNHHTTGRPLPESLAGSPALLHLGSLPKSSTARPELPAYRGCLRK 3581
Db 1558 LAVMKSQNVLRLEVDQASNHTVGPLLAAAGAPAPLYLGGLEPMAVQPPWPAYCGCMRR 1617
QY 3582 LLIN-GAPVNVTVASVQIQGAVGMRCPCSGTGLA--LSKQKALTQRHAKPSVSP 3631
Db 1618 LAVNRSPVAVNTRSVVEHGVAGVAGSGCPSPTRTQTPAPCQAPAAAASHRPLCSP 1670

RESULT 13

US-10-037-417-8
; Sequence 8, Application US/10037417
; Publication No. US20040052806A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E

; APPLICANT: Eisen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/10/037,417
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 1640
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-037-417-8

Query Match 30.7%; Score 6092; DB 12; Length 1640;
Best Local Similarity 72.7%; Pred. No. 0;
Matches 1197; Conservative 156; Mismatches 278; Indels 16; Gaps 5;

QY 1970 CDRLEGYGFEGCGCRPCACGPAKSGECHPQSGQCHQCGTGTGQCLECAPGYWGLP 2029
Db 1 CDRCEGHFGFNGCGCRPCACGPAKSGECHPQSGQCHQCGTGTGQCLECAPGYWGLP 60
QY 2030 EKGCRRCQCPRGHCDPHTGCTCPGSLGGERCDTCSQQHQVPPGKPGGHHGHCVCDC 2089
Db 61 EKGCRRCQCPRGHCDPHTGCTCPGSLGGERCDTCSQQHQVPPGKPGGHHGHCVCDC 120
QY 2090 VVLLDDLERAGALLPAIREQLQGINASSAAMARLHRLNASIADLQSLRRPPGPRYQAA 2149
Db 121 VVLLDDLERAGALLPAIREQLQGINASSAAMARLHRLNASIADLQSLRRPPGPRYQAA 180
QY 2150 QQLQLEQQSISLQDTERLGSGQATGVQCGAGQLDITESTILGKRAKLLSVRAVGRALN 2209
Db 181 QQLQLEQQSISLQDTERLGSGQATGVQCGAGQLDITESTILGKRAKLLSVRAVGRALN 240
QY 2210 ELASRMGQSGPDALVPSGEOLRWALAEVERLLWDMRTRDLGAQGAFAEAELAAQRLMA 2269
Db 241 ELMSQTGHLGLANASAPSGEQLLRTLAVERLLWDMRTRDLGAQGAFAEAELAAQRLMA 300
QY 2270 RVQEQLTSEWENQSLATHIRDQLAQYESGLMDLREALNOAVNTTREAELNSRNQERVK 2329
Db 301 RVQEQLTSEWENQSLATHIRDQLAQYESGLMDLREALNOAVNTTREAELNSRNQERVK 360
QY 2330 EALQWKQELSQDNATLKATLQAASLIIGHVSELQIGIDQAKEDLEHLLASLDGAWTPLLK 2389
Db 361 EALQWKQELSQDNATLKATLQAASLIIGHVSELQIGIDQAKEDLEHLLASLDGAWTPLLK 420
QY 2390 RMOAFSPASSKVDLVEAAEAHAQKLNQALNLSGIILGINQDRFIQRAVEASNAYSILQ 2449
Db 421 RMOAFSPASSKVDLVEAAEAHAQKLNQALNLSGIILGINQDRFIQRAVEASNAYSILQ 480
QY 2450 AVQAAEDAGQALRQASRTWETVVRGLAAGARQLLANSALLETILGHQGRGLGAQGR 2509
Db 481 AVQAAEDAGQALRQASRTWETVVRGLAAGARQLLANSALLETILGHQGRGLGAQGR 540
QY 2510 QAAGIQHNVWARKNQLAAQIQEAQAMLANDTSETSEKIAHAKAVAAEALSTATHVQSOL 2569

Db 541 QGARTQLRDVRAKKDQLEAHIAQAQAMLAMDTDETSKIAHAKAVAAEAQDTATRVQSQL 600

Qy 2570 QGMQKNVERWQSLGGLOQDLSQVERDASSVSTLEKTLPQLLAKLSRLNRGVHNASL 2629

Db 601 QAMQENVERWQGYEGLRGDQLCQAVLDAGHSVSTLEKTLPQLLAKLSILENRGVHNASL 660

Qy 2630 ALSANIGRVRKLIQAARSAASKVKVSMKFNRSRGVRLRPPRDLADLAAYTALKFHIQSPV 2689

Db 661 ALSASIGRVELIAQAARGAASKVKVPMKFNRSRGVQLRTPRDLADLAAYTALKFVLQG-- 718

Qy 2690 PAPERCKNTGDHFVLYMGSRQATGDMGVSLRNQKVHVYVRLKAGPTTLSIDENIGEQQF 2749

Db 719 PEPEQOGTDFVVMYMGSRQATGDMGVSLRDKKVHVYVQLGEAGPAVLSIDENIGEQQF 778

Qy 2750 AAVSIDRTLOFCHMSVTVEKQMVHEIKGDTVAPGSEGLNLNLPDDFVFYVGGYPSNFTPP 2809

Db 779 AAVSLDRTLQFCHMSVTVERQMIQETKGDVAPGAEGLLNLNRPDDFVFYVGGYPSFTPP 838

Qy 2810 EPLRFPGLGCIEMETLNEEVVSLYNFEQTFMLDTAVDKPCARSKATGDPWLTDGSYLDG 2869

Db 839 PLLRFPYRGCIEMDTLNEEVVSLYNFERTFQDLDTAVDRCARSKSTGDPWLTDGSYLDG 898

Qy 2870 SGFARISFEKQFSNTRKFDQELRLVSYNGIIFFLKQESQFLCLAVQEGTLVLFYDFGSGL 2929

Db 899 TGFARISFDSQISTTKRFEQELRLVSYSGVFLFLKQSQSFLCLAVQEGSLVLLYDFGAGL 958

Qy 2930 KKADPLQPPQALTAASKAIQVFLLAGNRKRVLRVERATVFSVDODNMLEMADAYILGGV 2989

Db 959 KXAVPLQPPPLTSASKAIQVFLLAGSRKRVLRVERATVYSVEQDNLDLADAYILGGV 1018

Qy 2990 PPEQLPLSLRQLFPPSGSVRGCIKGIKALGKYVDLKRNTTGISFGCTADLLVGRMTTFH 3049

Db 1019 PPDQLPPLSLRWLFPTGGSVRGVCVKIGKALGKYVDLKRNTTGVSAGCTADLLVGRAMTFH 1078

Qy 3050 GHGFLPLALPDVAPITEVYSGFGERGTQDNLLYYRTSDPGYQVSLRGHVTILRFMNQ 3109

Db 1079 GHGFLRLALSNAVPLTGNVYSGFGFSAQDSALLYRASPDCLCQVSLQQGRVSLQLLRT 1138

Qy 3110 EVETORVFADGAPHYVAFYSNVTVGMVLYVDDQLQLVKSHERTTLMQLQPEEPSRLLLGG 3169

Db 1139 EVKTOAGFADGAPHYVAFYSNATVGMVLYVDDQLQOMKPHRPPPELQPPQEGPPRLLLGG 1198

Qy 3170 LPVSGTFHNPFGCISNVFVQRLRGQRFVFDLHQNMGSVNVSVGCTPAQLIETS----- 3222

Db 1199 LPESGTIYNFSGCISNVFVQRLRGQRFVFDLQNNLGSVNVSTGCAPALQAQTPGLGRGL 1258

Qy 3223 RATAQVSRSRQPSQDLACTTPWLPGTIQDAYQFGGFLPSYLVQFVIGISPSHRNRLHLSM 3282

Db 1259 QATARKASRSRQPARHPACMLPPHLRTTRDSYQFGGSLSHLEFVGLARHNWPSLSM 1318

Qy 3283 LVRPHAAASQGLLLSTAPMSGRSPSLVFLNHHGFVAQTEGPGRLQVQSRQHSRAGOWHR 3342

Db 1319 HVLPR-SSRGLLLFTARLRPGSPSLALFLSNHGFVAQMEGLGTRLRQAQSRQRSPRGWHK 1377

Qy 3343 VSVRWGMQQLQVVDGQTSQKALHHRVPRAERPQPYTILSVGGLPASSYSSKLPVSVGF 3402

Db 1378 VSVRWKXNRIILLVTDGARAWSQEGPHRQHQAEHPQHTLFFVGLPASSHSSKLPVTVG 1437

Qy 3403 SGCLKKLQDKQPLRTPQMVGVTPTCVSGPLEDGLFFPGSEGVVTLLELPKAKMPYVLSLEL 3462

Db 1438 SGCVKRLRLHGRPLGAPTRMAGVTPCILGPLEAGLFFPGSGGVITLPLPGATLPDVGLEL 1497

Qy 3463 EMRPLAAAGLIFHLGOALATPYMQLKVLTEQVLLQANDGAGFFSTWVTPK-LCDGRWHR 3521

Db 1498 EVRPLAVTGLIFHLGOARTPPYLQ-----QVLLRADDGAGEFSTSVTRPSVLCDCQWHR 1552

Qy 3522 VAVIMGRDTRLLEVDTQSNHTTGRLPESLAGSPALLHLGLSPKSSSTARPELPAYRGCLRK 3581

Db 1553 LAVMKSGNVLRLEVDAQSNHTVGPLLAAAAGAPAPLYLGLPBPMAVQPPFPAYCGCMRR 1612

Qy 3582 LLINGAPVNVVTSVQIQGAVGMRGCP 3608

Db 1613 LAVNRSVPVAMTRSVVEHGAVGASGCEPA 1639

RESULT 14

US-10-037-417-49

; Sequence 49, Application US/10037417

; Publication No. US20040052806A1

; GENERAL INFORMATION:

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Alsobrook II, John P

; APPLICANT: Tchernev, Velizar T

; APPLICANT: Liu, Xiaohong

; APPLICANT: Spytek, Kimberly A

; APPLICANT: Patturajan, Meera

; APPLICANT: Grosse, William M

; APPLICANT: Lepley, Denise M

; APPLICANT: Burgess, Catherine E

; APPLICANT: Vernet, Corine A.M.

; APPLICANT: Li, Li

; APPLICANT: Gorman, Linda

; APPLICANT: Edinger, Shlomit R

; APPLICANT: Sciore, Paul

; APPLICANT: Ellerman, Karen

; APPLICANT: Malyankar, Uriel M

; APPLICANT: Rothenberg, Mark

; APPLICANT: Stone, David J

; APPLICANT: Boldog, Ferenc L

; APPLICANT: Guo, Xiaojia

; APPLICANT: Shenoy, Suresh G

; APPLICANT: Anderson, David W

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Taupier Jr, Raymond J

; APPLICANT: Miller, Charles E

; APPLICANT: Eisen, Andrew J

; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-235

; CURRENT APPLICATION NUMBER: US/10/037,417

; CURRENT FILING DATE: 2002-09-20

; PRIOR APPLICATION NUMBER: 60/260,018

; PRIOR FILING DATE: 2001-01-05

; PRIOR APPLICATION NUMBER: 60/260,360

; PRIOR FILING DATE: 2001-01-08

; PRIOR APPLICATION NUMBER: 60/272,411

; PRIOR FILING DATE: 2001-02-28

; PRIOR APPLICATION NUMBER: 60/272,817

; PRIOR FILING DATE: 2001-03-02

; PRIOR APPLICATION NUMBER: 60/291,186

; PRIOR FILING DATE: 2001-05-15

; PRIOR APPLICATION NUMBER: 60/303,231

; PRIOR FILING DATE: 2001-07-05

; PRIOR APPLICATION NUMBER: 60/305,060

; PRIOR FILING DATE: 2001-07-12

; PRIOR APPLICATION NUMBER: 60/318,405

; PRIOR FILING DATE: 2001-09-10

; PRIOR APPLICATION NUMBER: 60/318,700

; PRIOR FILING DATE: 2001-09-12

; NUMBER OF SEQ ID NOS: 227

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 49

; LENGTH: 1634

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-037-417-49

Query Match 27.6%; Score 5495.5; DB 12; Length 1634;

Best Local Similarity 70.1%; Pred.No. 0;

Matches 1107; Conservative 157; Mismatches 278; Indels 37; Gaps 6;

Qy 2051 TCPPLSGRCDTCSQHQVFPVPGKPGCGHGHIC-----EVCDCVVLDDDL 2097

Db 71 TAPRGSAGS-----AATPAASSIRCLFQAGLWATATVVKVCDHCVVLLDDDL 117

Qy 2098 ERAGALLPAIREQLQGINASSAAWALHRLNASIADLQSKLRPPGPRYQAAQQLTLEQ 2157

Db	118	ERAGALLPAIHEQLRGINASSMAWARLHRLNASIADLQSLRSPGLPRHETAQQLVLEQ	177
Qy	2158	QSIISLQODTERLGSQATGVQGAQLDOTTSTILGRAQKLLSVRAVGRALNELASRMGQ	2217
Db	178	QSTSLGQDARRLGGQAVGTRDQASQLLAGTEATLGHAKTLLAAIRAVDRTLSELMSQTGH	237
Qy	2218	GSPGDALVPSGEQLRWALAEVERLLWDMRTRDLGACGAVAEAEALAEAOQLMARVQEQLTS	2277
Db	238	LGLANASAPSGEQLLRTLAEVERLLWEMRARDLGAPOAAAEALAAQRLARVQEQLSS	297
Qy	2278	FWEENQSLATHIRDQLAQYESGLMDLREALNQAVNTTREAEEELNSRNQERVKEALQWKQE	2337
Db	298	LWEENQALATQTRDRLLACHEAGLMDLREALNRAVDATREAQELNSRNQERLEALQKQE	357
Qy	2338	LSQDNATLKATLOAASLILGHVSELLQIDQAKEDIEHLAASLDGAWTPLLKRMQAFSPA	2397
Db	358	LSRDNATLOATHARDTLASVFRLLHSLDQAKELERLAASLDGARTPLLQRMQTFSPA	417
Qy	2398	SSKVDLVEAAEAHAQKLNQALAINLSGIILGINQDRFIQRAVEASNAYSSILCAVQAAEDA	2457
Db	418	GSKRLVEAAEAHAQQLQALNLSSIIIDVNQDRLTQRAIEASNAYSRIQAVQAAEDA	477
Qy	2458	AGQALRQASRTWEMVQVRGLAAGAROLLANSSALEETILGHQGRGLAQGRLOAAGIQLH	2517
Db	478	AGQALQADHTWATVVVRQGLVDRAQOLLANSTALEEAMLOEQORLGLVWALQGARTQLR	537
Qy	2518	NVWARKNQLAAQIQEAQAMLAMDTSETSEKIAHAKAVAAEALSTATHVQSOLQGMQKNVE	2577
Db	538	DVRAKKQDLEAHIQAAQAMLAMDTDETSKKIAHAKAVAAEAQDATRVQSOLQAMQENVE	597
Qy	2578	RWQSQGLGLOQDLSQVERDASSSVSTLEKTLPLLAKLSRLNRGVHNASLALSANIGR	2637
Db	598	RWQGYEGLRGQDLGQAVLDAGHSVSTLEKTLPLLAKLSILENRGVHNASLALSASIGR	657
Qy	2638	VRKLIQAARSAASKVKVSMKFNRSRGVRLRPDRDLADLAAYTALKFHIQSPVPAPEPGKN	2697
Db	658	VRELIAQARGAASKVKVPMKFNRSRGVQLRTPRDLADLAAYTALKFYLOG--PEPEPGQG	715
Qy	2698	TGDHFVLYMGSRQATGYMGVSLRNQKVHVYRLGKAGPTTLSIDENIGEFAAVSIDRT	2757
Db	716	TEDRFVYMGSRQATGYMGVSLRDKKVHVYQLGEAGPAVLSIDEDIGEFAAVSLDRT	775
Qy	2758	LQFGHMSVTVEKQMVHEIKGDTVAPGSEGLNLNHPDDVFYVGGYPSNFTPEPLRFPGY	2817
Db	776	LQFGHMSVTVERQMIQETKGMTVAPGAEGLLNLRPDDVFYVGGYPSFTFPPLLRFPGY	835
Qy	2818	LGCIMETLNEEVVSLNFEQTFMLDTAVDKPCARSKATGDPWLTDGSLDGSGPARISF	2877
Db	836	RGCIEMDTLNEEVVSLNFEFTFQDТАVDRPCARSKSTGDPWLTDGSLDGTGPARISF	895
Qy	2878	EKQFSNTKRFDOELRLVSYNGIIFELKQESQFCLCLAVQEGTLVLFYDFGSLGKKADPLQP	2937
Db	896	DSQISTTKRFEQELRLVSGVLFELKQSQFCLCLAVQEGSLVLLYDFGAGLKKAVPLQP	955
Qy	2938	PQALTAASKAIOVFLLAGNPKRVLVRVERATVFSVDQDNMLEMADAYILGGVPEQLPLS	2997
Db	956	PPPLTSASKAIOVFLLGSRKRVLVRVERATVYSVEQDNLDLEADAYILGGVPPDQLPPS	1015
Qy	2998	LRQLPPSGSVRGCIKIGKALGVYDVKRLNNTTIGISFGCTADLLVGRMTTFHGHGFLPLA	3057
Db	1016	LRRLPFTGGSVRGCVKIGKALGVYDVKRLNNTTGSAGCTADLLVGRAMTFHGHGFLRLA	1075
Qy	3058	LPDVAPITEVVYSGFGRGTQDNLLYYRTSPDGPYQVSLREGHVTLRFMNOQEVETQRFV	3117
Db	1076	LSNVAPLTGNVYSGFGFHSQDSALLYRASPDGLCQVSLQQGRVSLQLLRETEVKTAQGF	1135
Qy	3118	ADGAPHYVAFYSNVTGVWLYYDDQLQVLKSHERTTPEMLQLOPEEPSRLLLGGLPVSGTFH	3177
Db	1136	ADGAPHYVAFYSNATGVWLYYDDQLQQMKPHRGPPPELQPQPEGPPRLLLGGLPESGTIY	1195
Qy	3178	NFSGCISNVFVQRLRGPQRFVDLHQNMGSVNVSVCCTPAQLIETS-----RATAQKVS	3230
Db	1196	NFSGCISNVFVORLLGPORVFDLOONLGSVNVS TGCAFPALQAOPTGLGPRGLQATARKAS	1255

RESULT 15

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; TITLE OF INVENTION: PROTEIN-SENSITIVE POLYMERIZATION OF VINYL MONOMERS 21103 2325

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; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-037-417-48

Query Match      25.2%; Score 5018.5; DB 12; Length 3712;
Best Local Similarity 31.3%; Pred. No. 7.9e-305;
Matches 1227; Conservative 595; Mismatches 1527; Indels 569; Gaps 122;

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Qy      60  EYNEVNTLDLGOVFHVAIVLIKFPANSPRPDLVLERSTDGHTYQWPQWQFPAASSKRDCL 119
      :|||||:
Db      111  KFEVNLNTINFEQEFHVAIVLIRMGNSPRPGLTWLEKSTDYDKTWTWQHFSDTPADCET 170

Qy      120  RFGPRTLERITQDDDDVICITEYSRIIVPLENGEIVVSLVNGRPGALNFSYSPLLRDFTKAT 179
      |||:|||||:
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Qy      180  NTRLRFLRTNTLLHLMGKALRDPTVTRRRYYYSIKDISIGGRVCVCHGHADVCDKADPLDP 239
      |||:|||||:
Db      231  NVRIILLRTKNLLGLHMSVARQDPTVTRRRYFYSIKDISIGGRCMCNHGHADTCDVQDKXSP 290

Qy      240  FR-LQACQHNTCGGSCDRCPGFNQPKPATTPDSANECQSCNCHGHAYDCYDPEVDR 298
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Qy      299  RNASONQDNVYQGGVCLDCQHTTGINCERCLPGFPRAPDQPLDSPHVCRPCDCESDFT 358
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Db      351  KGLSLDIHGYDGGVGCNQHNVTGINCNCCKPKYRPGKHWNEDTVCSQCQDYFFS 410

Qy      359  DGTCEDLTGRCYCRPNFTGBLCAACAEGYTDFPHCYPLPSFPHNDRREQVLPAQIVNCD 418
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Db      411  TGHCEETGNCECRAAFQPPSCDSAYGYYPNC-----RE-----CE 449

Qy      419  CNAAGTQGNACRKDPRLGRVCVKPNFRGAHCELCAPGFHG-PSCHPCQCSSPGVANSLCD 477
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Db      450  CNLNGTNGYHCEAESG-QQCPCKINFAGAYCKQCAEGYGFPECKACECNKIGSITNDON 508

Qy      478  PESGQCMCRTGFEGRDCHCALGYFHFPLCQLCGCSPAGTLPBGCD-EAGRCQCRPGFDG 536
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Db      509  VTGECCKLTNFGDNCERCKHGYFNYPTCSYCDNDQGTSEI CNKQSGQCICREGFGG 568

Qy      537  PHCDRCLPGYHGYPDCHACADPRGALDQQCGVGLCHCRPGNTGATCQECSPGFYGFPS 596
      :|||||:
Db      569  PRCDQCLPGFYNYPDCKPCNCSSTGSSAITCDNTGKCNCLNFAKGQCTLTAGYYSYD 628

Qy      597  CIPCHCSADGSLHTTCDPTTGQCRCRPRVTGLHCDMCPVPGAYNFPYCEAGSCHPAGLAP- 655
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Db      629  CLPCHCDSHSGQVSCN-SDGQCLCPNFDGRQDCSCKEGFYNFPFSCDCNCDPAGVIDK 687

Qy      656  -ANPALPETQAPCMCRAHVEGPGSCDRCKPGYWGLSASNPEGCTRCSCDPRGLGGVTECQ 714
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Db      688  FAGCGSVPGELCKCKERVTRGICNECKPLYWNLNISNTEGCEICDCWTDGTISALDTCT 747

Qy      715  G-NGQCFCKAHVCGKTAACKDGGFFGLDYADYFGCRSCRCDDVGGALGQCGCEPKTGACRCR 773
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Db      748  SKSGQCPCKPHTQRRRCQECRDGTFDLDSASLFGCKDCSDVGGSMQSVCDKISGQCKXCH 807
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Qy      834  IQPRIVARLNVTSPLFLRIVFRVYVNRGSTSVNGQISVREEGKLSSTCNCTEQSQPVAFPP 893
      :|||||:
Db      868  IQNDVRNEVNVFKSSLYRIVLRVYVNPNAENVATATISVSDNPLE-----VDQHVKVLLQP 922

Qy      894  STEPAPVTV--PQGFGEPPFLNPGIWallVEA-EGVLLDYVLLPSTYYEAAALQHRVT 950
      :|||||:
Db      923  TSEPQVTVAGPLGVKPSAIVLDPRYVFTTKANKNVMLDYFVLLPAAAYEAGILTRHIS 982

Qy      951  EACTYRPSALHSTENCLVYAHLPDLGFPSPAAGTEALCRHDSNLSRPRCPTEQLSFSH---- 1006
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Db      983  NPC-----ELGNMELCRHYKYASVEVFSPAATPFVI--GENSKPTNPVETYTDPEHLQIV 1035

Qy      1007  -----PPLATCFGSDVDIOLEMAVPQPGQYVLVVEYVGE-----DSHQEMGVAVHTPORA 1056
      :|||||:
Db      1036  SHVGDIPLVS---GSQNELHYIVDVPRSGRYIFVIDYISDRNFPDSYY---INLKLKDNF 1089

Qy      1057  PQQGVNLHPCPYSSSLCRSPARDTQHHLAIFHLDS--ASIRLTA---EQAHFFLHSTVL 1111
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Db      1090  DSETSVLLYPCLYSTICTRTSVNEDGMEKS-FYINKEDLPVVIISADIEDGSRFPFIISVTA 1148

Qy      1112  VPVEEFSTEFVEPRVFCVSSHGTFNPPSSAACLASRFPKPPQPIILKDCQVLPPLPDLPLT 1171
      :|||||:
Db      1149  IPVDQWSIDYINPSPCVI-----HDQQCATPKFRSVP-----DSKKIEPETD---- 1191

Qy      1172  QSQELSPGAPPEGPQRPPTAVDPNAEPTLL-RHPQGTVVVFTTQV---PTLGRYAFLLH 1226
      :|||||:
Db      1192  HEDRIATNKPPY-----ASLDERVKLVHLDSONEATIVIESKVDATKPNL--FVILVK 1242

Qy      1227  GYQPVHPSFPVEVLINGGR-IWQGHANASFCPHGYGCGRTLVLCGQTMLDVTNDELTVTV 1285
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Db      1243  YYQSPHPKYQVYVYTLTAGKNQYDGKFDIOHCPSSSGRGVIRPAGEGSFEI-DDEFKFTI 1301

Qy      1286  RVPEGRWLWDYVLIVPEDAYSSSYLOEPLDKSYDFISHCATQGYHISPPSSSSPFCRNA 1345
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Db      1302  TTDRSQSVWLDYLVVWPLKQYNDLLVEETFDQTKFEIQNCGHDHFHIT-HNASDFCKKS 1360

Qy      1346  ATSLSLFYNNGALPCGCHEVCAVSPTCEPFGGQCPCRGHVIGRDCSRCATGYWGFNCRP 1405
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Db      1361  VFSLTADYNSGALPCNCDYAGSTSFECHPFGGQCQCKPNVIERTCGRCRSRYGFPDCKP 1420

Qy      1406  CDC-GARLDELGTQCI CPRTVPDPCLVCQPOSFGCHPLVGCEECNCSPGQVQELTDPT 1464
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Db      1421  CKCENSAMCEPTTGECMCPNVIGDLCEKCAPNTYGFHQVIGCEECACNPMGIAN-GNSQ 1479

Qy      1465  CMDSDGQCRCPNVAGRRCDTCAPGYGYPSRCPDCHEAGTMASVCDPLTGQCHCKENV 1524
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Db      1480  CDLENGTCECRQNIIEGRACDVCSNGYFNFPHCEQCSCHKPGTELEVCDKIDGACFCCKNV 1539

Qy      1525  QGSRCDQCRVGTFSLDAANPKGCTRCFCGATERCG-----NSNLARH-----EFVD 1571
      :|||||:
Db      1540  VGRDCDQCVDTYNLQESNPDGCTTCFCFGKTSRCDsAYLRVYNVSLLKHVSITTFEFHE 1599

Qy      1572  MEGWVLLSSDRQVVPHEHREIEL----LHAD--LFSVADTFSELYWQAPPSYLG----- 1620
      :|||||:
Db      1600  ES-----IKFDMWVPVPAD---EILLNETTLKADFTLREVND-----ERPAYFGVLDYL 1644

Qy      1621  ---DRVSSYGGTLLHYELHSETQRGDI FIPYESRPDVLVQLGNQMSIAFLELAYPPPGQVH 1676
      :|||||:
Db      1645  LNQNHNISAYGGDLAYTLHFTSGFDGKYI---VAPDVILFSEHNALVHTSYEQPSRNEPF 1701

Qy      1677  RGQLQVEGNFRHLETHNPVSREELMMVLAGLEQLQIRALFSQTSSSVSLRRVVLEVASE 1736
      :|||||:
Db      1702  TNRVNIVESNFQTI-SGKPVSRADFMVLRDLKVIPIRANYWEQTLVTHLSDVYLTLADE 1760

Qy      1737  AGRGPPASN--VELCMCPANVRGDSQCECAPGYRDTKGLFLGRCVPCQCHGHSRCLP 1793
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Db      1761  DADGTGEYQFLAVERCSPFGYSGHSCEDCAPGYRDPSPGYGICYIPCCECNHSETCDC 1820
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QY	1794	GS	GICVGCQHNTG	QDCERC	RP	GFVSSDP	SPN	PASPC	PLAVPS	NNFADG	CVLRNGR	1853
Db	1821	AT	GICKCKCHGT	GDHCHC	ER	CVSGYYG	NA	TGTPG	DCMICAC	PLPFD	SNFATSCE	1880
QY	1854	TQ	--CLCR	PGYAGAS	CERC	CAP	FFGNPL	VLGSS	CQPCDC	SGNGDP	NMIFSD	1911
Db	1881	DQ	IHCEK	PGYTG	PRCES	CANGFY	GEPE	SIGVCK	PC	CSGNIN	PEDQGS	1939
QY	1912	GCLR	HTTGH	CERC	CAP	FYGNALL	PGN	CTRCD	SPCGT	TETCD	PQSGRCL	1971
Db	1940	RCLN	NTFGA	CNLC	CAP	FYGD	AIK	KNCS	CD	DDLTGT	CDPFGV	1999
QY	1972	RC	LEGYF	GEQ	CC	RC	PCAC	GPAAK	SGE	CHPQ	SGCHCQ	2031
Db	2000	RCKP	DHYG	FES	GV	CRAC	DCGA	ASNST	QC	DHTGH	CAKSGVT	2059
QY	2032	GRR	CCQ	PRGH	----	CDP	HTG	CTCP	PG	LSGER	CDTCS	2086
Db	2060	GCTP	CNCN	QGY	S	R	FGC	GNPTG	KCQ	CLPG	VIGDR	2112
QY	2087	DHCV	VLLDD	LER	AGALL	PA	IREQ	LO	GIN	ASSA	WARL	2141
Db	2113	NNCH	HALDD	V	TRM	RYQ	IDS	V--	LED	FN	SVTLA	2169
QY	2142	PGPR	YQAAQ	LQ	T	LE	QO	SIS	LQ	QD	TERL	2201
Db	2170	----	NSVD	L	SPSK	ANSE	LES	DA	KS	YAKV	QNTLAN	2220
QY	2202	RAVGR	ALNEL	AS	RM	GQ	SP	GD	AL	VP	SGEQL	2261
Db	2221	----	----	----	----	----	----	----	----	----	----	2256
QY	2262	AEAQ	RLMAR	VQ	----	----	----	----	----	----	----	2305
Db	2257	EQ	AQHIL	G	ING	T	S	I	E	L	T	2316
QY	2306	ALNQ	AVNTT	REA	EEL	NS	R	Q	ER	VKEAL	QWQEL	2352
Db	2317	HLED	LF	N	WS	--	EAS	Q	AKS	AD	V	2375
QY	2353	SLIL	GHV	SEL	LQ	GID	AKED	LE	HLA	ASLD	GA	2412
Db	2376	DLTL	NI	Q	IN	Q	KL	N	LD	AL	N	2426
QY	2413	KL	NQ	LAIN	S	G	I	L	G	--	INQDR	2471
Db	2427	KA	ELAI	KAQ	D	LAAQ	Y	T	D	T	ASA	2486
QY	2472	--	VQ	RGLAA	--	GAR	QLLANS	--	SAL	EETIL	G	2525
Db	2487	TD	GIEER	AHL	AD	T	G	S	T	D	L	2539
QY	2526	LAAQ	IOE	AQ	AM	L	AM	D	T	S	E	2584
Db	2540	TEH	Q	KD	IN	K	L	D	L	I	D	2599
QY	2585	G	----	--	LQ	Q	D	L	S	O	V	2635
Db	2600	GINR	D	L	T	N	K	D	V	S	O	2654
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Db	2655	ENL	K	A	Q	E	A	A	R	L	A	2710
QY	2696	KNTG	D	H	F	V	L	Y	M	G	----	2749
Db	2711	----	G	F	L	L	Y	L	G	N	D	2764
QY	2750	AAV	S	I	D	R	T	L	Q	F	G	2803
Db	2765	QAV	--	VDR	--	MGP	NA	K	L	T	I	2818
QY	2804	--	SNFT	P	P	P	E	P	L	R	F	2850

Db	2819	GISDFNAPDLT	TNSFSGDIEDLKIGDES	VGLWNFVYGGDDNDQGRERDVLLEKKKPV	TG 2878	
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Qy	2911	CLAVQEGILV	FDGSGCLKKADPLQPPQAL	TAASKAIQVFLLAGNRKRV-----LVRV	2964	
Db	2927	SIEMIDGAI	FFNISLGE	-----GGVQ-----SGSQDRYNDNQWHKVQA	2965	
Qy	2965	ER-----	ATVFSVDQDNMLEMADAY	YLGVPPE-QLPILSLRQLFPSGGSV	3008	
Db	2966	ERENRGLLK	VDDIVISRTNAPLEAD	LELPKLRLYFGGHPRRRLNTSISLQPNFD	3020	
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Db	3021	-GCIDNVIN	QGVVDL	TEYVTGGVEEGCSAKFST	VVSYPHEYGFLRMNVSSDNNLHV 3079	
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Qy	3214	-----	-----	-----TPAQL	3218	
Db	3241	SGDNEVES	PWSNADTLP	PKPDIESTL	PETPTTTTTTTTTTTTSTTTSTTTTTPSPI 3300	
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Qy	3265	LQFVGIS	PSHRNRLHLS	MLVRPHAA	SQGLLSTAPMSGRSPSLVLFLNHGHFVAQTEGPG 3324	
Db	3360	LQINSLP	VKVRHHDIG	ISFRTERPN-GLLI-YAG	SKQRDDFIAVYLLDGRVYVEIR-VG 3416	
Qy	3325	PRLQ--	VQSRQHSRAGQ	MHRVSVRWGMQOIQL	VVDGSGTWSQKALHHRVPRAE	RPOP---3379
Db	3417	AQLQAKIT	TEAELNDGT	WHTVEVVRTQKVS	LLIDKLEQPGSVDLN-----AERSAPVLA 3471	
Qy	3380	--YTL	SVGGL-----	PASSYSKLP	SVSGFSGCLKKLQDKQLR	TPTQMVGVTPC 3428
Db	3472	VELPIY	LG	VKNKFLSEVKNLTD	FKTEVPY--FNGCLKNIKFDAM	DLPTPEEFGVVP 3528
Qy	3429	VSGPLED	GLFFPGSEGV	VTLELPKAKMPY	VVSLEMLRPLAAAGLIF--HLGQALA	-----3481
Db	3529	-SEOVER	GLFFENNQAF	VKIFDHF	DVGTEMKISDFRPRDPNGLL	FSVHGKNSYAILLEV 3587
Qy	3482	--TPYMQL	KVLTEQVLLQ	ANDGAGEF	STWVTYP--KLCDGRWHR	VAVIMGRDILRLLEV 3536
Db	3588	DNTLYFT	VTKTDLKNIV	-----STNYKL	PNNESFCDGKTRNVQAIK	SKFVINIAVD 3637
Qy	3537	-TQSNHTT	GRLPESLAGS	PALLHLGS-----LPKS	STARPELPAYRGCLRKLLINGAPV	3589
Db	3638	FISSNP	GVNGE	SVITRTNRPL	FLGGHVAFORAPGIKTKK	----SFKGCISKVEVNQMI 3693
Qy	3590	NVTASVQ	IQGAVGMR	GCP 3607		
Db	3694	NITPNM	-VVGDI	WQGYCP 3710		

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6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	20118	100.0	3695	14	US-10-037-182-2
2	20104	99.9	3695	12	US-10-312-352-22
3	20060.5	99.7	3696	15	US-10-312-088-31
4	20035.5	99.6	3690	12	US-10-112-944-347
5	20030	99.6	3705	15	US-10-312-088-30
6	18254.5	90.7	3600	12	US-10-037-417-2
7	18231	90.6	3597	12	US-10-037-417-6
8	15839	78.7	3635	9	US-09-845-583-2
9	15839	78.7	3635	12	US-10-037-417-47
10	15839	78.7	3635	14	US-10-037-182-4
11	15120	75.2	2743	14	US-10-037-182-36
12	8504.5	42.3	1677	12	US-10-112-944-801
13	8499.5	42.2	1640	12	US-10-037-417-8
14	7804.5	38.8	1634	12	US-10-037-417-49
15	5097	25.3	3712	12	US-10-037-417-48

16	5097	25.3	3712	13	US-10-108-605-103	Sequence 103, Appl
17	5093	25.3	3712	12	US-10-037-417-51	Sequence 51, Appl
18	5002	24.9	953	9	US-09-845-583-4	Sequence 4, Appl
19	5002	24.9	953	12	US-10-037-417-50	Sequence 50, Appl
20	4974	24.7	3672	15	US-10-369-493-6146	Sequence 6146, Ap
21	4756.5	23.6	908	12	US-10-037-417-4	Sequence 4, Appl
22	3069.5	15.3	3070	10	US-09-961-403-7	Sequence 7, Appl
23	2933	14.6	3084	9	US-09-938-275-4	Sequence 4, Appl
24	2933	14.6	3084	14	US-10-262-670-2	Sequence 2, Appl
25	2854	14.2	3075	9	US-09-938-275-5	Sequence 5, Appl
26	2514	12.5	2823	15	US-10-369-493-5220	Sequence 5220, Ap
27	2514	12.5	2823	15	US-10-369-493-5221	Sequence 5221, Ap
28	2260.5	11.2	1693	15	US-10-603-725-4	Sequence 4, Appl
29	2260.5	11.2	1693	15	US-10-603-725-8	Sequence 8, Appl
30	2260.5	11.2	1713	14	US-10-171-311-113	Sequence 113, App
31	2260.5	11.2	1713	15	US-10-372-683-10	Sequence 10, Appl
32	2260.5	11.2	1713	15	US-10-603-725-6	Sequence 6, Appl
33	2260.5	11.2	1724	15	US-10-603-725-2	Sequence 2, Appl
34	2249	11.2	1694	15	US-10-603-725-12	Sequence 12, Appl
35	2249	11.2	1725	15	US-10-603-725-10	Sequence 10, Appl
36	2153.5	10.7	1816	14	US-10-299-058-4	Sequence 4, Appl
37	2149	10.7	1823	12	US-10-363-616-457	Sequence 457, App
38	2147.5	10.7	1816	14	US-10-299-058-2	Sequence 2, Appl
39	2136.5	10.6	1816	15	US-10-372-683-4	Sequence 4, Appl
40	1995	9.9	463	15	US-10-264-049-3039	Sequence 3039, Ap
41	1729	8.6	634	10	US-09-949-029-134	Sequence 134, App
42	1667	8.3	342	15	US-10-264-049-3068	Sequence 3068, Ap
43	1633	8.1	365	9	US-09-925-299-1007	Sequence 1007, Ap
44	1633	8.1	365	10	US-09-925-299-1007	Sequence 1007, Ap
45	1618.5	8.0	483	15	US-10-108-260A-3715	Sequence 3715, Ap

ALIGNMENTS

RESULT 1
US-10-037-182-2
; Sequence 2, Application US/10037182 -
; Publication No. US20030044899A1
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Doi, Masayuki
; APPLICANT: Thyboll, Jill
; TITLE OF INVENTION: Recombinant Laminin 10
; FILE REFERENCE: 99-274-F
; CURRENT APPLICATION NUMBER: US/10/037,182
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,449
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/279,282
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 3695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-037-182-2

QY	1	MAKRLCAGSALCVRGPRGAPAPLLLVGLALLGAARAREEAGGGFSLHPPYFNLAEGARIAA	60	Sequence 2, Appl
Db	1	MAKRLCAGSALCVRGPRGAPAPLLLVGLALLGAARAREEAGGGFSLHPPYFNLAEGARIAA	60	Sequence 2, Appl
QY	61	SATCEEAPARGSPRPTELYCKLVGGPVAGGDPNQIRGOYCDICTAANSNKAHPASNA	120	Sequence 4, Appl
Db	61	SATCEEAPARGSPRPTELYCKLVGGPVAGGDPNQIRGOYCDICTAANSNKAHPASNA	120	Sequence 4, Appl
QY	121	IDGTERWQSPPLSRGLEYNVNTLDLGOVHVAVYLIKFPANSPRDLWLERSMDFGR	180	Sequence 8, Appl

Db	121	IDGTERWWQSPPLSRGLEYNVNVTLDLGQVHFHVAVLKFNANSPRDLWVLSRSMDFGR	180
QY	181	TYQPWFQFFASSKRDCLERFGPQTLEIRTRDDAICTTEYSRIVPLENGEIVVSVLNGRPG	240
Db	181	TYQPWFQFFASSKRDCLERFGPQTLEIRTRDDAICTTEYSRIVPLENGEIVVSVLNGRPG	240
QY	241	AMNFSYSPLLRFTKATNVLRFLRNTLLGHLMGKALRDPVTVRRYYISIKDISIGRC	300
Db	241	AMNFSYSPLLRFTKATNVLRFLRNTLLGHLMGKALRDPVTVRRYYISIKDISIGRC	300
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QY	361	CYGHATDCYYDPEVDRRRASQSLDGTYYQGGVVICDQHHTAGVNCERCLPGFYRSPNHPL	420
Db	361	CYGHATDCYYDPEVDRRRASQSLDGTYYQGGVVICDQHHTAGVNCERCLPGFYRSPNHPL	420
QY	421	DSPHVRRNCNCESDFTDGTCEDLTGRCYCRPNFSGERCDVCAEGFTGFPSCYPTPSSND	480
Db	421	DSPHVRRNCNCESDFTDGTCEDLTGRCYCRPNFSGERCDVCAEGFTGFPSCYPTPSSND	480
QY	481	TREQVLPAGQIVNCDCSAAGTOGNACRKPVRVGRCLCKPNFQGTCHCELCAFGYGGCQP	540
Db	481	TREQVLPAGQIVNCDCSAAGTOGNACRKPVRVGRCLCKPNFQGTCHCELCAFGYGGCQP	540
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Db	601	EAGRCLCQPEFAGPHCDRCRPGYHGFPPNCQACTCDPRGALDQLCGAGGLCRCPGYTGTA	660
QY	661	CQECSPGFHGFPPSCVPCHCSAEGSLHAAACDPRSGQCSCEPRVTGLRCDTCTVPGAYNFPYC	720
Db	661	CQECSPGFHGFPPSCVPCHCSAEGSLHAAACDPRSGQCSCEPRVTGLRCDTCTVPGAYNFPYC	720
QY	721	EAGSCHPAGLAPVDPALPEAQVPCMCRAHVEGPSCDRCRPGFWGLSPSNPEGCTRCSCDL	780
Db	721	EAGSCHPAGLAPVDPALPEAQVPCMCRAHVEGPSCDRCRPGFWGLSPSNPEGCTRCSCDL	780
QY	781	RGTLGGVAECQPGTGQCFCKPHVCQACASCKDGGFLDQADYFGCRSCRCIDIGGALQOS	840
Db	781	RGTLGGVAECQPGTGQCFCKPHVCQACASCKDGGFLDQADYFGCRSCRCIDIGGALQOS	840
QY	841	CEPRTGVCRCRPNQPTCSEPARDHYLPDLHLRLLELEEAATPEGHAVRFGFNPLEFEN	900
Db	841	CEPRTGVCRCRPNQPTCSEPARDHYLPDLHLRLLELEEAATPEGHAVRFGFNPLEFEN	900
QY	901	FSWRGYAQMVPQPRIVARLNLTSPLDLFWLVFRYVNRGAMSVSGRVSREEGRSAAACANC	960
Db	901	FSWRGYAQMVPQPRIVARLNLTSPLDLFWLVFRYVNRGAMSVSGRVSREEGRSAAACANC	960
QY	961	TAQSQPVAFPPSTEPAFITVPQRGFGEPFVLNPGTVALRVEAGVLLDYVLLPSAYYEA	1020
Db	961	TAQSQPVAFPPSTEPAFITVPQRGFGEPFVLNPGTVALRVEAGVLLDYVLLPSAYYEA	1020
QY	1021	ALLQLRVTEACTYRPSAQSGDNCLLYTHPLDGFPSAAGLEALCRQDNSLPRPCPTEQL	1080
Db	1021	ALLQLRVTEACTYRPSAQSGDNCLLYTHPLDGFPSAAGLEALCRQDNSLPRPCPTEQL	1080
QY	1081	SPSHPPPLITCTGSDVDVQLQVAVPQGRVALVVEYANEDARQEVGVAVHTPQAPQOGLL	1140
Db	1081	SPSHPPPLITCTGSDVDVQLQVAVPQGRVALVVEYANEDARQEVGVAVHTPQAPQOGLL	1140
QY	1141	SLHPCLYSTLCRGTAQDTQDHLAVFHLDSASVRLTAEQARFFLHGVTLPVIEEFSPEFV	1200
Db	1141	SLHPCLYSTLCRGTAQDTQDHLAVFHLDSASVRLTAEQARFFLHGVTLPVIEEFSPEFV	1200
QY	1201	EPRVSCISSHGAFGNNSAACLPSPFKPQPIILRDCQVILPPLPGILPLTHAQDLTPATSP	1260
Db	1201	EPRVSCISSHGAFGNNSAACLPSPFKPQPIILRDCQVILPPLPGILPLTHAQDLTPATSP	1260

QY	1261	AGPRPRPPTAVDPDAEPTLLREPOATVFTTHVPTLGRYAFLLHHGYQPAHPTFPVEVLIN	1320
Db	1261	AGPRPRPPTAVDPDAEPTLLREPOATVFTTHVPTLGRYAFLLHHGYQPAHPTFPVEVLIN	1320
QY	1321	AGRWVQGHANASFCPHGYGCRTLVVCEGQALLDVTHSELTVTVRVPEGRWLWLDYVVLVVP	1380
Db	1321	AGRWVQGHANASFCPHGYGCRTLVVCEGQALLDVTHSELTVTVRVPEGRWLWLDYVVLVVP	1380
QY	1381	ENVYSFGYLREEPLDKSYDFISHCAAQGYHISPSSSSSLFCRNAAAASLSLFYNNGARPCGC	1440
Db	1381	ENVYSFGYLREEPLDKSYDFISHCAAQGYHISPSSSSSLFCRNAAAASLSLFYNNGARPCGC	1440
QY	1441	HEVGATGPTCEPFGGQCPCHAHVIGRDCSRCATGYWGFPPNCRPCDCGARLCCDELTCQCIC	1500
Db	1441	HEVGATGPTCEPFGGQCPCHAHVIGRDCSRCATGYWGFPPNCRPCDCGARLCCDELTCQCIC	1500
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Db	1501	PPRTIPDCLLCQPQTFGCHPLVGCCECNCSGPGIQBELTDPTCDTDSGQCKCRPNVTGRR	1560
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Db	1561	CDTCSPGFHGYPRCPCDCHEAGTAPGVCDPLTGQCYCKENVQGPCKDCQCSLGTFSLDA	1620
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Db	1621	NPKGCTRCFCFGATERCRSSSYTRQEFVDMEGWVLLSTDQVWPPHERQPGTEMLRADLRH	1680
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Db	1681	VPEAVPEAFPELYWQAPPSYLGDRVSSYGGTLRLYELHSETQRQDVVFVPMESRPDVVLQGN	1740
QY	1741	QMSITFLEPAYPTPGHVHRGQIQLVVEGNFRHTETRTNVTYSREELMMVLASLEQLQIRALFS	1800
Db	1741	QMSITFLEPAYPTPGHVHRGQIQLVVEGNFRHTETRTNVTYSREELMMVLASLEQLQIRALFS	1800
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Db	1801	QISSAVSLRRVALEVASPAGQALASNVELCLCPASVYRSDSCQECAPGFYRDVKGFLGR	1860
QY	1861	CVPCQCHGSHDRCLPGSGVCVDCQHNTEGAHCERCQAGFMSSRDDPSAPCVSCPCPLSVP	1920
Db	1861	CVPCQCHGSHDRCLPGSGVCVDCQHNTEGAHCERCQAGFMSSRDDPSAPCVSCPCPLSVP	1920
QY	1921	SNNFAEGCVLRGGRTQCLCKPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSNGNDPNLL	1980
Db	1921	SNNFAEGCVLRGGRTQCLCKPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSNGNDPNLL	1980
QY	1981	FSDCDPLTGACRGCLRHTTGPRCEICAPGFYGNALLPGNCTRCDCTPCGTEACDPHSGHC	2040
Db	1981	FSDCDPLTGACRGCLRHTTGPRCEICAPGFYGNALLPGNCTRCDCTPCGTEACDPHSGHC	2040
QY	2041	LCKAGVTGRRCDRCQEGHFGFNGCGCRPCACGPAEAGSECHPQSGQCHCRPGTMGPQCR	2100
Db	2041	LCKAGVTGRRCDRCQEGHFGFNGCGCRPCACGPAEAGSECHPQSGQCHCRPGTMGPQCR	2100
QY	2101	ECAPGYWGLPEQGCRRCCQPGGRCDPHTGRNCNCPPLSGERCDCSQQHQVVPVPGGPVGH	2160
Db	2101	ECAPGYWGLPEQGCRRCCQPGGRCDPHTGRNCNCPPLSGERCDCSQQHQVVPVPGGPVGH	2160
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Db	2161	SIHCEVCDHCVVLLDDLERAGALLPAIHEQLRGINASSMAWARLHRLNASIADLQSQLR	2220
QY	2221	SPLGPRHETAQOLEVLEQQSTSLGQDARLGGQAVGTRDQASQLLAGTEATLGHAKTLLA	2280
Db	2221	SPLGPRHETAQOLEVLEQQSTSLGQDARLGGQAVGTRDQASQLLAGTEATLGHAKTLLA	2280
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Db	2281	AIRAVDRTLSELMSQTGHLGLANASAPSGEQLLRTLAEVERLLWEMRARDLGAPOAAAEA	2340

QY 2341 ELAAAQRLRLARVQEQSSLWEEENQALATQTRDELAQHEAGLMDLREALNRAVDATREAOE 2400
Db 2341 ELAAAQRLRLARVQEQSSLWEEENQALATQTRDRRLAQHEAGLMDLREALNRAVDATREAOE 2400
QY 2401 LNSRNOERLEEALQRKQELSRDNATLQATLHAARDTLASVFRLLHSLDQAKEELERLAAS 2460
Db 2401 LNSRNOERLEEALQRKQELSRDNATLQATLHAARDTLASVFRLLHSLDQAKEELERLAAS 2460
QY 2461 LDGARTPLLRQMOTFSPAGSKLRLVEAAEAHAQQLQALNLSSIIILDVNDRLTQRAIE 2520
Db 2461 LDGARTPLLRQMOTFSPAGSKLRLVEAAEAHAQQLQALNLSSIIILDVNDRLTQRAIE 2520
QY 2521 ASNAYSRILOAVQAAEDAAQALQADHTWATVVROGLVDRAQQLLANSTALEEAMLOEQ 2580
Db 2521 ASNAYSRILOAVQAAEDAAQALQADHTWATVVROGLVDRAQQLLANSTALEEAMLOEQ 2580
QY 2581 QRLGLVWAALQGARTQLRDVRAKKDQLEAHIQAAQAAMLMDTDETSKKIAHAKAVAAEAQ 2640
Db 2581 QRLGLVWAALQGARTQLRDVRAKKDQLEAHIQAAQAAMLMDTDETSKKIAHAKAVAAEAQ 2640
QY 2641 DTATRVQSOLQAMOENVERWQGYEGLRGDGLQAVLDAGHSVSTLEKTLPLQALLSIL 2700
Db 2641 DTATRVQSOLQAMOENVERWQGYEGLRGDGLQAVLDAGHSVSTLEKTLPLQALLSIL 2700
QY 2701 ENRGVHNASLALSASIGRVRELIQAARGAASKVKVPKFNKNGRSGVQLRTPRDLADLAAYT 2760
Db 2701 ENRGVHNASLALSASIGRVRELIQAARGAASKVKVPKFNKNGRSGVQLRTPRDLADLAAYT 2760
QY 2761 ALKFYLGQPEPEPGQGTEDRFVMYMGSRQATGDMYGVSLRDKKVVHVVYQLGEAGPAVLSI 2820
Db 2761 ALKFYLGQPEPEPGQGTEDRFVMYMGSRQATGDMYGVSLRDKKVVHVVYQLGEAGPAVLSI 2820
QY 2821 DEDICEQFAAVSLDRTLQFGHMSVTVVEROMIQETKGDITVAPGAEGLLNLRDPPDFVYVGG 2880
Db 2821 DEDICEQFAAVSLDRTLQFGHMSVTVVEROMIQETKGDITVAPGAEGLLNLRDPPDFVYVGG 2880
QY 2881 YPSTFTPPPLLRFPYRGYRGCIEMDTLNEEVVSLYNFERTFQDITAVDRPCARSKSTGDPWL 2940
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Db 3001 LYDFGAGLKKAVPLQPPPLPPTSASKAIQVFLGGSRKRVLRVERATVYSVEQDNDLELA 3060
QY 3061 DAYVLGSGVPPDQLPPSLRWLFPTGGSVRGCVKGIKALGKYVDLKRNTTGVSACTADLL 3120
Db 3061 DAYVLGSGVPPDQLPPSLRWLFPTGGSVRGCVKGIKALGKYVDLKRNTTGVSACTADLL 3120
QY 3121 VGRAMTFHGHGFLRLALSNAVPLTGNVYSGFGFHSQAQDSALLYRASPDGLCQVSLQOQR 3180
Db 3121 VGRAMTFHGHGFLRLALSNAVPLTGNVYSGFGFHSQAQDSALLYRASPDGLCQVSLQOQR 3180
QY 3181 VSLQLLRTEVKTOAGFADGAPHYVAFYSNATGVWLYVDDQLQMKPHRGPPPELQPOPEG 3240
Db 3181 VSLQLLRTEVKTOAGFADGAPHYVAFYSNATGVWLYVDDQLQMKPHRGPPPELQPOPEG 3240
QY 3241 PPRLLILGGLPESGTIYNFSGCISNVFVQRLLGQRVFDLQONLGSVNVSTGCAPALQAQT 3300
Db 3241 PPRLLILGGLPESGTIYNFSGCISNVFVQRLLGQRVFDLQONLGSVNVSTGCAPALQAQT 3300
QY 3301 PGLGPRGLQATARKASRRSRQPARHPACMLPPHLRTRTRDSYQFGGSLSSHLEFFVGILARH 3360
Db 3301 PGLGPRGLQATARKASRRSRQPARHPACMLPPHLRTRTRDSYQFGGSLSSHLEFFVGILARH 3360
QY 3361 RNWPSLSMHVLPRSSRGLLLFTARLPPGSPSLALFLSNGHFVAQMEGLGTRLRAQSRQRS 3420
Db 3361 RNWPSLSMHVLPRSSRGLLLFTARLPPGSPSLALFLSNGHFVAQMEGLGTRLRAQSRQRS 3420
QY 3421 RPGRWHKVSVRWEKNRILLVTDGARAWSQEGPHRQHQAHPQHTLTFVGGLPASSSHSSK 3480

Db 3421 RPGRWHKVSVRWEKNRILLVTDGARAWSQEGPHRQHQAHPQHTLTFVGGLPASSSHSSK 3480
QY 3481 LPVTYGFSGCVKRLRLHGRPLGAPTRMAGVTPCILGPLEAGLFFPGSGGVITLPLPGATL 3540
Db 3481 LPVTYGFSGCVKRLRLHGRPLGAPTRMAGVTPCILGPLEAGLFFPGSGGVITLPLPGATL 3540
QY 3541 PDVGLLEVRPLAVTGLIFHLGQARTPPYLQLVTEKQVLLRADDDGAGEFSTSVTRPSVL 3600
Db 3541 PDVGLLEVRPLAVTGLIFHLGQARTPPYLQLVTEKQVLLRADDDGAGEFSTSVTRPSVL 3600
QY 3601 CDGQWHLRLAVMKSGNVLRLEVDQAQSNHTVGPLLAAAAGAPAPLYLGLLPEPMAVQWPWPPA 3660
Db 3601 CDGQWHLRLAVMKSGNVLRLEVDQAQSNHTVGPLLAAAAGAPAPLYLGLLPEPMAVQWPWPPA 3660
QY 3661 YCGCMRRLAVNRSVPVAMTRSVEVHGAVGASGCPAA 3695
Db 3661 YCGCMRRLAVNRSVPVAMTRSVEVHGAVGASGCPAA 3695

RESULT 2

US-10-312-352-22
; Sequence 22, Application US/10312352
; Publication No. US20040053824A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; TANG, Y. Tom
; APPLICANT: YUE, Henry; AZIMZAI, Yalda
; APPLICANT: HE, Ann; BATRA, Sajeev
; APPLICANT: LO, Terence P.; NGUYEN, Danniell B.
; APPLICANT: BURRILL, John D.; MARCUS, Gregory A.
; APPLICANT: ZINGLER, Kurt A.; GANDHI, Ameena R.
; APPLICANT: LAL, Preeti G.; KEARNEY, Liam
; APPLICANT: BURFORD, Neil; YAO, Monique G.
; APPLICANT: CHAWLA, Narinder K.; ELLIOT, Vicki S.
; APPLICANT: ARVIZU, Chandra S.; KHAN, Farrah A.
; APPLICANT: BAUGHN, Mariah R.; HAFALIA, April, J.A.
; APPLICANT: POLICKY, Jennifer L.; AU-YOUNG, Janice K.
; APPLICANT: LU, Yan; BOROWSKY, Mark L.
; APPLICANT: LU, Dyung Aina M.; RAMKUMAR, Jayalaxmi
; APPLICANT: YANG, Junming; GURURAJAN, Rajagopal
; APPLICANT: WARREN, Bridget A.; GIETZEN, Kimberly J.
; APPLICANT: XU, Yuming; KALLICK, Deborah A.
; APPLICANT: LEE, Ernestine A.; THANGAVELU, Kavitha
; APPLICANT: DELEGANE, Angelo M.; LEE, Sally
; TITLE OF INVENTION: EXTRACELLULAR MATRIX AND CELL ADHESION MOLECULES
; FILE REFERENCE: PE-0794 USN
; CURRENT APPLICATION NUMBER: US/10/312,352
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: PCT/US01/21067
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,454
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/219,462
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 60/240,111
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: US 60/240,106
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: US 60/244,021
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/248,887
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/249,570
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PERL Program
; SEQ ID NO 22
; LENGTH: 3695
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040053824A1 6382722CD1

US-10-312-352-22

Query Match		99.9%;	Score 20104;	DB 12;	Length 3695;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 3694;		Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1	MAKRLCAGSALCVGPRGPAPLLLVGLALLGAARAREEAGGFSLHPPYFNLAEGARIAA	60		
Db	1	MAKRLCAGSALCVGPRGPAPLLLVGLALLGAARAREEAGGFSLHPPYFNLAEGARIAA	60		
QY	61	SATCGEEAPARGSPRPTEGLYCKLVGGPVAGGDPNQTIRGOYCDICTAANSNKAHPASNA	120		
Db	61	SATCGEEAPARGSPRPTEGLYCKLVGGPVAGGDPNQTIRGOYCDICTAANSNKAHPASNA	120		
QY	121	IDGTERWQSPPLSRGLEYNVNVTLDLGOVHFVAYVLIKFNANSPRDLWLERSMDFGR	180		
Db	121	IDGTERWQSPPLSRGLEYNVNVTLDLGOVHFVAYVLIKFNANSPRDLWLERSMDFGR	180		
QY	181	TYQPWQFFASSKRDCLERFGPQTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRPG	240		
Db	181	TYQPWQFFASSKRDCLERFGPQTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRPG	240		
QY	241	AMNFSYSPLLEBFTKATNVRLEFLRNTLLGLHLMGKALRDPVTTRYYYSIKDISIGGRC	300		
Db	241	AMNFSYSPLLEBFTKATNVRLEFLRNTLLGLHLMGKALRDPVTTRYYYSIKDISIGGRC	300		
QY	301	VCHGHADACDAKDPDTPFRLOCTCOHNTCGGTCDCRCCGFGNQPKPATANSANECQSCN	360		
Db	301	VCHGHADACDAKDPDTPFRLOCTCOHNTCGGTCDCRCCGFGNQPKPATANSANECQSCN	360		
QY	361	CYGHATDCYDPEVDRRRASQSLDGTYYQGGVCIDCQHHTAGVNCERCLPGFYRSPNHPL	420		
Db	361	CYGHATDCYDPEVDRRRASQSLDGTYYQGGVCIDCQHHTAGVNCERCLPGFYRSPNHPL	420		
QY	421	DSPHVCRRCNCESDFTDGTCTEDLTGRCYCRPNFSGERCDCVCAEGFTGPPSCYPTPSSND	480		
Db	421	DSPHVCRRCNCESDFTDGTCTEDLTGRCYCRPNFSGERCDCVCAEGFTGPPSCYPTPSSND	480		
QY	481	TREQVLPAQIIVNCDCSAAAGTQGNACRKPVRVGRCLCKPNFQTHCELCAPIFYGPGCQP	540		
Db	481	TREQVLPAQIIVNCDCSAAAGTQGNACRKPVRVGRCLCKPNFQTHCELCAPIFYGPGCQP	540		
QY	541	CQCSSPGVADDDCDPDTGQCRCRVGFEGATCDRCAPGYFHFPLCQLCGCSPAGTLPBGCD	600		
Db	541	CQCSSPGVADDDCDPDTGQCRCRVGFEGATCDRCAPGYFHFPLCQLCGCSPAGTLPBGCD	600		
QY	601	EAGRLCQPEFAGPHCDRCRPGYHGFNQCQACTDPRGALDQLCGAGGLCRCPGYTGTA	660		
Db	601	EAGRLCQPEFAGPHCDRCRPGYHGFNQCQACTDPRGALDQLCGAGGLCRCPGYTGTA	660		
QY	661	CQECSPGFHGFPPSCVPCCHCSAEGSLHAAACDPRSGQSCRPRTGLRCDTCVPGAYNFPYC	720		
Db	661	CQECSPGFHGFPPSCVPCCHCSAEGSLHAAACDPRSGQSCRPRTGLRCDTCVPGAYNFPYC	720		
QY	721	EAGSCHPAGLAPVDPALPEAQVPCMCRAHVEGPSCDRCCKPGFWGLSPSNPEGCTRCSCDL	780		
Db	721	EAGSCHPAGLAPVDPALPEAQVPCMCRAHVEGPSCDRCCKPGFWGLSPSNPEGCTRCSCDL	780		
QY	781	RGTLGGVAECQPGTGQCFCKPHVCGQACASCKDGFGLDQADYFGCRSCRCIDIGGALQOS	840		
Db	781	RGTLGGVAECQPGTGQCFCKPHVCGQACASCKDGFGLDQADYFGCRSCRCIDIGGALQOS	840		
QY	841	CEPRTGVCRCPNTQGTCEBPARDHYLPDLHLRLLELEBAATPEGHAVRFGFNPLEFEN	900		
Db	841	CEPRTGVCRCPNTQGTCEBPARDHYLPDLHLRLLELEBAATPEGHAVRFGFNPLEFEN	900		
QY	901	FSWRYAQMAPVQPRIVARLNLTSPDLFWLVFRVYNRGAMSVSGRVSREGRSAACANC	960		
Db	901	FSWRYAQMAPVQPRIVARLNLTSPDLFWLVFRVYNRGAMSVSGRVSREGRSAACANC	960		
QY	961	TAQSQVAFPPSPTEPAFITVQRFGEPPFVLPNGTVALRVEAEGVLLDYVLLPSPAYYEA	1020		
Db	961	TAQSQVAFPPSPTEPAFITVQRFGEPPFVLPNGTVALRVEAEGVLLDYVLLPSPAYYEA	1020		

QY	1021	ALLQLRVTEACTYRPSAQSGDNCLLYTHPLDGFPSAAGLEALCRQDNSLPRPCPTEQL	1080
Db	1021	ALLQLRVTEACTYRPSAQSGDNCLLYTHPLDGFPSAAGLEALCRQDNSLPRPCPTEQL	1080
QY	1081	SPSHPLITCTGSDVDVQLQVAVPQPGRYALVVEYANEDARQEVGVAVHTPQRAPOQGLL	1140
Db	1081	SPSHPLITCTGSDVDVQLQVAVPQPGRYALVVEYANEDARQEVGVAVHTPQRAPOQGLL	1140
QY	1141	SLHPCLYSTLCRGFTARDTQDHLAVFHLDSASVRLTAEQARFFHLHGVTLPVPIEESPEFV	1200
Db	1141	SLHPCLYSTLCRGFTARDTQDHLAVFHLDSASVRLTAEQARFFHLHGVTLPVPIEESPEFV	1200
QY	1201	EPRVSCISSHGAFGPNSAACLPSPFPKPPPIILRDCQVILPPLPGILPLTHAODLTATSP	1260
Db	1201	EPRVSCISSHGAFGPNSAACLPSPFPKPPPIILRDCQVILPPLPGILPLTHAODLTATSP	1260
QY	1261	AGPRPRPPTAVDPDAEPTLLREPOATVVFTTHVPTLGRYAFLLHGVQPAHPTFPVEVLIN	1320
Db	1261	AGPRPRPPTAVDPDAEPTLLREPOATVVFTTHVPTLGRYAFLLHGVQPAHPTFPVEVLIN	1320
QY	1321	AGRVWQGHANASFCPHGYGCRTLVCEGQALLDVTHSELTVTVRVEGRWLWDYVLVVP	1380
Db	1321	AGRVWQGHANASFCPHGYGCRTLVCEGQALLDVTHSELTVTVRVEGRWLWDYVLVVP	1380
QY	1381	ENVYSFGLREELDKSYDFISHCAAQGYHISPSSSLFCRNNAAASLSLFYNNGARPCGC	1440
Db	1381	ENVYSFGLREELDKSYDFISHCAAQGYHISPSSSLFCRNNAAASLSLFYNNGARPCGC	1440
QY	1441	HEVGATGPTCEPFGGQCPCHAHVIGRDCSRCATGYWGFNCRPCDCGARLCELTGQCIC	1500
Db	1441	HEVGATGPTCEPFGGQCPCHAHVIGRDCSRCATGYWGFNCRPCDCGARLCELTGQCIC	1500
QY	1501	PPRTIPDCLLCOPTFGCHPLVGCCECNSGPGIQELTDTPTDTSQCKCRPNVTGRR	1560
Db	1501	PPRTIPDCLLCOPTFGCHPLVGCCECNSGPGIQELTDTPTDTSQCKCRPNVTGRR	1560
QY	1561	CDTCSPGFHGYPRCRPCDCHAGTAPGVCDPLTGQCYCKENQVQPKDCQCSLGTFSLDAA	1620
Db	1561	CDTCSPGFHGYPRCRPCDCHAGTAPGVCDPLTGQCYCKENQVQPKDCQCSLGTFSLDAA	1620
QY	1621	NPKGTRCFCFGATERCRSSSYTRQEFVDMEGVWLLSTDROVVPHERQPGTEMLRADLRH	1680
Db	1621	NPKGTRCFCFGATERCRSSSYTRQEFVDMEGVWLLSTDROVVPHERQPGTEMLRADLRH	1680
QY	1681	VPEAVPEAFPELYWQAPPSYLGDRVSSYGGTLRYELHSETQGDVFPVMESESRPDVVLQGN	1740
Db	1681	VPEAVPEAFPELYWQAPPSYLGDRVSSYGGTLRYELHSETQGDVFPVMESESRPDVVLQGN	1740
QY	1741	QMSITFLEPAYTPGHVHRGQLQVVEGNFRHTETRTNTVSEELMMVLASLEQLQIRALFS	1800
Db	1741	QMSITFLEPAYTPGHVHRGQLQVVEGNFRHTETRTNTVSEELMMVLASLEQLQIRALFS	1800
QY	1801	QISSAVSLRRVALEVASPAGQALASNVLELCLCPASVYRSDSCQECAPGFYRDVKGLFLGR	1860
Db	1801	QISSAVSLRRVALEVASPAGQALASNVLELCLCPASVYRSDSCQECAPGFYRDVKGLFLGR	1860
QY	1861	CVPCQCHGHSRCLPGSGVCVDCQHNTEGAHCERCAQAGFMSRRDDPSAPCVSCPCPLSVP	1920
Db	1861	CVPCQCHGHSRCLPGSGVCVDCQHNTEGAHCERCAQAGFMSRRDDPSAPCVSCPCPLSVP	1920
QY	1921	SNNFAEGCVLRGGRTQCLCKPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSGNGDPNLL	1980
Db	1921	SNNFAEGCVLRGGRTQCLCKPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSGNGDPNLL	1980
QY	1981	FSDCDPLTGACRGCLRHTTGPCEICAPGFYGNALLPGNCTRCDCCTPCGTEACDPHSGHC	2040
Db	1981	FSDCDPLTGACRGCLRHTTGPCEICAPGFYGNALLPGNCTRCDCCTPCGTEACDPHSGHC	2040
QY	2041	LCKAGVTGRRCDRCQEGHFGFNGCGGCRPCACGPAEAGESECHPQSQGCHCRPGTMGPQCR	2100
Db	2041	LCKAGVTGRRCDRCQEGHFGFNGCGGCRPCACGPAEAGESECHPQSQGCHCRPGTMGPQCR	2100

2101 ECAPGYWGLPEOGCRRCCQPCGRCDPHTGRCNCPPGLSGERCDCSTCQQHQVVPVGGPVGH 2160
2101 ECAPGYWGLPEOGCRRCCQPCGRCDPHTGRCNCPPGLSGERCDCSTCQQHQVVPVGGPVGH 2160
2161 STHCEVCDHCVVLLDDLERAGALLPAIHEQLRGINASSMAWARLHRLNASIADLQSQLR 2220
2161 STHCEVCDHCVVLLDDLERAGALLPAIHEQLRGINASSMAWARLHRLNASIADLQSQLR 2220
2221 SPLGPRHETAQOQLEVLQEQSTSLGQDARRLGGQAVGTRDQASQLLAGTEATLGHAKTLLA 2280
2221 SPLGPRHETAQOQLEVLQEQSTSLGQDARRLGGQAVGTRDQASQLLAGTEATLGHAKTLLA 2280
2281 AIRAVDRITLSELMSTGHLGLANASAPSGEQLLRTLAEVERLLWEMRARDLGAPOAAAEA 2340
2281 AIRAVDRITLSELMSTGHLGLANASAPSGEQLLRTLAEVERLLWEMRARDLGAPOAAAEA 2340
2341 ELAAQRLRLARVQEQSLSSLWEENQALATQTRDRLAQHEAGLMDLREALNRAVDATREAOE 2400
2341 ELAAQRLRLARVQEQSLSSLWEENQALATQTRDRLAQHEAGLMDLREALNRAVDATREAOE 2400
2401 LNSNRQERLEALQKQELSRDNATLQATLHAARDTLASVFRLLHSLDQAKEELERLAAS 2460
2401 LNSNRQERLEALQKQELSRDNATLQATLHAARDTLASVFRLLHSLDQAKEELERLAAS 2460
2461 LDGARTPLLRQMOTFSPAGSKRLVBAABAAQQLGQALNLSIIILDVNQDRLTQRAIE 2520
2461 LDGARTPLLRQMOTFSPAGSKRLVBAABAAQQLGQALNLSIIILDVNQDRLTQRAIE 2520
2521 ASNAYSRILOAVQAAEDAAGQALQQAADHTWATVVRQGLVDRAQQLLANSTALEEAMLOEQ 2580
2521 ASNAYSRILOAVQAAEDAAGQALQQAADHTWATVVRQGLVDRAQQLLANSTALEEAMLOEQ 2580
2581 QRLGLVWAALQAGARTQLRDVRAKQDQLEAHIQAAQAMLMDTDETSKKIAHAKAVAAEAQ 2640
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2641 DTATRVQSQLQAMQENVERWQGYEGLRGDQGLQAVLDAGHSVSTLEKTLPLQLLAKLSIL 2700
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2701 ENRGVHNASLALSASIGRVRELIAQARGAASKVKVPMKFNRSVQLRTPRDLADLAAYT 2760
2701 ENRGVHNASLALSASIGRVRELIAQARGAASKVKVPMKFNRSVQLRTPRDLADLAAYT 2760
2761 ALKFYLOQPEPEPGGTEDRFVVMYMSRQATGDMYMSLRDKKHWVYQLGEAGPAVLSI 2820
2761 ALKFYLOQPEPEPGGTEDRFVVMYMSRQATGDMYMSLRDKKHWVYQLGEAGPAVLSI 2820
2821 DEDIGEQAFAAVSLDRTLOFGHMSVTVERQMIQETKGTDTAPGAEGLLNLRPPDDFVYVGG 2880
2821 DEDIGEQAFAAVSLDRTLOFGHMSVTVERQMIQETKGTDTAPGAEGLLNLRPPDDFVYVGG 2880
2881 YPSTFTPPPLRFPYRGCIEMDTLNEEVVSLYNFERTFQDLDTAVDRCARSKSTGDPWL 2940
2881 YPSTFTPPPLRFPYRGCIEMDTLNEEVVSLYNFERTFQDLDTAVDRCARSKSTGDPWL 2940
2941 TDGSYLDGTGFARISFDSQISTTKRFEQELRLVSYSGVLFFLKQOSQFLCLAVQEGSLVL 3000
2941 TDGSYLDGTGFARISFDSQISTTKRFEQELRLVSYSGVLFFLKQOSQFLCLAVQEGSLVL 3000
3001 LYDFGAGLKKAVPLQPPPLTSASKAIQVFLGGSRKRVLRVERATVYSVEQDNDLELA 3060
3001 LYDFGAGLKKAVPLQPPPLTSASKAIQVFLGGSRKRVLRVERATVYSVEQDNDLELA 3060
3061 DAYYLGGVPPDQLPPSLRWLPTGGSVRGCVKGKALGKYVDLKRNLTTGVSAGCTADLL 3120
3061 DAYYLGGVPPDQLPPSLRWLPTGGSVRGCVKGKALGKYVDLKRNLTTGVSAGCTADLL 3120
3121 VGRAMTFHGHGFLRLALSNAVPLTGNVYSGFGFHSQADSALLYRASPDGLCQVSLQOGR 3180
3121 VGRAMTFHGHGFLRLALSNAVPLTGNVYSGFGFHSQADSALLYRASPDGLCQVSLQOGR 3180
3181 VSLQLLRTEVKTQAGFADGAPHYVAFYSNATGVWLYVDDQLQOMKPHRGPPELQPOPEG 3240

3181 VSLQLLRTEVKTQAGFADGAPHYVAFYSNATGVWLYVDDQLQOMKPHRGPPELQPOPEG 3240
3241 PPRLLGGLPESGTTYNFSGCISNVFQRLGQVDFDLQCNLGSVNVSTGCAPALQAQT 3300
3241 PPRLLGGLPESGTTYNFSGCISNVFQRLGQVDFDLQCNLGSVNVSTGCAPALQAQT 3300
3301 PGLGPRGLQATARKASRRSRQPARHPACMLPPHLRTRTRDSYQFGGSLSSHLEFVGILARH 3360
3301 PGLGPRGLQATARKASRRSRQPARHPACMLPPHLRTRTRDSYQFGGSLSSHLEFVGILARH 3360
3361 RNWPSLSMHVLPSSRGLLFFARLRPGSPSLALFLSNHGFVAQMEGLGTRLRAQSRORS 3420
3361 RNWPSLSMHVLPSSRGLLFFARLRPGSPSLALFLSNHGFVAQMEGLGTRLRAQSRORS 3420
3421 RPGRWHKVSVRWEKNRILLVTDGARAWSQEGPHRQHQAHPQPHHTLFGGGLPASSHSSK 3480
3421 RPGRWHKVSVRWEKNRILLVTDGARAWSQEGPHRQHQAHPQPHHTLFGGGLPASSHSSK 3480
3481 LPVTGVFGSGCVKRLRLHGRPLGAPTRMAGVTPCILGLEAGLFFPGSGGVITLPLPGATL 3540
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3541 PDVGLELEVRPLAVTGLIFHLGQARTPPYLQVTEKQVLLRADDGAGEFSTSVTRPSVL 3600
3541 PDVGLELEVRPLAVTGLIFHLGQARTPPYLQVTEKQVLLRADDGAGEFSTSVTRPSVL 3600
3601 CDGQWHRLAVMKSGNVLRLEVDQAQSNHTVGPPLAAAGAPAPLYLGGCLPEPMAVQPPPPA 3660
3601 CDGQWHRLAVMKSGNVLRLEVDQAQSNHTVGPPLAAAGAPAPLYLGGCLPEPMAVQPPPPA 3660
3661 YCGMRRRLAVNRSPVAMTRSVVEVHGAVGASGCPAA 3695
3661 YCGMRRRLAVNRSPVAMTRSVVEVHGAVGASGCPAA 3695

RESULT 3

US-10-312-088-31
; Sequence 31, Application US/10312088
; Publication No. US20030219862A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Cogswell, John P.
; APPLICANT: Kabnic, Karen S.
; APPLICANT: Lai, Ying-Ta
; APPLICANT: Martensen, Shelby A.
; APPLICANT: Murdock, Paul R.
; APPLICANT: Smith, Randall F.
; APPLICANT: Strum, Jay C.
; APPLICANT: Xiang, Zhaoying
; APPLICANT: Xie, Qing
; APPLICANT: Rizni, Safia K.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50029
; CURRENT APPLICATION NUMBER: US/10/312,088
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/19929
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,161
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/213,156
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 3696
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-312-088-31

Query Match 99.7%; Score 20060.5; DB 15; Length 3696;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3687; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 1081 SPSHPPLITCTGSDVDVQLQVAVPQPGRYALVVEYANEDARQEVGVAVHTPQAPQOGLL 1140
Dd 1081 SPSHPPLITCTGSDVDVQLQVAVPQPGRYALVVEYANEDARQEVGVAVHTPQAPQOGLL 1140
QY 1141 SLHPCLYSTLCRGRTARDTQDHLAVFHLDSASVRLTAEOARFFLHGVTLPVPIEFSPEFV 1200
Dd 1141 SLHPCLYSTLCRGRTARDTQDHLAVFHLDSASVRLTAEOARFFLHGVTLPVPIEFSPEFV 1200
QY 1201 EPRVSCISSHGAFGPNSSAACLPSPFPKPPQPIILRDCQVPLPPLPGLLTHAODLTPATSP 1260
Dd 1201 EPRVSCISSHGAFGPNSSAACLPSPFPKPPQPIILRDCQVPLPPLPGLLTHAODLTPAMSP 1260
QY 1261 AGPRPRPPTAVDPDAEPTLLREPOATVVFTHVPTLGRYAFLLHGYQPAHPTFPVEVLIN 1320
Dd 1261 AGPRPRPPTAVDPDAEPTLLREPOATVVFTHVPTLGRYAFLLHGYQPAHPTFPVEVLIN 1320
QY 1321 AGRVWQGHANASFCPHGYGCRITLVCEGOALLDVTHSELTTVTVRVPBGRWLWDYVLVVP 1380
Dd 1321 AGRVWQGHANASFCPHGYGCRITLVCEGOALLDVTHSELTTVTVRVPBGRWLWDYVLVVP 1380
QY 1381 ENVYSFGYLREEPDKSYDFISHCAAQGYHISPSSSSSLFCRNAASLSLFYNNGARPCGC 1440
Dd 1381 ENVYSFGYLREEPDKSYDFISHCAAQGYHISPSSSSSLFCRNAASLSLFYNNGARPCGC 1440
QY 1441 HEVGATGPTCEPFPGGQCPCHAHVIGRDCSRCATGYWGFNCRPCDCGARLDELGTQCIC 1500
Dd 1441 HEVGATGPTCEPFPGGQCPCHAHVIGRDCSRCATGYWGFNCRPCDCGARLDELGTQCIC 1500
QY 1501 PPRITPPDCLLCQPTFCGCHPLVGECECNSGPGIQELTDPTCDTDSGQCKCRPNVTGRR 1560
Dd 1501 PPRITPPDCLLCQPTFCGCHPLVGECECNSGPGIQELTDPTCDTDSGQCKCRPNVTGRR 1560
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Dd 1561 CDTCSPGFHGYPRCRPCDCEAGTAPGVCDPLTGQCYCKENVOGPKDQCCLGTFSLDAA 1620
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Dd 1621 NPKGCTRCFCFGATERCRSSSYTROEFVDMEGVLLSTDRQVVPHERQPGTEMLRADLRH 1680
QY 1681 VPEAVPEAFPELYWQAPPSYLGDRVSSYGGTLYRLEHSETQRGDVFPVPMESRPDVVLQGN 1740
Dd 1681 VPEAVPEAFPELYWQAPPSYLGDRVSSYGGTLYRLEHSETQRGDVFPVPMESRPDVVLQGN 1740
QY 1741 QMSITFLEPAYPTPGHVHRGQLQVLEGNFRHTETRTNTVSREELMMVLASLEQLQIRALFS 1800
Dd 1741 QMSITFLEPAYPTPGHVHRGQLQVLEGNFRHTETRTNTVSREELMMVLASLEQLQIRALFS 1800
QY 1801 QISSAVSLRRVALEVASPAGQALASNVELCLCPASYRGDSQCECAPGFYRDVKGLFLGR 1860
Dd 1801 QISSAVFLRRVALEVASPAGQALASNVELCLCPASYRGDSQCECAPGFYRDVKGLFLGR 1860
QY 1861 CVPCQCHGHSRCLPGSGVCVDQHNTEGAHCERCOAGFMSSRDDPSAPCVSCPCPLSVP 1920
Dd 1861 CVPCQCHGHSRCLPGSGVCVDQHNTEGAHCERCOAGFMSSRDDPSAPCVSCPCPLSVP 1920
QY 1921 SNNFAEGCVLRGGRTQCLCKPGYAGASCRCAPGFFGNPLVLGSSCQPCDCSGNGDPNLL 1980
Dd 1921 SNNFAEGCVLRGGRTQCLCKPGYAGASCRCAPGFFGNPLVLGSSCQPCDCSGNGDPNLL 1980
QY 1981 FSDCDPLTGACRGCLRHHTTGPCEICAPGFYGNALLPGNCTRCDCCTPCGTEACDPHSGHC 2040
Dd 1981 FSDCDPLTGACRGCLRHHTTGPCEICAPGFYGNALLPGNCTRCDCCTPCGTEACDPHSGHC 2040
QY 2041 LCKAGVTGRRCDRCQBGHFGFNGCGGRPCACGPAAGSECHPSQGGCHCRPMTGPOCR 2100
Dd 2041 LCKAGVTGRRCDRCQBGHFGFNGCGGRPCACGPAAGSECHPSQGGCHCRPMTGPOCR 2100
QY 2101 ECAPGYWGLPEQGGRRCCQPGGRCDPHTGRNCNPPGLSGERCDCSCQHQVVPVGGPVGH 2160
Dd 2101 ECAPGYWGLPEQGGRRCCQPGGRCDPHTGRNCNPPGLSGERCDCSCQHQVVPVGGPVGH 2160
QY 2161 SIHCEVCDHCVVLLDDLERAGALLPAIHEQLRGINASSMAWARLHRLNASIADLQSQLR 2220

QY 1 MAXRLCAGSALCVRGPRGAPLLLVGLALGAARAREEAGGFSLHPPYFNLAEGARITAA 60
Dd 1 MAXRLCAGSALCVRGPRGAPLLLVGLALGAARAREEAGGFSLHPPYFNLAEGARITAA 60
QY 61 SATCGEEAPARGSPRPTELYCKLVGGPVAGDPNQITIRGQYCDICTAANSNKAHPASNA 120
Dd 61 SATCGEEAPARGSPRPTELYCKLVGGPVAGDPNQITIRGQYCDICTAANSNKAHPASNA 120
QY 121 IDGTERWQSPPLSRGLEYNVNVTLDLGQVHFVAYVLIKFANSRPDLWLVSMDPGR 180
Dd 121 IDGTERWQSPPLSRGLEYNVNVTLDLGQVHFVAYVLIKFANSRPDLWLVSMDPGR 180
QY 181 TYQPWQFFASSXKRDCLERFPGPTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRPG 240
Dd 181 TYQPWQFFASSXKRDCLERFPGPTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRPG 240
QY 241 AMNFSYSPLLREFTKATNVRLRFLRTNTLLGHLMGKALRDPVTTRYYYSIKDISIGRC 300
Dd 241 AMNFSYSPLLREFTKATNVRLRFLRTNTLLGHLMGKALRDPVTTRYYYSIKDISIGRC 300
QY 301 VCHGHADACDAKDPDTPRLQCTCQHNCTCGTCDRCPCPGFNQOPWKPATANSANECOSCN 360
Dd 301 VCHGHADACDAKDPDTPRLQCTCQHNCTCGTCDRCPCPGFNQOPWKPATANSANECOSCN 360
QY 361 CYGHATDCYYDPEVDRRRASQSLDGTYYQGGVCIDCQHHTTAGVNCERCLPGFYRSPNHPL 420
Dd 361 CYGHATDCYYDPEVDRRRASQSLDGTYYQGGVCIDCQHHTTAGVNCERCLPGFYRSPNHPL 420
QY 421 DSPHVCRRNCNCESEDFTDGTCEDLTGRCYCRPNFSGERCDCVCAEGTGFPPSCYPTPSSND 480
Dd 421 DSPHVCRRNCNCESEDFTDGTCEDLTGRCYCRPNFSGERCDCVCAEGTGFPPSCYPTPSSND 480
QY 481 TREQVLPAGQIVNCDCSAAGTQGNACRDKPRVGRCLCKPNFQGHCELCAPGFYGGCQP 540
Dd 481 TREQVLPAGQIVNCDCSAAGTQGNACRDKPRVGRCLCKPNFQGHCELCAPGFYGGCQP 540
QY 541 CQCSSPGVADDDCDPTDGTQCRCRVGFEGATCDRCAPGYFHFPLCQLCGCSPAGTLPBGCD 600
Dd 541 CQCSSPGVADDDCDPTDGTQCRCRVGFEGATCDRCAPGYFHFPLCQLCGCSPAGTLPBGCD 600
QY 601 EAGRCLCOPEFAGPHCDRCRPGYHGFNPNQACTDPRGALDQLCGAGGLCRCRPBYGTGA 660
Dd 601 EAGRCLCOPEFAGPHCDRCRPGYHGFNPNQACTDPRGALDQLCGAGGLCRCRPBYGTGA 660
QY 661 COECSPGFHGFPSCVPCCHCSAEGSLHAACDPRSGQCSRRPVTGLRCDTCTVPGAYNFPYC 720
Dd 661 COECSPGFHGFPSCVPCCHCSAEGSLHAACDPRSGQCSRRPVTGLRCDTCTVPGAYNFPYC 720
QY 721 EAGSCHPAGLAPVDPALPEAQVPCMCRAHVVEGSPCDRCCKPGFWGLSPSNPEGCTRCSCDL 780
Dd 721 EAGSCHPAGLAPVDPALPEAQVPCMCRAHVVEGSPCDRCCKPGFWGLSPSNPEGCTRCSCDL 780
QY 781 RGTLLGGVAECQPGTGQCFCKPHVCGQACASCKDGFGLDQADYFGCRSCRCIDIGGALGQS 840
Dd 781 RGTLLGGVAECQPGTGQCFCKPHVCGQACASCKDGFGLDQADYFGCRSCRCIDIGGALGQS 840
QY 841 CEPRTGVCRCRNPNTQGTCTSEPARDHYLPDLHLRLLELEAATPEGHAVRFGFNPLEFEN 900
Dd 841 CEPRTGVCRCRNPNTQGTCTSEPARDHYLPDLHLRLLELEAATPEGHAVRFGFNPLEFEN 900
QY 901 FSWRGYAQMAMPVQPRIVARLNLTSPLDFWLVFRYVNRGAMSVSGRVSVREEGRSATCANC 960
Dd 901 FSWRGYAQMAMPVQPRIVARLNLTSPLDFWLVFRYVNRGAMSVSGRVSVREEGRSATCANC 960
QY 961 TAQSQPVAFPPSTEPATITVPQRGFGEFVLPNGTVALRVAEGVLLDYVVLPSAYYEA 1020
Dd 961 TAQSQPVAFPPSTEPATITVPQRGFGEFVLPNGTVALRVAEGVLLDYVVLPSAYYEA 1020
QY 1021 ALLQLRVTEACTYRPSAQQSGDNCLLYTHPLDGFPSAAGLEALCRQDNLSPRECPTQL 1080
Dd 1021 ALLQLRVTEACTYRPSAQQSGDNCLLYTHPLDGFPSAAGLEALCRQDNLSPRECPTQL 1080

Db 2161 SIHCEVCDHCVVLLDDLERAGALLPAIHEQLRGINASSMAWARLHRLNASIADLQSOLR 2220
QY 2221 SPLGPRHETAQOOLEVLEQQSTSLGQDARRLGGQ-AVGTRDQASOLLAGTEATLGHAKTLL 2279
Db 2221 SPLGPRHETAQOOLEVLEQQSTSLGQDARRLGGQAAVGTRDQASOLLAGTEATLGHAKTLL 2280
QY 2280 AAIRAVDRTLSELMSTCHLGLANASAPSGEQLLRTLAEVERLLWEMRARDLGAPOAAAE 2339
Db 2281 AAIRAVDRTLSELMSTCHLGLANASAPSGEQLLRTLAEVERLLWEMRARDLGAPOAAAE 2340
QY 2340 AELAAQRLLARVQEQLSSLWEENQALATQTRDRLAQHEAGLMDLREALNRAVDATREAQ 2399
Db 2341 AELAAQRLLARVQEQLSSLWEENQALATQTRDRLAQHEAGLMDLREALNRAVDATREAQ 2400
QY 2400 ELNSNQERLEALQKQELSRDNATLQATLHAARDTLASVFRLLHSLDQAKESLERLAA 2459
Db 2401 ELNSNQERLEALQKQELSRDNATLQATLHAARDTLASVFRLLHSLDQAKESLERLAA 2460
QY 2460 SLDGARTPLLQRMQTFSAGSKLRLVEAAEAHAQQLGQALNLSIIILDVNQRLTQRAI 2519
Db 2461 SLDGARTPLLQRMQTFSAGSKLRLVEAAEAHAQQLGQALNLSIIILDVNQRLTQRAI 2520
QY 2520 EASNAYSRILOAVQAAEDAAGQALQOQADHTWATVVRQGLVDRAQQLLANSTALEEAMLQE 2579
Db 2521 EASNAYSRILOAVQAAEDAAGQALQOQADHTWATVVRQGLVDRAQQLLANSTALEEAMLQE 2580
QY 2580 QORLGLVWAALQGARTQLRDVRAKKDQLEAHIQAAQAMLAMDTDETSKKIAHAKAVAAEA 2639
Db 2581 QORLGLVWAALQGARTQLRDVRAKKDQLEAHIQAAQAMLAMDTDETSKKIAHAKAVAAEA 2640
QY 2640 QDTATRVQSOLQAMQENVERWQGYEGLRGQDLGQAVLDAGHSVSTLEKTLPLQILAKLSI 2699
Db 2641 QDTATRVQSOLQAMQENVERWQGYEGLRGQDLGQAVLDAGHSVSTLEKTLPLQILAKLSI 2700
QY 2700 LENRGVHNASLALSASIGRVRELLAQARGAASKVKVPMKFNGRSGVQLRTPRDLADLAAY 2759
Db 2701 LENRGVHNASLALSASIGRVRELLAQARGAASKVKVPMKFNGRSGVQLRTPRDLADLAAY 2760
QY 2760 TALKFYLOQPEPEPGOGTDRFVMYMGSRQATGDYMGVSLRDKKVHWVYQLGEAGPAVLS 2819
Db 2761 TALKFYLOQPEPEPGOGTDRFVMYMGSRQATGDYMGVSLRDKKVHWVYQLGEAGPAVLS 2820
QY 2820 IDEDIGEQAASVSLDRTLQFGHMSVTVVERQMIQETKGDTVAPGAEGLLNLRPDDFVFYVG 2879
Db 2821 IDEDIGEQAASVSLDRTLQFGHMSVTVVERQMIQETKGDTVAPGAEGLLNLRPDDFVFYVG 2880
QY 2880 GYPSTFTPPPLLRFPYRGCIEMDTLNEEVVSLYNFERTFQDLTAVDRPCARSKSTGDPW 2939
Db 2881 GYPSTFTPPPLLRFPYRGCIEMDTLNEEVVSLYNFERTFQDLTAVDRPCARSKSTGDPW 2940
QY 2940 LTDGSYLDGTGFARISFDSQISTTKRFEQELRLVSYSGVLFELKQOQSOFCLLAVQEGSLV 2999
Db 2941 LTDGSYLDGTGFARISFDSQISTTKRFEQELRLVSYSGVLFELKQOQSOFCLLAVQEGSLV 3000
QY 3000 LLYDFGAGLKKAVPLQPPPLTSASKAIQVFLLLGGSRRKRVLVRVERATVYSVEQDNDLEL 3059
Db 3001 LLYDFGAGLKKAVPLQPPPLTSASKAIQVFLLLGGSRRKRVLVRVERATVYSVEQDNDLEL 3060
QY 3060 ADAYYLGVPDPDQLPPSLRWLFPPTGGSVRGCVKGIKALGVYDLKRLNTTGVSAAGCTADL 3119
Db 3061 ADAYYLGVPDPDQLPPSLRWLFPPTGGSVRGCVKGIKALGVYDLKRLNTTGVSAAGCTADL 3120
QY 3120 LVGRAMTFHGHGFLRLALSNAVPLTGNVYSGFGFHSQAQDSALLYRASPDGLCQVSLQOQ 3179
Db 3121 LVGRAMTFHGHGFLRLALSNAVPLTGNVYSGFGFHSQAQDSALLYRASPDGLCQVSLQOQ 3180
QY 3180 RVSLQLLRTEVKTQAGFADGAPHYVAFYSNATGVWLVDLQLOQMKGPHRGPPPELOQPOE 3239
Db 3181 RVSLQLLRTEVKTQAGFADGAPHYVAFYSNATGVWLVDLQLOQMKGPHRGPPPELOQPOE 3240
QY 3240 GPRLLILGGLPESGTIYNFSGCISNVFVQRLLPQRFVFDLQQLGSVNVSTGCPALQAAQ 3299

Db 3241 GPRLLILGGLPESGTIYNFSGCISNVFVQRLLPQRFVFDLQQLGSVNVSTGCPALQAAQ 3300
QY 3300 TPGLGPRGLQATARKASRRSQPARHPACMLPPHLRITTRDSYQFGGSLSSHLEFVFGILAR 3359
Db 3301 TPGLGPRGLQATARKASRRSQPARHPACMLPPHLRITTRDSYQFGGSLSSHLEFVFGILAR 3360
QY 3360 HRNWPSSLMHVLPSSRGLLFTARLRPGSPSLALFLSNHGFVAQMEGLGTRLRAQSRQR 3419
Db 3361 HRNWPSSLMHVLPSSRGLLFTARLRPGSPSLALFLSNHGFVAQMEGLGTRLRAQSRQR 3420
QY 3420 SRPGRWHKVSVRWEKNRILLVTDGARAWSQEGPHRQHOGAEHPQPHTLFFVGGLPASSHSS 3479
Db 3421 SRPGRWHKVSVRWEKNRILLVTDGARAWSQEGPHRQHOGAEHPQPHTLFFVGGLPASSHSS 3480
QY 3480 KLPVTVGFSGCVKRLRLHGRPLGAPTRMAGVTPCILGPLEAGLFFPGSGGVITLPLPGAT 3539
Db 3481 KLPVTVGFSGCVKRLRLHGRPLGAPTRMAGVTPCILGPLEAGLFFPGSGGVITLPLPGAT 3540
QY 3540 LPDVGLELEVRPLAVTGLIFHLGOARTPPYLQLOVTEKQVLLRADDGAGEFSTSVTRPSV 3599
Db 3541 LPDVGLELEVRPLAVTGLIFHLGOARTPPYLQLOVTEKQVLLRADDGAGEFSTSVTRPSV 3600
QY 3600 LCDGQWHLRAWKMSGNVLRLEVDQSNHTVGPLLLAAAGAPAPLYLGGLPEPMAVQPWPP 3659
Db 3601 LCDGQWHLRAWKMSGNVLRLEVDQSNHTVGPLLLAAAGAPAPLYLGGLPEPMAVQPWPP 3660
QY 3660 AYCGRMRRLAVNRSPVAMTRSRVEHGAVGASGCPAA 3695
Db 3661 AYCGRMRRLAVNRSPVAMTRSRVEHGAVGASGCPAA 3696

RESULT 4
US-10-112-944-347
; Sequence 347, Application US/10112944
; Publication No. US20040048249A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Weng, Gezhi
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyang
; APPLICANT: Xue, Aigong J.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Zhiwei
; TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and
; TITLE OF INVENTION: Secreted Polypeptides
; FILE REFERENCE: 805A
; CURRENT APPLICATION NUMBER: US/10/112,944
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
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; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/519,705
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 09/552,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 924
; SOFTWARE: pt_FL_genes Version 5.0
; SEQ ID NO 347
; LENGTH: 3690

TYPE: PRT
ORGANISM: Homo sapiens
US-10-112-944-347

Query Match 99.6%; Score 20035.5; DB 12; Length 3690;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3682; Conservative 3; Mismatches 5; Indels 5; Gaps 1;

QY 1 MAKRLCAGSALCVRGPRGPAPLLVGLALLGAARAREEAGGFSLHPPYFNLAEGARIAA 60
Db 1 MAKRLCAGSALCVRGPRGPAPLLVGLALLGAARAREEAGGFSLHPPYFNLAEGARIAA 60

QY 61 SATCGEEAPARGSPRPTECLYCKLVGGPVAGDPNQITRGQYCDICTAANSNKAHPASNA 120
Db 61 SATCGEEAPARGSPRPTECLYCKLVGGPVAGDPNQITRGQYCDICTAANSNKAHPASNA 120

QY 121 IDGTERWWQSPPLSRGLYNEVNVTLDLGQVHFVAYVLIKFANSPRPDLWVLSRMDGFR 180
Db 121 IDGTERWWQSPPLSRGLYNEVNVTLDLGQVHFVAYVLIKFANSPRPDLWVLSRMDGFR 180

QY 181 TYQWQFFASSKRDCLERFGPQTLERITRDDAAICTTEYSRIIVPLENGEIVVSLVNGRPG 240
Db 181 TYQWQFFASSKRDCLERFGPQTLERITRDDAAICTTEYSRIIVPLENGEIVVSLVNGRPG 240

QY 241 AMNFSYSPLLREFTKATNVRLRFLRNTLLGLHMGKALRDPVTTRYYYSIKDISIGRC 300
Db 241 AMNFSYSPLLREFTKATNVRLRFLRNTLLGLHMGKALRDPVTTRYYYSIKDISIGRC 300

QY 301 VCHGHADACDAKDPDTPFRLQCTCOHNTCGGTCDCRCGFNFQWPWKATANSANECQSCN 360
Db 301 VCHGHADACDAKDPDTPFRLQCTCOHNTCGGTCDCRCGFNFQWPWKATANSANECQSCN 360

QY 361 CYGHATDCYDPEVDRRRASQSLDGTYYQGGVVICDQHTTAGVNCERCLPGYRSPNHPL 420
Db 361 CYGHATDCYDPEVDRRRASQSLDGTYYQGGVVICDQHTTAGVNCERCLPGYRSPNHPL 420

QY 421 DSPHVCRRNCESDFTDGTCEDLTGRCYCRPNFSGERCDVCAEGTFGPSYPTPSSND 480
Db 421 DSPHVCRRNCESDFTDGTCEDLTGRCYCRPNFSGERCDVCAEGTFGPSYPTPSSND 480

QY 481 TREQVLPAGQIVNDCSAAAGTQGNACRKDPVGRCLCKPNFQGTGTHCELAPGYGPGCQP 540
Db 481 TREQVLPAGQIVNDCSAAAGTQGNACRKDPVGRCLCKPNFQGTGTHCELAPGYGPGCQP 540

QY 541 CQCSSPGVADRCDDPTGQCRVGFEGATCDRCAPGYFHFPLCQLCGCSPAGTLPEGCD 600
Db 541 CQCSSPGVADRCDDPTGQCRVGFEGATCDRCAPGYFHFPLCQLCGCSPAGTLPEGCD 600

QY 601 EAGRCLCQEFAGPHCDRCRPGYHGFNQCQACTDPRGALDQLCGAGGLCRCPGYTGTA 660
Db 601 EAGRCLCQEFAGPHCDRCRPGYHGFNQCQACTDPRGALDQLCGAGGLCRCPGYTGTA 660

QY 661 CQECSPGFHGFPPSCVPCCHCSAEGSLHAACDPRSGQSCRPRTVGLRCDTCVPGAYNFPYC 720
Db 661 CQECSPGFHGFPPSCVPCCHCSAEGSLHAACDPRSGQSCRPRTVGLRCDTCVPGAYNFPYC 720

QY 721 EAGSCHPAGLAPVDPALPEAQVPCMCRAHVEGPSCDRCCKPGFWGLSPSNPEGCTRCSCDL 780
Db 721 EAGSCHPAGLAPVDPALPEAQVPCMCRAHVEGPSCDRCCKPGFWGLSPSNPEGCTRCSCDL 780

QY 781 RGTLLGVAECQPGTGQCFCFKPHVCGQACASCKDGFGLDQADYFGCRSCRCIDIGGALQS 840
Db 781 RGTLLGVAECQPGTGQCFCFKPHVCGQACASCKDGFGLDQADYFGCRSCRCIDIGGALQS 840

QY 841 CEPRTGVCRCRPNTQGTCTSEPARDHYLPDLHLRLLELEAAATPEGHAVRFGFNPLEFEN 900
Db 841 CEPRTGVCRCRPNTQGTCTSEPARDHYLPDLHLRLLELEAAATPEGHAVRFGFNPLEFEN 900

QY 901 FSWRGYAQMAPVQPRIVARLNLTSPDLFWLVRYNVRGAMSVSGRVSVREGRSAAACANC 960
Db 901 FSWRGYAQMAPVQPRIVARLNLTSPDLFWLVRYNVRGAMSVSGRVSVREGRSAAACANC 960

QY 961 TAQSQPVAFPPSTEPAFITVPQRGFGEFVLPNPGTVALRVEAEGVLLDYVLLPSAYYEA 1020

Db 961 TAQSQPVAFPPSTEPAFITVPQRGFGEFVLPNPGTVALRVEAEGVLLDYVLLPSAYYEA 1020

QY 1021 ALLQLRVTEACTYRPSAQSGDNCLLYTHLPDGFPSAAAGLEALCRQDNSLPRPCPTQL 1080
Db 1021 ALLQLRVTEACTYRPSAQSGDNCLLYTHLPDGFPSAAAGLEALCRQDNSLPRPCPTQL 1080

QY 1081 SPSHPPLITCTGSDVDVQLQVAVPQPGRYALVVEYANEDARQEVGVAVHTPQAPQOGLL 1140
Db 1081 SPSHPPLITCTGSDVDVQLQVAVPQPGRYALVVEYANEDARQEVGVAVHTPQAPQOGLL 1140

QY 1141 SLHPCLYSTLCRGTAARDTQDHLAVFHLDEASVRLTAEQARFFLHGVTLVPIEFSPEFV 1200
Db 1141 SLHPCLYSTLCRGTAARDTQDHLAVFHLDEASVRLTAEQARFFLHGVTLVPIEFSPEFV 1200

QY 1201 EPRVSCISSHGAFGPNSAACLPSPRFPKPPQPIILRDCQVILPPLGLPLTHAQDLTPATSP 1260
Db 1201 EPRVSCISSHGAFGPNSAACLPSPRFPKPPQPIILRDCQVILPPLGLPLTHAQDLTPAMSP 1260

QY 1261 AGPRPRPPTAVDDAEPTLLREPQATVVVTHVPTLGRYAFLLHGYQPAHPTFPVEVLIN 1320
Db 1261 AGPRPRPPTAVDDAEPTLLREPQATVVVTHVPTLGRYAFLLHGYQPAHPTFPVEVLIN 1320

QY 1321 AGRVWQGHANASFCPHGYGCRITLVCEGQALLDVTHSELVTTVRVPBEGRWLWLDYVLVVP 1380
Db 1321 AGRVWQGHANASFCPHGYGCRITLVCEGQALLDVTHSELVTTVRVPBEGRWLWLDYVLVVP 1380

QY 1381 ENVYSFGYLRREPLDKSYDFISHCAAQGYHISPSSSSSLFCRNAAASLSLFYNNGARPCGC 1440
Db 1381 ENVYSFGYLRREPLDKSYDFISHCAAQGYHISPSSSSSLFCRNAAASLSLFYNNGARPCGC 1440

QY 1441 HEVGATGPTCEPFGGQCPCHAHVIGRDCSRCATGYWGFNCRPCDCCGARLCELTGQCIC 1500
Db 1441 HEVGATGPTCEPFGGQCPCHAHVIGRDCSRCATGYWGFNCRPCDCCGARLCELTGQCIC 1500

QY 1501 PPRTIPPDCLLQCPQTFGCHPLVGCCECNCSPGQIELTDTCTDSDGQCKCRPNVTGRR 1560
Db 1501 PPRTIPPDCLLQCPQTFGCHPLVGCCECNCSPGQIELTDTCTDSDGQCKCRPNVTGRR 1560

QY 1561 CDTCSPGFHHYPRCRPCDCHEAGTAPGVCDPLTGQCYCKENVQGPCKDQCSLGTFSLDAA 1620
Db 1561 CDTCSPGFHHYPRCRPCDCHEAGTAPGVCDPLTGQCYCKENVQGPCKDQCSLGTFSLDAA 1620

QY 1621 NPKGCTRCFCGATERCRSSSYTRQEFVDMEGVLLSTDRQVVPHERQPGTEMLRADLRH 1680
Db 1621 NPKGCTRCFCGATERCRSSSYTRQEFVDMEGVLLSTDRQVVPHERQPGTEMLRADLRH 1680

QY 1681 VPEAVPEAFPELYWQAPPSYLGDRVSSYGGTLRYELHSETQRGDVFVPMESRPDVVLQGN 1740
Db 1681 VPEAVPEAFPELYWQAPPSYLGDRVSSYGGTLRYELHSETQRGDVFVPMESRPDVVLQGN 1740

QY 1741 QMSITFLEPAYTPGHVHRGQLQVVEGNFRHTETRTNVSREELMMVLASLEQLQIRALFS 1800
Db 1741 QMSITFLEPAYTPGHVHRGQLQVVEGNFRHTETRTNVSREELMMVLASLEQLQIRALFS 1800

QY 1801 QISSAVSLRRVALEVASPAGQGALASNVVELCLCPASVYRGDSQECAPGFYRDVKGLFLGR 1860
Db 1801 QISSAVSLRRVALEVASPAGQGALASNVVELCLCPASVYRGDSQECAPGFYRDVKGLFLGR 1860

QY 1861 CVPCQCHGHSRCLPLGSGVCDVCOHNTGHAHCERCQAGFMSSRDDPSAPCVSCPCPLSVP 1920
Db 1861 CVPCQCHGHSRCLPLGSGVCDVCOHNTGHAHCERCQAGFMSSRDDPSAPCVSCPCPLSVP 1920

QY 1921 SNNFAEGCVLRGGRTQCLCKPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSNGDNPILL 1980
Db 1921 SNNFAEGCVLRGGRTQCLCKPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSNGDNPILL 1980

QY 1981 FSDCDPLTGACRGCLRHHTTGPCEICAPGYGNALLPGNCTRCDCCTPCGTEACDPHSGHC 2040
Db 1981 FSDCDPLTGACRGCLRHHTTGPCEICAPGYGNALLPGNCTRCDCCTPCGTEACDPHSGHC 2040

QY 2041 LCKAGVTGRRCRCQEGHFGNCGGCRPCACGPAAGSECHPQSGQCHCRPGTMGPQCR 2100

Db 2041 LCKAGVTGRRCDRCQEGHFGFDGGCGGRCPCACGPAAGSECHPQSGQCHCRPGTGMGPQCR 2100
QY 2101 ECAPGYWGLPEQGRRCQCPCGGRCDPHTGRNCNPPGLSGERCDCSCQQHQVPVPGGPVGH 2160
Db 2101 ECAPGYWGLPEQGRRCQCPCGGRCDPHTGRNCNPPGLSGERCDCSCQQHQVPVPGGPVGH 2160
QY 2161 SIHCEVCDHCVVLLDDDLERAGALLPAIHEQURGINASSMAWARLHRLNASIADLQSLR 2220
Db 2161 SIHCEVCDHCVVLLDDDLERAGALLPAIHEQURGINASSMAWARLHRLNASIADLQSLR 2220
QY 2221 SPLGPRHETAQQLVELEQOQSTSLGQDARRLGGQAVGTRDQASQLLAGTEATLGHAKTLLA 2280
Db 2221 SPLGPRHETAQQLVELEQOQSTSLGQDARRLGGQAVGTRDQASQLLAGTEATLGHAKTLLA 2280
QY 2281 AIRAVDRITLSEMSQTHGLGLANASAPSGEQLLRTLAEVERLLWEMRARDLGAPQAAAEA 2340
Db 2281 AIRAVDRITLSEMSQTHGLGLANASAPSGEQLLRTLAEVERLLWEMRARDLGAPQAAAEA 2340
QY 2341 ELAAAQRLRLARVQEQSLSLWEENQALATQTRDRLAQHEAGLMDLREALNRAVDATREAOE 2400
Db 2341 ELAAAQRLRLARVQEQSLSLWEENQALATQTRDRLAQHEAGLMDLREALNRAVDATREAOE 2400
QY 2401 LNSRNQERLEEALQRKQELSRDNATLQATLHAARDTLASVFRLLHSLDQAKEELERLAAS 2460
Db 2401 LNSRNQERLEEALQRKQELSRDNATLQATLHAARDTLASVFRLLHSLDQAKEELERLAAS 2460
QY 2461 LDGARTPLLRQMOTFSPAGSKRLRVEAAEAHAQQLQALNLSIIILDVNQDRLTORAIE 2520
Db 2461 LDGARTPLLRQMOTFSPAGSKRLRVEAAEAHAQQLQALNLSIIILDVNQDRLTORAIE 2520
QY 2521 ASNAYSRILOAVQAAEDAAGALQQADHTWATVVROGLVDRAQQLLANSTALEEAMLOEQ 2580
Db 2521 ASNAYSRILOAVQAAEDAAGALQQADHTWATVVROGLVDRAQQLLANSTALEEAMLOEQ 2580
QY 2581 QRLGLVWAALOGARTQLRDVRAKDKQLEAHIQAAQAMLAMDTDETSKKIAHAKAVAAEAQ 2640
Db 2581 QRLGLVWAALOGARTQLRDVRAKDKQLEAHIQAAQAMLAMDTDETSKKIAHAKAVAAEAQ 2640
QY 2641 DTATRVQSOLQAMQENVERWQOYEGRLGQDGLQAVILDAGHSVSTLEKTLPLLAKLSIL 2700
Db 2641 DTATRVQSOLQAMQENVERWQOYEGRLGQDGLQAVILDAGHSVSTLEKTLPLLAKLSIL 2700
QY 2701 ENRGVHNASLALSASIGRVRELIAQARGAASKVKVPMKFNRSRGVQLRTPRDLADLAAYT 2760
Db 2701 ENRGVHNASLALSASIGRVRELIAQARGAASKVKVPMKFNRSRGVQLRTPRDLADLAAYT 2760
QY 2761 ALKFYLQGEPEPEPGQGTEDRFVVMGMSRQATGDYMGVSLRDKKVHVWYQLGEAGPAVLSI 2820
Db 2761 ALKFYLQGEPEPEPGQGTEDRFVVMGMSRQATGDYMGVSLRDKKVHVWYQLGEAGPAVLSI 2820
QY 2821 DEDIGEQAFAVSLDRTLQFGHMSVTVERQMIQETKGDTPVAPGAEGLLNLRPDDFVFYVGG 2880
Db 2821 DEDIGEQAFAVSLDRTLQFGHMSVTVERQMIQETKGDTPVAPGAEGLLNLRPDDFVFYVGG 2880
QY 2881 YPSTFTPPPLLRFPYRGCIEMDTLNEEVVSLYNFERTFQDQTAVDRPCARSKSTGDPWL 2940
Db 2881 YPSTFTPPPLLRFPYRGCIEMDTLNEEVVSLYNFERTFQDQTAVDRPCARSKSTGDPWL 2940
QY 2941 TDGSYLDGTGFPARISFDSQISTTKRFEQELRLVSYSGVLFLLKQSQFCLLAVQEGSLVL 3000
Db 2941 TDGSYLDGTGFPARISFDSQISTTKRFEQELRLVSYSGVLFLLKQSQFCLLAVQEGSLVL 3000
QY 3001 LYDFGAGLKKAVPLQPPPLTSASKAIQVFLGGSRKRVLYRVERATVYSVEQDNDLELA 3060
Db 3001 LYDFGAGLKKAVPLQPPPLTSASKAIQVFLGGSRKRVLYRVERATVYSVEQDNDLELA 3060
QY 3061 DAYYLGGVPPDQLPPSLRWLFPPTGGSVRGCVKGIKALGKYVDLKRNLNTTGVSAAGCTADLL 3120
Db 3061 DAYYLGGVPPDQLPPSLRWLFPPTGGSVRGCVKGIKALGKYVDLKRNLNTTGVSAAGCTADLL 3120
QY 3121 VGRAMTFHGHGFLRLALSNVAPLTGNVYSGFGFHSQAQDSALLYRASPDGLCQVSLQOGR 3180
Db 3121 VGRAMTFHGHGFLRLALSNVAPLTGNVYSGFGFHSQAQDSALLYRASPDGLCQVSLQOGR 3180

QY 3181 VSLQLLRTEVKTQAGPADGAPHYVAFYSNATGVWLTVDDQLQOMKPHRGPPPELQPOPEG 3240
Db 3181 VSLQLLRTEVKTQAGPADGAPHYVAFYSNATGVWLTVDDQLQOMKPHRGPPPELQPOPEG 3240
QY 3241 PPRLLLGGLPESGTTYNFSGCISNVFVQRLILGPORVFDLQQNLGSVNVSTGCAPALQAQT 3300
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QY 3301 PGLGPRGLQATARKASHRSRQPARHPACMLPPLHLRTRTDSYQFGGSLSSHLEFVVGILARH 3360
Db 3301 PGLGPRGLQ-----ASRRSRQPARHPACMLPPLHLRTRTDSYQFGGSLSSHLEFVVGILARH 3355
QY 3361 RNWPSLSMHVLPRSSRGILLFTARLRPGSPSLALFLSNGHFVAQMEGLGTRLRAQSRQRS 3420
Db 3356 RNWPSLSMHVLPRSSRGILLFTARLRPGSPSLALFLSNGHFVAQMEGLGTRLRAQSRQRS 3415
QY 3421 RPCRWHKVSVRWEKNRILLVTDGARAWSQEGPHROHQGAHPQPHHTLFGVGLPASHSSK 3480
Db 3416 RPCRWHKVSVRWEKNRILLVTDGARAWSQEGPHROHQGAHPQPHHTLFGVGLPASHSSK 3475
QY 3481 LPVTVFGSGCVKRLRLHGRPLGAPTRMAGVTPCILGPLEAGLFFPGSGGVITILDLPGATL 3540
Db 3476 LPVTVFGSGCVKRLRLHGRPLGAPTRMAGVTPCILGPLEAGLFFPGSGGVITILDLPGATL 3535
QY 3541 PDVGLLEVRPLAVTGLIFHLGQARTPPYLQLVTEKQVLLRADDGAGEFSTSVTRPSVL 3600
Db 3536 PDVGLLEVRPLAVTGLIFHLGQARTPPYLQLVTEKQVLLRADDGAGEFSTSVTRPSVL 3595
QY 3601 CDGQWHRILAVMKSGNVLRLEVDAQSNHTVGPLLLAAAGAPAPLYLGLPEPMAVQWPWPPA 3660
Db 3596 CDGQWHRILAVMKSGNVLRLEVDAQSNHTVGPLLLAAAGAPAPLYLGLPEPMAVQWPWPPA 3655
QY 3661 YCGCMRRLAVNRSVPAMTRSVEVHGAVGASGCPAA 3695
Db 3656 YCGCMRRLAVNRSVPAMTRSVEVHGAVGASGCPAA 3690

RESULT 5
US-10-312-088-30
; Sequence 30, Application US/10312088
; Publication No. US20030219862A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Cogswell, John P.
; APPLICANT: Kabnic, Karen S.
; APPLICANT: Lai, Ying-Ta
; APPLICANT: Martensen, Shelby A.
; APPLICANT: Murdock, Paul R.
; APPLICANT: Smith, Randall F.
; APPLICANT: Strum, Jay C.
; APPLICANT: Xiang, Zhaoying
; APPLICANT: Xie, Qing
; APPLICANT: Rizni, Safia K.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GF50029
; CURRENT APPLICATION NUMBER: US/10/312,088
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/19929
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,161
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; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 3705
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-312-088-30
Query Match 99.6%; Score 20030; DB 15; Length 3705;

Best Local Similarity 99.4%; Pred. No. 0;									
Matches 3683; Conservative 3; Mismatches 9; Indels 10; Gaps 1;									
QY	1	MAKRLCAGSALCVPRGPPAPLLVGLALLGAARAREEAGGGSLSLHPPYFNLAEGARIAA	60						
Db	1	MAKRLCAGSALCVPRGPPAPLLVGLALLGAARAREEAGGGSLSLHPPYFNLAEGARIAA	60						
QY	61	SATCGEEAPARGSPREPTEDLYCKLVGGPVAGDPPNOTIRGQYCDICTAANSNKAHPASNA	120						
Db	61	SATCGEEAPARGSPREPTEDLYCKLVGGPVAGDPPNOTIRGQYCDICTAANSNKAHPASNA	120						
QY	121	IDGTERWQSPPLSRGLEYNVNTLDLQGVFHVAYVLIKFANSRPPDLWLERSMDFGR	180						
Db	121	IDGTERWQSPPLSRGLEYNVNTLDLQGVFHVAYVLIKFANSRPPDLWLERSMDFGR	180						
QY	181	TYQPWQFFASSKRDCLERFGPQTLERITRDAAICTTEYSRIVPLENGEIVVSLVNGRPG	240						
Db	181	TYQPWQFFASSKRDCLERFGPQTLERITRDAAICTTEYSRIVPLENGEIVVSLVNGRPG	240						
QY	241	AMNFSYSPLLRREFTKATNVRLRFLRTNTLLGHLMGKALRDPVTRRYYSIKDISIGGRC	300						
Db	241	AMNFSYSPLLRREFTKATNVRLRFLRTNTLLGHLMGKALRDPVTRRYYSIKDISIGGRC	300						
QY	301	VCHGHADACDAKDPDPRLOCTCQHNCTGGTCDRCPCGPNQPKPATANSANECQSCN	360						
Db	301	VCHGHADACDAKDPDPRLOCTCQHNCTGGTCDRCPCGPNQPKPATANSANECQSCN	360						
QY	361	CYGHATDCYYDPEVDRRRASQSLDGTGQGGVCIDCQHHTAGVNCERCLPGFYRSPNHPL	420						
Db	361	CYGHATDCYYDPEVDRRRASQSLDGTGQGGVCIDCQHHTAGVNCERCLPGFYRSPNHPL	420						
QY	421	DSPHVRRRCNCSDFDTGTCEDLTGRCYCRPNFSGERCDCVCAEGFTGFPSCYPTPSSND	480						
Db	421	DSPHVRRRCNCSDFDTGTCEDLTGRCYCRPNFSGERCDCVCAEGFTGFPSCYPTPSSND	480						
QY	481	TREQVLPAQIIVNDCSAAAGTOGNACRDXPRVGRCLCKPNFQGTCHCELCAFGFYGPCQP	540						
Db	481	TREQVLPAQIIVNDCSAAAGTOGNACRDXPRVGRCLCKPNFQGTCHCELCAFGFYGPCQP	540						
QY	541	CQCSSPGVADDDRCDDTGTQCRVGVPEGATCDRCAPGYFHFPLCQLCGCSPAGTLPPEGCD	600						
Db	541	CQCSSPGVADDDRCDDTGTQCRVGVPEGATCDRCAPGYFHFPLCQLCGCSPAGTLPPEGCD	600						
QY	601	EAGRLCQPEFAGPHCDRCRPGYHGFNPNQACTCDPRGALDOLCGAGGLCRRCRPGYTGA	660						
Db	601	EAGRLCQPEFAGPHCDRCRPGYHGFNPNQACTCDPRGALDOLCGAGGLCRRCRPGYTGA	660						
QY	661	CQECSPGFHGFPSVCPCHCSAEGSLHAAACDPRSGQCSRRPVTLGLRCDTCTVPGAYNFPYC	720						
Db	661	CQECSPGFHGFPSVCPCHCSAEGSLHAAACDPRSGQCSRRPVTLGLRCDTCTVPGAYNFPYC	720						
QY	721	EAGSCHPAGLAPVDPALPEAQVPCMCRAHVEGSPCDRCCKPGFWGLSPSNPEGCTRCSCDL	780						
Db	721	EAGSCHPAGLAPVDPALPEAQVPCMCRAHVEGSPCDRCCKPGFWGLSPSNPEGCTRCSCDL	780						
QY	781	RGTLGGVAECQPGTGQCFCKPHVCGQACASCKDGGFFGLDQADYFGCRSCRCDDIGGALGQS	840						
Db	781	RGTLGGVAECQPGTGQCFCKPHVCGQACASCKDGGFFGLDQADYFGCRSCRCDDIGGALGQS	840						
QY	841	CEPRTGVCRCRNTQGTCTSEPARDHYLPDLHLRLLELEAATPEGHAVRFGFNPLEFEN	900						
Db	841	CEPRTGVCRCRNTQGTCTSEPARDHYLPDLHLRLLELEAATPEGHAVRFGFNPLEFEN	900						
QY	901	FSWRGYAQMAPPQPRIVARLNLTSPLDFWLVFVRYVNRGAMSVSGRVSREEGRSAAACANC	960						
Db	901	FSWRGYAQMAPPQPRIVARLNLTSPLDFWLVFVRYVNRGAMSVSGRVSREEGRSAAACANC	960						
QY	961	TAQSQPVAFPPSPTEPAFITVQPGFGFEPVLPNGTVALRVEAEGVLLDYVLLPSAYYEA	1020						
Db	961	TAQSQPVAFPPSPTEPAFITVQPGFGFEPVLPNGTVALRVEAEGVLLDYVLLPSAYYEA	1020						
QY	1021	ALLQLRVTEACTYRPSAQSGDNCLLYTHLPDGFPSAAGLEALCRQDNSLPRPCPTEQL	1080						

Db	1021	ALLQLRVTEACTYRPSAQSGDNCLLYTHLPDGFPSAAGLEALCRQDNSLPRPCPTEQL	1080						
QY	1081	SPSHPLITCTGSDVDVQLQVAVPQPGRYALVVEYANEDARQEVGVAHTPQRAPOQGLL	1140						
Db	1081	SPSHPLITCTGSDVDVQLQVAVPQPGRYALVVEYANEDARQEVGVAHTPQRAPOQGLL	1140						
QY	1141	SLHPCLYSTLCRGRTARDTQDLHAFVHLDSEASVRLTAEQARFFLHGVTLPVIEEFSPEFV	1200						
Db	1141	SLHPCLYSTLCRGRTARDTQDLHAFVHLDSEASVRLTAEQARFFLHGVTLPVIEEFSPEFV	1200						
QY	1201	EPVSCISSHGAFGPNAAACLPSPRFPKPOPIILRDCQVILPLPGLPLTHAQDLTPATSP	1260						
Db	1201	EPVSCISSHGAFGPNAAACLPSPRFPKPOPIILRDCQVILPLPGLPLTHAQDLTPATSP	1260						
QY	1261	AGPRPRPPTAVDPDAEPTLLREPOATVVFTTHVPTLGRYAFLLHGYQPAHPTFPVEVLIN	1320						
Db	1261	AGPRPRPPTAVDPDAEPTLLREPOATVVFTTHVPTLGRYAFLLHGYQPAHPTFPVEVLIN	1320						
QY	1321	AGRWQGHANASFCPHGYGCRTLVVCEGOALLDVTHSELTVTVRVEGRWLWLDYVLVVP	1380						
Db	1321	AGRWQGHANASFCPHGYGCRTLVVCEGOALLDVTHSELTVTVRVEGRWLWLDYVLVVP	1380						
QY	1381	ENVYSGYLREELDKSYDFISHCAAQGYHISPSSSSSLFCRNAASLSLFFYNNGARPCGC	1440						
Db	1381	ENVYSGYLREELDKSYDFISHCAAQGYHISPSSSSSLFCRNAASLSLFFYNNGARPCGC	1440						
QY	1441	HEVGATGPTCEPFGGQCPCHAHVIGRDCSRCATGYWGFPPNCRPCDCGARLDELGTQCIC	1500						
Db	1441	HEVGATGPTCEPFGGQCPCHAHVIGRDCSRCATGYWGFPPNCRPCDCGARLDELGTQCIC	1500						
QY	1501	PRRTIPDCLLCQPTFGCHPLVGECECNSGPGIQELTDTPTDTSQCKCRPNVTGRR	1560						
Db	1501	PRRTIPDCLLCQPTFGCHPLVGECECNSGPGIQELTDTPTDTSQCKCRPNVTGRR	1560						
QY	1561	CDTCSPGFHGYPRCRPCDCHAGTAPGVCDPLTGQCYCKENVOGPKCDQCSLGTFSLDAA	1620						
Db	1561	CDTCSPGFHGYPRCRPCDCHAGTAPGVCDPLTGQCYCKENVOGPKCDQCSLGTFSLDAA	1620						
QY	1621	NPXGCTRCFCFGATERCRSSSYTRQEFVDMEGVWLLSTDRQVVPHERQPGTEMLRADLRH	1680						
Db	1621	NPXGCTRCFCFGATERCRSSSYTRQEFVDMEGVWLLSTDRQVVPHERQPGTEMLRADLRH	1680						
QY	1681	VPEAVPEAFPELYWQAPPSSYLGDVSVSSGCTLRYLHSETQRQGVFVPMESRDPVVLQGN	1740						
Db	1681	VPEAVPEAFPELYWQAPPSSYLGDVSVSSGCTLRYLHSETQRQGVFVPMESRDPVVLQGN	1740						
QY	1741	QMSITFLEPAYTPGHVHRGQLQLVEGNFRHTTETRTNTVSREELMMVLASLEQLQIRALFS	1800						
Db	1741	QMSITFLEPAYTPGHVHRGQLQLVEGNFRHTTETRTNTVSREELMMVLASLEQLQIRALFS	1800						
QY	1801	QISSAVSLRRVALEVASPAGQALASNVLCCLCPASVYRSDSCQECAPGFYRDVKGLFLGR	1860						
Db	1801	QISSAVSLRRVALEVASPAGQALASNVLCCLCPASVYRSDSCQECAPGFYRDVKGLFLGR	1860						
QY	1861	CVPCQCHGHSRCLPFGSGVCDVCOHNTGHAHCERCAQAGFVSSRDDPSAPCVSCPLSVP	1920						
Db	1861	CVPCQCHGHSRCLPFGSGVCDVCOHNTGHAHCERCAQAGFVSSRDDPSAPCVSCPLSVP	1920						
QY	1921	SNNFABGCVLRGGRTQCLCKPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSNGDPLNLL	1980						
Db	1921	SNNFABGCVLRGGRTQCLCKPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSNGDPLNLL	1980						
QY	1981	FSDCDPLTGACRCGLRHTTGPCEICAPGFYGNALLPGNCTRCDCPTCGTEACDPSHSHC	2040						
Db	1981	FSDCDPLTGACRCGLRHTTGPCEICAPGFYGNALLPGNCTRCDCPTCGTEACDPSHSHC	2040						
QY	2041	LCXAGVTGRRCDRCQEGHFGFNGCGGRPCACGPAAGSECHPQSGQCHCRPGTGMGPQCR	2100						
Db	2041	LCXAGVTGRRCDRCQEGHFGFNGCGGRPCACGPAAGSECHPQSGQCHCRPGTGMGPQCR	2100						
QY	2101	ECAPGYWGLPEQGCRCRCQPGGRCDPHTGRNCNPPGLSGERCDTCSQHQHVPVPGGPVGH	2160						
Db	2101	ECAPGYWGLPEQGCRCRCQPGGRCDPHTGRNCNPPGLSGERCDTCSQHQHVPVPGGPVGH	2160						

; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
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; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
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; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 2
; LENGTH: 3600
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-037-417-2

Query Match 90.7%; Score 18254.5; DB 12; Length 3600;
Best Local Similarity 91.8%; Pred. No. 0;
Matches 3433; Conservative 18; Mismatches 103; Indels 187; Gaps 23;

QY	1	MAKRLCAGSALCVRGRGPAPLLLVGLALLGAARAREEAGGFSLHPPYFNLAEGARIAA	60
Db	1	MAKRLCAGSALCVRGRGPAPLL-----LHPPYFNLAEGARIAA	39
QY	61	SATCGEEAPARGSPRTEDLYCKLVGGPVAGDPNQITIRGOYCDICTAANSNKAHPASNA	120
Db	40	SATCGEEAPARGSPRTEDLYCKLVGGPVAGDPNQITIRGOYCDICTAANSNKAHPASNA	99
QY	121	IDGTERWWQSPPLSLRGLEYNEVNVTLDLGVFHVAYVLIKFANSRPDLVWLMERSMDFGR	180
Db	100	IDGTERWWQSPPLSLRGLEYNEVNVTLDLGVFHVAYVLIKFANSRPDLVWLMERSMDFGR	159
QY	181	TYQPWFQFFASSKRDCLERFGPQTLEIRTRDDAAICTTEYSRIVPLENGEIVVSLVNGRPG	240
Db	160	TYQPWFQFFAASKRDCLERFGPQTLEIRTRDDAAICTTEYSRIVPLENGEIVVSLVNGRPG	219
QY	241	AMNFSYSPLLRFTKATNVRLRFLRNTLLGLHMGKALRDPVTVTRYYYSIKDISIGGRC	300
Db	220	AMNFSYSPLLRFTKATNVRLRFLRNTLLGLHMGKALRDPVTVTRYYYSIKDISIGGRC	279
QY	301	VCHGHADACDAKOPTDFRLQCTCOHNTCGTCDRCPCPGFNQOPWKPEATANSANECQSCN	360
Db	280	VCHGHADACDAKOPTDFRLQCTCOHNTCGTCDRCPCPGFNQOPWKPEATANSANECQ-CE	338
QY	361	CYGHATDCYYDPEVDRRRASQSLDGTYYGGGVGVCIDCQHHTAGVNCERCLPGFYRSPNHPL	420
Db	339	CYGHATDCYYDPEVDRRRASQSLDGTYYGGGVGVCIDCQHHTAGVNCERCLPGFYRSPNHPL	398
QY	421	DSPHVCRRCNCESDFTDGTCEDLTGRCYCRPNFSGERCDVCAEGFTGPPSCYPTPSSND	480
Db	399	DSPHVCRGCNCESDFTDGTCEDLTGRCYCRPNFSGERCDVCAEGFTGPPSCYREHLPGND	458
QY	481	TREQVLPAGQIVNCDCSAAGTQGNACRKPVRGRCCLKPNFQGTCHCELCAPGFYGPGCQP	540
Db	459	TREQVLPAGQIVSCDCAAGTQGNACRKPVRGRCCLKPNFQGTCHCELCAPGFYGPGC-P	517
QY	541	CQCSS---PGVADDDCDPDTGQCRVGFEGATCDRCAPGYF-----HFPLCQLCGCSP	591
Db	518	ASVPALEWPMATAVTLTQASAG---AEWASRGPHVIAVPPATFTSLSASHPLRSVAVCGCSP	574
QY	592	AGTLPFGCDEAGRCCLQPEFAGPHCDRCRPGYHGFENCACTCDPRGALDQLCGAGGLCR	651
Db	575	AGTLPFGCDEAGRCCLQPEFAGPHCDRCRPGYHGFENCACTCDPRGALDQLCGAGGLCR	634
QY	652	CRPGYGTACQECSPGFHGFSCVPCHCSAEGSLHAAC-----DPRSGQCSGRP-RVTGLR	706
Db	635	CRPGYGTACQECSPGFHGFPS-----CPATALLKAPCTQPTVPGVGSAAAGPVRGCGVT	689

QY	707	--CDTCVPGAYNFPYCEAGSCHPAGLAPVDPALPEAQVPCMCRAHVEGSPCDRCKPGFWG	764
Db	690	HVCPVPTTSPTAKPLFTAGSCHPAGLAPVDPALPEVSPPCMCRAHVEGSPCDRCKPGFWG	749
QY	765	LSPSNPEGCTRCSCDLRGLTGGVAECQPGTQCFCCKPHVCQACASCKDGFGLDQADYF	824
Db	750	LSPSNPEGCTRCSCDLRGLTGGVAECQ-CTGQCFCCKPHVCQACASCKDGFGLDQADYF	808
QY	825	GCRSCRCDIGGALQSCSEPRTGVCRCRPNQTGPTCSEPARDHYLPDLHHLRLELEEAATP	884
Db	809	GCRSCRCDIGGALQSCSEPRTGVCRCRPNQTGPTCSEPARDHYLPDLHHLRLELEEAATP	868
QY	885	EGHAVRFGFNPLEFENFWSRGYAQMAYQAPVQPRIVARLNTLSPDLFWLFRYVNRGAMSVSG	944
Db	869	EGHAVRFGFNPLEFENFWSRGYAQMAYQAPVQPRIVARLNTLSPDLFWLFRYVNRGAMSVSG	928
QY	945	RVSUREGRSAACANCTAQSQPVAFPPSTEPAFITVPQRGFGEPPFVLNPGTVALRVEAEG	1004
Db	929	RVSUREGRSATCANCTAQSQPVAFPPSTEPAFITVPQRGFGEPPFVLNPGTVALRVEAEG	988
QY	1005	VLLDYVWLLPSAYVEAALLQLRVTEACTVPSAQSQSGDNCLLYTHLPDGFPSAAGLEAL	1064
Db	989	VLLDYVWLLPSAYVEAALLQLRVTEACTVPSAQSQSPSCLLYTHLPDGFPSAAGLEAL	1048
QY	1065	CRQDNLPRPCPTQOLSPSHPLITCTGSDVDVQLQVAVPQPGRYALVVEYANEDARQEV	1124
Db	1049	CRQDNLPRPCPTQOLSPSHPLITCTGSDVDVQLQVAVPQPGRYALVVEYANEDARQEV	1108
QY	1125	GVAVHTPORAPQOGLLSLHPCLYSTLCRGTAARDTQDHLAVFHLDSASVRLTAEQARFFL	1184
Db	1109	GVAVHTPORAPQOGLLSLHPCLYSTLCRGTAARDTQDHLAVFHLDSASVRLTAEQARFFL	1168
QY	1185	HGVTLPVPIEEFSPFEVPRVSCISSHGAFGPNASAACLPSRFKPPQPIILRDCQVPLPP	1244
Db	1169	HGVTLPVPIEEFSPFEVPRVSCISSHGAFGPNASAACLPSRFKPPQPIILRDCQVPLPP	1228
QY	1245	GLPLTHAQDLTPATSPAGPRPRPPTAVDPAEPTLLREPOATVVFTHVPTLGRYAFLLH	1304
Db	1229	GLPLTHAQDLTPAMSPAGPRPRPPTAVDPAEPTLLREPOATVVFTHVPTLGRYAFLLH	1288
QY	1305	GYQPAHPTFPVEVLINAGRWWQHANASFCPHGYGCRTLVCEGOALLDVTHSELTVTVR	1364
Db	1289	GYQPAHPTFPVEVLINAGRWWQHANASFCPHGYGCRTLVCEGOALLDVTHSELTVTVR	1348
QY	1365	VPEGRWLWLDYLVVVPENVYSFGYLREEPLDKSYDFISHCAAQGYHISPSSSSLFCRNAA	1424
Db	1349	VPKGRWLWLDYLVVVPENVYSFGYLREEPLDKSYDFISHCAAQGYHISPSSSSLFCRNAA	1408
QY	1425	ASLSLFYNNGARPCGCHVEGATGPTCEPFGGQPCCHAHVIGRDCSRCATGYWGFPCNCRPC	1484
Db	1409	ASLSLFYNNGARPCGCHVEGATGPTCEPFGGQPCCHAHVIGRDCSRCATGYWGFPCNCRAC	1468
QY	1485	DCGARLDELGTQCICPPRTIPDCLLCCQPTFGCHPLVGCCECNCSGPGIQBELTDPTCD	1544
Db	1469	DCGARLDELGTQCICPPRTIPDCLLCCQPTFGCHPLVGCCECNCSGPGIQBELTDPTCD	1528
QY	1545	TDGQCKCRPNVTGRRCDTCSPGFHGYPRCPCDCHEAGTAPGVCDPLTGQCYCKENVQG	1604
Db	1529	TDGQCKCRPNVTGRRCDTCSPGFHGYPRCPCDCHEAGTAPGVCDPLTGQCYCKENVQG	1588
QY	1605	PKDQCSLGTFSLDAAANPKGCTRCFCFGATERCRSSSYTRQEFVDMEGWVLLSTDRQVVP	1664
Db	1589	PKDQCSLGTFSLDAAANPKGCTRCFCFGATERCRSSSYTRQEFVDMEGWVLLSTDRQVVP	1648
QY	1665	HEROPGTEMLRADLRHVPEAVPEAFPELYWQAPPSYLGDRVSSYGGTLRYELHSETQRGD	1724
Db	1649	HEROPGTEMLRADLRHVPEAVPEAFPELYWQAPPSYLGDRVSSYGGTLRYELHSETQRGD	1708
QY	1725	VFVPMESRPDVVLQGNQMSITFLEPAYPTPGHVHRGQLQLVEGNFRHTETRTNVSREELM	1784
Db	1709	VFVPMESRPDVVLQGNQMSITFLEPAYPTPGHVHRGQLQLVEGNFRHTETRTNVSREELM	1768
QY	1785	MVLASLEQLQIRALFSQISSAVSLRRVALEVASPACQAGALASNVLCCLCPASVYRGDSQCE	1844

1769 Db MVLASLEQLRALFSQISSAVFLRRVALEVASPAGQALASNVELCLCPASYRGDSQOE 1828
1845 QY CAPGFYRDVKGLFLGRVCVPCQCHGHSRDLCPGSGVCVDCQHNTGEGHCHERCQAGFMSSRD 1904
1829 Db CAPGFYRDVKGLFLGRVCVPCQCHGHSRDLCPGSGVCV - CQHNTGEGHCHERCQAGFVSSRD 1887
1905 QY DPSAPCVSCPCPLSVPSNNFAEGCVLRGGRTQCLCKPGYAGASCERCAPGFFGNPLVLGS 1964
1888 Db DPSAPCVSCPCPLSVPSN-----RCAPGFFGNPLVLGS 1920
1965 QY SCQPCDCSGNDPNLLFSDCDPLTGACRGCLRHHTGPRCEICAPGFYGNALLPGNCTRCD 2024
1921 Db SCQPCDCSGNDPNLLFSDCDPLTGACRGCLRHHTGPRCEICAPGFYGNALLPGNCTRCD 1980
2025 QY CTPCGTEACDPHSGHCLCKAGVTGRRCCDRCEGHFGNGCGCRPCACGPAEGSECHPQ 2084
1981 Db CTPCGTEACDPHSGHCLCKAGVTGRRCCDRCEGHFGDFGCGGCRPCACGPAEGSECHPQ 2040
2085 QY SGQCHCRPGTMGPQCHRECAPGYWGLPEQGCRRCQCPGGRCDPHTGRCNCPPLGLSGERCDT 2144
2041 Db SGQCHCRPGTMGPQCHRECAPGYWGLPEQGCRRCQCPGGRCDPHTGRCNCPPLGLSGERCDT 2100
2145 QY CSQQHQPVPVGGPVGHSIHCEVCDHCVVLLDDLERAGALLPAIHEQLEGINASSMAWAR 2204
2101 Db CSQQHQPVPVGGPVGHSIHCEVCDHCVVLLDDLERAGALLPAIHEQLEGINASSMAWAR 2160
2205 QY LHRLNASIADL-----QSQRSPGLPRHETAQOLEVLEQQST 2241
2161 Db LHRLNASIADLQVLSVLAPPPQPGPVQAFTRFLPQSQRSPGLPRHETAQOLEVLEQQST 2220
2242 QY SLQCDARRLGGQAVGTRDQASQLLAGTEATLGHAKTLAAIRAVDRITLSLMSQTGHGL 2301
2221 Db SLPP-----QAVGTRDQASQLLAGTEATLGHAKTLAAIRAVDRITLSLMSQTGHGL 2273
2302 QY ANASAPSGEQLLRLTLAEVERLLWEMRARDLGAPOAAAEAEALAAQORLLARVQEOQLSSLWE 2361
2274 Db ANASAPSGEQLLRLTLAEVERLLWEMRARDLGAPOAAAEAEALAAQORVLARVQEOQLSSLWE 2333
2362 QY ENQALATQTRDRRLAQHEAGLMDLREALNRAVDATREAEQELNSRNOERLEEALORKQELSR 2421
2334 Db ENQALATQTRDRRLAQHEAGLMDLREALNRAVDATREAEQELNSRNOERLEEALORKQELSR 2393
2422 QY DNATLQATLHAARDTLASVERLLHSLDQAK - EELERLAASLDGARTPLLQRMQTFSPAGS 2480
2394 Db DNATLQATLHAARDTLASVERLLEGLSPLKFQELERLAASLDGARTPLLQRMQTFSPAGS 2453
2481 QY KLRLVEAAEAHAQQLGQALNLSSIILDVNQDRLTQRAEASNAYSRILOAVQAAEDAAG 2540
2454 Db KLRLVEAAEAHAQQLGQALNL - SIILDVNQDRLTQRAEASNAYSRILOAVQAAEDAAG 2512
2541 QY QALQOQADHTWATVVRQGLVDRAQQLLANSTALEEMLQEQORLGL - -VWA - -ALQGART 2595
2513 Db QALQOQADHTWQTVVRQGLVDRAQQLLANSTALEEMLQEQORLGLGECWAPNGALRPAGT 2572
2596 QY QLRDVRAKKDQLEAHIAQAQAMLAMDTDETSKKIAHAKAVAAEAQDTATRVOSQLQAMQE 2655
2573 Db QLRDVRAKKDQLEAHIAQAQAMLAMDTGETSKKIAHAKAVAAEAQDTATRVOSQLQAMQE 2632
2656 QY NVERWQGYEGLRGQDLGQAVLDAGHSVSTLEKTLPOLLAKL SILENRGVHNASLALSAS 2715
2633 Db NVERWQGYEGLRGQDLGQAVLDAGSAVSTLEKTLPOLLAKL SILENRGVHNASLALSAS 2692
2716 QY IGRVRELIAQARGAASK - VKVPMKFNGRSGVQLRTPRDLADLAAYTALKFYLOQPEPEPG 2774
2693 Db IGRVRELIAQARGAASKVKVPMKFNGRSGVQLRTPRDLADLAAYTALKFYLOQPEPEPG 2752
2775 QY QGTEDRFVYMGSRQATGDYMGVSLRDKKVHVWVYQLGEAGPAVL S IDEDIGEQFAAVSLD 2834
2753 Db QGTEDRFVYMGSRQATGDYMGVSLRDKKVHVWVYQLGEAGPAVL S IDEDIGEQFAAVSLD 2812
2835 QY RTLOFGHMSVTVVERQMIQETKGDTVAPGAEGLLNLRPDDFVFYVGGYSTFTPPPLLRFP 2894

2813 Db RTLOFGHMSVTVVERQMIQETKGDTVAPGAEGLLNLRPDDFVFYVGGYSTFTPPPLLRFP 2872
2895 QY GYRGCIEMDTLNEEVVSLYNFERTFQOLDTAVDRPCARSKSTGDPWLTDGSYLDGTGFARI 2954
2873 Db GYRGCIEMDTLNEEVVSLYNFERTFQOLDTAVDRPCARSKSTGDPWLTDGSYLDGTGFARI 2932
2955 QY SFDSQISTTKRFEQELRLVSYSGVLFFFLKQSQOFLCLAVQEGSLVLLYDFGAGLKKAVPL 3014
2933 Db SFDSQISTTKRFEQELRLVSYSGVLFFFLKQSQOFLCLAVQEGSLVLLYDFGAGLKKAVPL 2992
3015 QY QPPPPLTSASKAIQVFLLLGGSRKRVLRVERATVYSVEQDNDELEADAYVILGGVPPDQLP 3074
2993 Db QPPPPLTSASKAIQVFLLLGGSRKRVLRVERATVYSVEQDNDELEADAYVILGGVPPDQL- 3051
3075 QY PSLRWLFPPTGGSVRGCVKGIKALGKYVDLKRINTTGVSAAGCTADLLVGRAMTFHGHGFLR 3134
3052 Db PSLRWLFPPTGGSVRGCVKGIKALGKYVDLKRINTTGVSAAGCTADLLVGRAMTFHGHGFLR 3111
3135 QY LALSNVAPLTGNVYSGFGFHSQAQDSALLYIRASPDGLCQVSLQQGRVSLQLLRTEVKTQA 3194
3112 Db LALSNVAPLTGNVYSGFGFHSQAQDSALLYIRASPDGLCQVSLQQGRVSLQLLRTEVKTQA 3171
3195 QY GFADGAPHYVAFYSNATGVWLYVDDQLQOMKPHRGPPPELOPQPEGPPRLLLGGLPESGT 3254
3172 Db GFADGAPHYVAFYSNATGVWLYVDDQLQOMKPHRGPPPELOPQPEGPPRLLLGGLPESGT 3231
3255 QY IYNFSGCISNVFVQRLGQPVFVDLQONLGSVNVSTGCAPALQAOTPGLPGRGLQATARK 3314
3232 Db IYNFSGCISNVFVQRLGQPVFVDLQONLGSVNVSTGCAPALQAOTPGLP-----RQ 3284
3315 QY ASRERSQPARHPACMLPPHLTRTRDSYQFGGSLSSHLEFVGILARHNWPSLSMHVLP RS 3374
3285 Db ASRERSQPARHPACMLPPHLTRTRDSYQFGGSLSSHLEFVGILARHN----- 3332
3375 QY SRGULLFTARLRPGSPSLALFLSNHGFVAQMEGLGTRLRAQSRQSRPRGRWHKVSVRWEK 3434
3333 Db -----VSVRWEK 3339
3435 QY NRILLVTDGARAWSQEGPHRQHQGAHPQPHTLFVGGIPASSHSSKLPVTVGFGCVKRL 3494
3340 Db NRILLVTDGARAWSQEGPHRQHQGAHPQPHTLFVGGIPASSHSSKLPVTVGFGCVKRL 3399
3495 QY RLHGRELGAPTRMAGVTPCILGPLEAGLFFPGSGGVTILDLPGATLPDVGLELEVRPLAV 3554
3400 Db RLHGRELGAPTRMAGVTPCILGPLEAGLFFPGSGGVTILDLPGATLPDVGLELEVRPLAV 3459
3555 QY TGLIFHLGQARTPPYLQLOVTEKQVLLRADDGAGEFSTSVTRPSVLCDGQWHRLAVMKSG 3614
3460 Db TGLIFHLGQARTPPYLQLOVTEKQVLLRADDGAGEFSTSVTRPSVLCDGQWHRLAVMKSG 3519
3615 QY NVLRLEVDAQSNHTVGPPLAAAGAPAPLYLGLLPEPMAVQPPWPPAYCGCMRRLAVNRSP 3674
3520 Db NVLRLEVDAQSNHTVGPPLAAAGAPAPLYLGLLPEPMAVQPPWPPAYCGCMRRLAVNRSP 3579
3675 QY VAMTRSVEVHGAVGASGCPAA 3695
3580 Db VAMTRSVEVHGAVGASGCPAA 3600

RESULT 7
US-10-037-417-6
; Sequence 6, Application US/10037417
; Publication No. US20040052806A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchiernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E

APPLICANT: Vernet, Corine A.M.
APPLICANT: Li, Li
APPLICANT: Gorman, Linda
APPLICANT: Edinger, Shlomit R
APPLICANT: Sciore, Paul
APPLICANT: Ellerman, Karen
APPLICANT: Malyankar, Uriel M
APPLICANT: Rothenberg, Mark
APPLICANT: Stone, David J
APPLICANT: Boldog, Ferenc L
APPLICANT: Guo, Xiaojia
APPLICANT: Shenoy, Suresh G
APPLICANT: Anderson, David W
APPLICANT: Padigaru, Muralidhara
APPLICANT: Tauplier Jr, Raymond J
APPLICANT: Miller, Charles E
APPLICANT: Eisen, Andrew J
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-235
CURRENT APPLICATION NUMBER: US/10/037,417
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/260,018
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/260,360
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/272,411
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/272,817
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/291,186
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/303,231
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/305,060
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 60/318,405
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/318,700
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 227
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 3597
TYPE: PRT
ORGANISM: Homo sapiens
US-10-037-417-6

Query Match 90.6%; Score 18231; DB 12; Length 3597;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 3428; Conservative 18; Mismatches 108; Indels 184; Gaps 21;
QY 1 MAKRLCAGSALCVRGPRGPAPLLVGLALLGAARABEAGGFSLHPPYFNLAEGARIAA 60
DB 1 MAKRLCAGSALCVRGPRGPAPLL-----LHPPYFNLAEGARIAA 39
QY 61 SATCGEEAPARGSPRPTEDELYCKLVGGPVAGGDPNOTIRGQYCDICTAANSNKAHPASNA 120
DB 40 SATCGEEAPARGSPRPTEDELYCKLVGGPVAGGDPNOTIQGYCDICTAANSNKAHPASNA 99
QY 121 IDGTERWQSPPLSRGLEYNVNVTLDLGQVHFVAXVLIKFANSRPDLWVLSRSMDFGR 180
DB 100 IDGTERWQSPPLSRGLEYNVNVTLDLGQVHFVAXVLIKFANSRPDLWVLSRSMDFGR 159
QY 181 TYQPWFQFASCKRDCLERFQPTLERITRDDAAICTEYSRIVPLENGEIVWSLVNRP 240
DB 160 TYQPWFQFASCKRDCLERFQPTLERITRDDAAICTEYSRIVPLENGEIVWSLVNRP 219
QY 241 AMNFSYSPLLREFTKATNVRLEFRITNTLLGLMKGALRDPVTTRRYYSIKDISIGRC 300
DB 220 AMNFSYSPLLREFTKATNVRLEFRITNTLLGLMKGALRDPVTTRRYYSIKDISIGRC 279
QY 301 VCHGHADACDAKPTDPRFRLQCTQHNTCGGTCDRCPCGFGNQPKPATANSANECQ-CE 360

Db 280 VCHGHADACDAKPTDPRFRLQCTQHNTCGGTCDRCPCGFGNQPKPATANSANECQ-CE 338
QY 361 CYGHATDCYDPEVDRRRASQSLDGTQGGVCIDCQHHTAGVNCERCLPGFYRSPNHPL 420
Db 339 CYGHATDCYDPEVDRRRASQSLDGTQGGVCIDCQHHTAGVNCERCLPGFYRSPNHPL 398
QY 421 DSPHVCRRNCESDFTDGTCELTGRCYCRPNFSGERCDCVCAEGFTGFPSCYTPSSND 480
Db 399 DSPHVCRRNCESDFTDGTCELTGRCYCRPNFSGERCDCVCAEGFTGFPSCYTPSSND 458
QY 481 TREQVLPAGQIVNCDSCAAGTQGNACKRDPVGRCLCKPNFQGTCHCELCAPGYGPGQP 540
Db 459 TREQVLPAGQIVNCDSCAAGTQGNACKRDPVGRCLCKPNFQGTCHCELCAPGYGPGQP 517
QY 541 CQCSS---PGVADDRCDPDTGQCRVGFEGATCDRCAPGYF-----HFPLCQLCGCSP 591
Db 518 ASVPALEWPMPTAVTLTQASAG---AEWASRGPHVIAVPEATFTLSASHPLSRAVCGCSP 574
QY 592 AGTLPEGCEAGRCCLCOPEFAGPHCDRCRPGYHGFNCOACTCDPRGALDQLCGAGGLCR 651
Db 575 AGTLPEGCEAGRCCLCOPEFAGPHCDRCRPGYHGFNCOACTCDPRGALDQLCGAGGLCR 634
QY 652 CRPGYTGTACQECSPGFHGFPPSCVPHCHCSAEGSLHAAC---DPRSGQCSCRPRVTGLRC 707
Db 635 CRPGYTGTACQECSPGFHGFPPSCVPHCHCSAEGSLHAAC---CPATALLKAPCTQPTVPGVSAAGP-VRGCGV 688
QY 708 DTCVPGAYNPYCEAGSCHPAGLAPVDPALPEAQVPCMCRAHVEGSPCDRCCKPGFWGLSP 767
Db 689 TRVCPVPTTSPTAKLALATLPVWPPVDPALPEAQVPCMCRAHVEGSPCDRCCKPGFWGLSP 748
QY 768 SNPEGCTRCSCDLRGTLGGVAECQPGTGQCFCKPHVCCQACASCKDGFGLDQADYFGCR 827
Db 749 SNPEGCTRCSCDLRGTLGGVAECQPGTGQCFCKPHVCCQACASCKDGFGLDQADYFGCR 808
QY 828 SCRCDIGGALGQSCCEPRTGVCRCPNTQGTCTSEPARDHYLPDLHLRLLEDEEAATPEGH 887
Db 809 SCRCDIGGALGQSCCEPRTGVCRCPNTQGTCTSEPARDHYLPDLHLRLLEDEEAATPEGH 868
QY 888 AVRFGNPLEFENFWSRGYQAQMAPVQPRIVARLNTSPDLFWLVFRYVNRGAMSVGRVS 947
Db 869 AVRFGNPLEFENFWSRGYQAQMAPVQPRIVARLNTSPDLFWLVFRYVNRGAMSVGRVS 928
QY 948 VREGRSAACANCTAQSQPVAFPPSTPEAFITVPOQGFGEPPFVLPNGTVALRVEAEGVLL 1007
Db 929 VREGRSAACANCTAQSQPVAFPPSTPEAFITVPOQGFGEPPFVLPNGTVALRVEAEGVLL 988
QY 1008 DYVLLPSAYYEAALLQLRVTEACTYRPSAQSGDNCLLYTHLPDGFPSAAGLEALCRQ 1067
Db 989 DYVLLPSAYYEAALLQLRVTEACTYRPSAQSGDNCLLYTHLPDGFPSAAGLEALCRQ 1048
QY 1068 DNSLPRPCPTEQLSHPPLITCTGSDVDVQLQVAVPQGRYALVVEYANEDARQEVGVA 1127
Db 1049 DNSLPRPCPTEQLSHPPLITCTGSDVDVQLQVAVPQGRYALVVEYANEDARQEVGVA 1108
QY 1128 VHTPQRAPOQGLLSLHPCLYSTLCRGRTARDTQDHLAVFHLDSASVRLTAEQARFHLGV 1187
Db 1109 VHTPQRAPOQGLLSLHPCLYSTLCRGRTARDTQDHLAVFHLDSASVRLTAEQARFHLGV 1168
QY 1188 TLVPIEESPEFVEPRVSCISSHGAFGPNNSAACLSRPPKPPQPIILRDCQVILPPGLP 1247
Db 1169 TLVPIEESPEFVEPRVSCISSHGAFGPNNSAACLSRPPKPPQPIILRDCQVILPPGLP 1228
QY 1248 LTHAQDLTPATSPAGPRPRPTAVDPDAEPTLLREPOATVFTTHVPTLCRYAFLHGYQ 1307
Db 1229 LTHAQDLTPATSPAGPRPRPTAVDPDAEPTLLREPOATVFTTHVPTLCRYAFLHGYQ 1288
QY 1308 PAHPTFPVEVLINAGRVWQGHANASFCPHGYGCRTLVVCQGLLDVTHSELTVTVRVE 1367
Db 1289 PAHPTFPVEVLINAGRVWQGHANASFCPHGYGCRTLVVCQGLLDVTHSELTVTVRVE 1348
QY 1368 GRWLWLDYVLVVPENVYSGYLREEPLDKSYDFISHCAAQGYHISPSSSSLFCRNAAASL 1427
Db 1349 GRWLWLDYVLVVPENVYSGYLREEPLDKSYDFISHCAAQGYHISPSSSSLFCRNAAASL 1408

QY 1428 SLFYNNGARPCGCHEVGATGPTCEPFGGQCPCHAHVIGRDCSRCATGYWGPNCRCDCG 1487
Dd 1409 SLFYNNGARPCGCHEVGATGPTCEPFGGQCPCHAHVIGRDCSRCATGYWGPNCRCDCG 1468
QY 1488 ARLCDELGTGOCICPPRTIIPDCLLCQPOTFGCHPLVGCCECNCSPGIGIELTDPTCDTDS 1547
Dd 1469 ARLCDELGTGOCICPPRTIIPDCLLCQPOTFGCHPLVGCCECNCSPGIGIELTDPTCDTDS 1528
QY 1548 GQCKCRPNVTGRRCDTCSPGFHGYPRCRPCDCHAEAGTAPGVCDPLTGQCCKENVOGPKC 1607
Dd 1529 GQCKCRPNVTGRRCDTCSPGFHGYPRCRPCDCHAEAGTAPGVCDPLTGQCCKENVOGPKC 1588
QY 1608 DQCSLGTFSLDAANPKGCTRCFCFGATERCRSSSYTRQEFVDMEGWVLLSTDROVUPHER 1667
Dd 1589 DQCSLGTFSLDAANPKGCTRCFCFGATERCRSSSYTRQEFVDMEGWVLLSTDROVUPHER 1648
QY 1668 QPCTEMLRADLRHVPEAVPEAPPELYWQAPPSYLGDRVSSYGGTLRYELHSETQRGDVV 1727
Dd 1649 QPCTEMLRADLRHVPEAVPEAPPELYWQAPPSYLGDRVSSYGGTLRYELHSETQRGDVV 1708
QY 1728 PMESRPDVVLQGNQMSITFLEBPAYPTPGHVHRGQLQVVEGNFRHTETRTNVTBREELMMVL 1787
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QY 1788 ASLEQLQIRALFSQISSAVLRRVALEVASPAGQGALASNVELCLCPASYRGSCQECAP 1847
Dd 1769 ASLEQLQIRALFSQISSAVLRRVALEVASPAGQGALASNVELCLCPASYRGSCQECAP 1828
QY 1848 GFYRDVKGLFLGRCVPCQCHGHSRCLPGSGVCVDCQHNTEGAHCERCQAGFMSSRDDPS 1907
Dd 1829 GFYRDVKGLFLGRCVPCQCHGHSRCLPGSGVCV-CQHNTEGAHCERCQAGFMSSRDDPS 1887
QY 1908 APCVSCPCPLSVPSNFAEGCVLRRGGRTQCLCKPGYAGASCERCAPGFFGNPLVLGSSCQ 1967
Dd 1888 APCVSCPCPLSVPSN-----RCAPGFFGNPLVLGSSCQ 1920
QY 1968 PCDCSNGDPNLLFSDCDPLTGACRGCLRHTTGPRCEICAPGFYGNALLPGNCTRCDCTP 2027
Dd 1921 PCDCSNGDPNLLFSDCDPLTGACRGCLRHTTGPRCEICAPGFYGNALLPGNCTRCDCTP 1980
QY 2028 CGTEACDPHSGHCLCKAGVTGRRCDRCQEGHFGNGCGCRPCACGPAAEGSECHPQSGQ 2087
Dd 1981 CGTEACDPHSGHCLCKAGVTGRRCDRCQEGHFGNGCGCRPCACGPAAEGSECHPQSGQ 2040
QY 2088 CHCRPCTMGPOCRECAPGYWGLPEQGCRRCQCPGGRCDPHTGRNCNPPGLSGERCDTCSQ 2147
Dd 2041 CHCRPCTMGPOCRECAPGYWGLPEQGCRRCQCPGGRCDPHTGRNCNPPGLSGERCDTCSQ 2100
QY 2148 QHQPVPFGPVGHSIHCEVCDHCVVLLDDLERAGALLPAIHEQLRGINASSMAWARLHR 2207
Dd 2101 QHQPVPFGPVGHSIHCEVCDHCVVLLDDLERAGALLPAIHEQLRGINASSMAWARLHR 2160
QY 2208 LNASIADL-----QSOLRSPGLPRRHETAQOLEVLEQOSTSLG 2244
Dd 2161 LNASIADLQVLSVLAFFPPQPGPVQAFTFRLPQSOLRSPGLPRRHETAQOLEVLEQOSTSLP 2220
QY 2245 QDARRLGQOAVGTRDQASQLLAGTEATLGHAKTLLAAIRAVIDRTLSELMSQTGHLGLANA 2304
Dd 2221 P-----QAVGTRDQASQLLAGTEATLGHAKTLLAAIRAVIDRTLSELMSQTGHLGLANA 2273
QY 2305 SAPSGEQLLRTLAEVERLLWEMRARDLGAPQAAAEAEELAAQRLLARVQEBQLSSLWEENQ 2364
Dd 2274 SAPSGEQLLRTLAEVERLLWEMRARDLGAPQAAAEAEELAAQRLLARVQEBQLSSLWEENQ 2333
QY 2365 ALATQTRDLRAQHEAGLMDLREALNRAVDATREAQELNSRQERLEEALQRKQELSRDNA 2424
Dd 2334 ALATQTRDLRAQHEAGLMDLREALNRAVDATREAQELNSRQERLEEALQRKQELSRDNA 2393
QY 2425 TLQATLHAARDTLASVFRLLHSLDQAK-EELERLAASLDGARTPLLQRMQTFSPAGSKLR 2483
Dd 2394 TLQATLHAARDTLASVFRLLHSLDQAK-----EELERLAASLDGARTPLLQRMQTFSPAGSKLR 2453

QY 2484 LVEAAEAHAQQLGQLALNLSSIIILDVNQDRLTORAIEASNAYSRILOAVQAAEDAAGQAL 2543
Dd 2454 LVEAAEAHAQQLGQLALNL-SIIILDVNQDRLTORAIEASNAYSRILOAVQAAEDAAGQAL 2512
QY 2544 QADHTWATVVRQGLVDRAQOLLANSTALEEAMLEQOORLGL--VWA---ALQGARTQLR 2598
Dd 2513 QADHTWQTVVRQGLVDRAQOLLANSTALEEAMLEQOORLGLGECWAFMGALRPAQTQLR 2572
QY 2599 DVRAKDDOLEAHIQAAQAAMLAMDTDETSKKIAHAKAVAAEAQDTATRVQSQLOAQMOENVE 2658
Dd 2573 DVRAKDDOLEAHIQAAQAAMLAMDTGETSKKIAHAKAVAAEAQDTATRVQSQLOAQMOENVE 2632
QY 2659 RWQGYEGLRGQDLGOAVLDAGHSVSTLEKTLPLQLLAKISILENRGVHNASLALSASIGR 2718
Dd 2633 RWQGYEGLRGQDLGOAVLDAGSAVSTLEKTLPLQLLAKISILENRGVHNASLALSASIGR 2692
QY 2719 VRELIQAARGAASK-VKVPMEKNGRSGVQLRTPRDLADLAAYTALKFYLGQPEPEPGQST 2777
Dd 2693 VRELIQAARGAASKVKVPMEKNGRSGVQLRTPRDLADLAAYTALKFYLGQPEPEPGQST 2752
QY 2778 EDRFVYMGSRQATGDYMGVSLRDKKVHVYQOLGEAGPAVLSIDEDIGEQAFAAVSLDRTL 2837
Dd 2753 EDRFVYMGSRQATGDYMGVSLRDKKVHVYQOLGEAGPAVLSIDEDIGEQAFAAVSLDRTL 2812
QY 2838 QFGHMSVTVVERQMIQETKGDIVAPGAEGLLNLRPDDFVFYVGGYPSTFTPPPLLRFPFGR 2897
Dd 2813 QFGHMSVTVVERQMIQETKGDIVAPGAEGLLNLRPDDFVFYVGGYPSTFTPPPLLRFPFGR 2872
QY 2898 GCIEMDTLNEEWSLYNFERTFQDITAVDRPCARSKSTGDPWLTDGSLDGTGTFARISFD 2957
Dd 2873 GCIEMDTLNEEWSLYNFERTFQDITAVDRPCARSKSTGDPWLTDGSLDGTGTFARISFD 2932
QY 2958 SQISTTKRFEQELRLVSYSGVLFPLKQSQFLCLAVQESGLVLLYDFGAGLKKAVPLQPP 3017
Dd 2933 SQISTTKRFEQELRLVSYSGVLFPLKQSQFLCLAVQESGLVLLYDFGAGLKKAVPLQPP 2992
QY 3018 PPLTSASKAIQVFLLLGGSRKRVLRVERATVYSVEQDNDLEADAYYLGVPDPQLPPSL 3077
Dd 2993 PPLTSASKAIQVFLLLGGSRKRVLRVERATVYSVEQDNDLEADAYYLGVPDPQL-PSL 3051
QY 3078 RWLFTGSGSVRGCVKGIKALGVYDLKRLNTTGVSAAGCTADLLVGRAMTFHGHGFLRLAL 3137
Dd 3052 RRLFTGSGSVRGCVKGIKALGVYDLKRLNTTGVSAAGCTADLLVGRAMTFHGHGFLRLAL 3111
QY 3138 SNVAPLTGNVYSGFGFHSQAQDSALLYYRASPDGLCQVSLQOGRVSLQLLRTTEVKTOAGFA 3197
Dd 3112 SNVAPLTGNVYSGFGFHSQAQDSALLYYRAS-PVRPHQVSLQOGRVSLQLLRTTEVKTOAGFA 3171
QY 3198 DGAPHYVAFYSNATGVWLYVDDQLQOMKPHRGPPPELQOPQEGPPRLLLGGLPESGTIYN 3257
Dd 3172 DGAPHYVAFYSNATGVWLYVDDQLQOMKPHRGPPPELQOPQEGPPRLLLGGLPESGTIYN 3231
QY 3258 FSGCISNVFVQRLGLGPQRFVFDLQONLGSVNSTGCPALQACTPGLGPRGLQATARKASR 3317
Dd 3232 FSGCISNVFVQRLGLGPQRFVFDLQONLGSVNSTGCPALQACTPGLGP-----RQASR 3284
QY 3318 RSRQPARHPACMLPPHLRTRTSDSYQFGGSLSSHLEFVGILARHNWPSLSMHVLPSSRG 3377
Dd 3285 RSRQPARHPACMLPPHLRTRTSDSYQFGGSLSSHLEFVGILARHN----- 3329
QY 3378 LLLFTARLRPGSPSLALFLSNGHFVAQMEGLGTRLRLAQQRORSRPPGRWHKVSVRWEKNRI 3437
Dd 3330 -----VSVRWEKNRI 3339
QY 3438 LLVTDGARAWSQEGPHRQHGAEPHPHTLFGGLPASSHSSKLPVTVGFSGCVKRLRLH 3497
Dd 3340 LLVTDGARAWSQEGPHRQHGAEPHPHTLFGGLPASSHSSKLPVTVGFSGCVKRLRLH 3399
QY 3498 GRPLGAPTRMAGVTPCILGPLEAGLFFPGSGGGVITLDPGATLPDVGLELEVRPLAVTGL 3557
Dd 3400 GRPLGAPTRMAGVTPCILGPLEAGLFFPGSGGGVITLGLPGATLPDVGLELEVRPLAVTGL 3459
QY 3558 IFHLGQARTPPYLQVTEKQVLLRADDDGAGEFSTSVTRPSVLCDGQWHRLAVMKSGNVL 3617

Db 3460 IFHLGQARTPPYLQVLPRQVLLRADDDGAGEFSTSVTRPSVLCDGQWHLAVMKSGNVL 3519
Qy 3618 RLEVDAQSNHTVGPLLAAAAGAPAPLYLGGLPPEPMAVQWPWPAYCGCMRRLLAVNRSPVAM 3677
Db 3520 RLEVDAQSNHTVGPLLAAAAGAPAPLYLGGLPPEPMAVQWPWPAYCGCMRRLLAVNRSPVAM 3579
Qy 3678 TRSVEVHGAVGASGCPAA 3695
Db 3580 TRSVEVHGAVGASGCPAA 3597

RESULT 8

US-09-845-583-2
; Sequence 2, Application US/09845583
; Patent No. US20020142954A1
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Brunken, William Joseph
; APPLICANT: Champlaud, Marie-France
; APPLICANT: Hunter, Dale
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
; FILE REFERENCE: 10287-056001
; CURRENT APPLICATION NUMBER: US/09/845.583
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/200,863
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3635
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-845-583-2

Query Match 78.7%; Score 15839; DB 9; Length 3635;
Best Local Similarity 79.4%; Pred. No. 0;
Matches 2874; Conservative 277; Mismatches 452; Indels 18; Gaps 8;

Qy 79 DLYCKLVGGPVAGSDPNQITIRGOYCDICTAANSNKAHPASNAIDGTERWWQSPPLSRGLE 138
Db 1 DLYCKLVGGPVAGSDPNQITIRGOYCDICTAANSNKAHPASNAIDGTERWWQSPPLSRGLE 60
Qy 139 YNEVNVTLDLGOVHVAYVLIKFNASPRPDLVLESMDFGRTYQWPQFFASSKRDCLER 198
Db 61 YNEVNVTLDLGOVHVAYVLIKFNASPRPDLVLESMDFGRTYQWPQFFASSKRDCLER 120
Qy 199 FGPOTLERITRDDAICTTEYSRIVPLENGEIVVSLVNGRPGAMNFYSYPLIREFTKATN 258
Db 121 FGPOTLERITQDDDDVICTTEYSRIVPLENGEIVVSLVNGRPGALNFYSYPLLRDFTKATN 180
Qy 259 VRLRFLRTNTLLGLMKGALRDPVTTRRYIYSIKDISIGRCVCHGHADACDAKDPDPF 318
Db 181 IRLRFLRTNTLLGLMKGALRDPVTTRRYIYSIKDISIGRCVCHGHADVCDKDPDPF 240
Qy 319 RLQCTCQHNTCGGTCDRCPCGFNQPKPATANSANECQSCNCYGHATDCYYDPEVDRRR 378
Db 241 RLQCAQHNTCGGSCDRCCPCGFNQPKPATIDSANECQSCNCHGHAYDCYYDPEVDRRN 300
Qy 379 ASQSLDGTYYQGGVCIDCOHHTAGVNCERCLPGFYRSPNHPLDSPHYCRRNCESDFTDG 438
Db 301 ASQNDNVYQGGVCIDCOHHTGINCERCLPGFFRAPDQPLDSPHYCRPCDCESDFTDG 360
Qy 439 TCEDLTGRCYCRPNFSGERCIDVCAEGFTGFPSCVPTPS - SSNDTREQVLPAGQIVNCDCS 497
Db 361 TCEDLTGRCYCRPNFTGELCAACAEGYTDFFHCYPLPSFPHNDTREQVLPAGQIVNCDCN 420
Qy 498 AAGTQGNACRKOPRVGRCLCKPNFQGTCHCELCAFPFYGPCCQPCQSSPGVADDDRCDPDT 557
Db 421 AAGTQGNACRKOPRLGRVCCKPNFRGAHCELCAFPFHGSPCHPCQCSSPGVANSLCDPES 480
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; Sequence 47, Application US/10037417
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; GENERAL INFORMATION:
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TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
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Query Match 78.7%; Score 15839; DB 12; Length 3635;
Best local Similarity 79.4%; Pred. No. 0;
Matches 2874; Conservative 277; Mismatches 452; Indels 18; Gaps 8;
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Db 2216 GQGSFGDALVPSGEQLRWALAEVERLLWDMETRDLDGAQGAFAEAEALAEQRLMARVQEQL 2275
QY 2357 SSLWEENQALATQTRDLRAQHEAGLMDLREALNPAVDATREAQELNSRNQERLEALQK 2416
Db 2276 TSFWEENQSLATHIRDQLAQYESGLMDJREALNQAVENTTREAELNSRNQERVKEALQWK 2335
QY 2417 QELSRDNATLQATLHAARDTLASVFRLLHSLDQAKEELERLAASLDGARTPLIQRMQTF 2476
Db 2336 QELSQDNATLKATLOAASLILGHVSELQCIDQAKEDLEHLAASLDGAWTPLLKRMQAF 2395
QY 2477 PAGSKLRLVEAAEAHAQQLGQALNLSSIIILDVNDRLTORAIEASNAYSRILOAVQAAE 2536

Db 2396 PASSKVDLVEAAEAHAQKLNQLAINLSGIILGINQDRFIQRAVEASNAYSSILQAVQAAE 2455
QY 2537 DAAGQALQQADHTWATVVROGLVDRAQQLLANSTALEEAMLQEQORLGLVWALQQARTQ 2596
Db 2456 DAAGQALRQASRTWEMVQVORGLAAGARQOLLANSSALEETILGHQGRGLAQGRLOAAQIQ 2515
QY 2597 LRDVRAKDKQLEAHIQAAQAMLAMDTDETSKIAHAKAVAAEAQDTATRVQSOLQAMQEN 2656
Db 2516 LHNWARKNQLAAQIQEAQAMLAMDTSETSEKIAHAKAVAAEALSTATHVQSOLQGMQKN 2575
QY 2657 VERWQOYEGELRGQDLGQAVLDAGHSVSTLEKTLPOLAKLSILENRGVHNASLALSASI 2716
Db 2576 VERWQSOLGGLQGDLSQVERDASSVSTLEKTLPOLAKLSILENRGVHNASLALSANI 2635
QY 2717 GRVRELIAQARGAASKVKVPMKFNKNGRSGVQLRTPRDLADLAAYTALKFYLQG--PEPEPG 2774
Db 2636 GRVRKLLAQARSAASKVKVSMKFNKNGRSGVRLRPPRDLADLAAYTALKFHIQSPVPAPEPG 2695
QY 2775 QGTEDRFVMYMGSRQATGDYMGVSLRDKKVHWYQLGEAGPAVLSDIDEDIGEQAFAVSLD 2834
Db 2696 XNTGDHFVLYMGSRQATGDYMGVSLRNQKVHWYRLKAGPTLSDIDENIGEQAFAVSID 2755
QY 2835 RTLQFGHMSVTVERQMIQETKGDIVAPGAEGLLNLRPDDDFVYVGGYPSFTTTPPLLRFP 2894
Db 2756 RTLQFGHMSVTVEKQMVHEIKGDIVAPGSEGLLNLRHPDDDFVYVGGYPSNFTTPEPLRFP 2815
QY 2895 GYRGCIEMDTLNEEVVSLYNPERTFQDLDTAVDRPCARSKSTGDPWLTGSLYDGTGFARI 2954
Db 2816 GYLGCIEMETLNEEVVSLYNFEQTFMLDTAVDKPCARSKATGDPWLTGSLYDGSGFARI 2875
QY 2955 SFDSQISTTKRFEQELRLVSYSGVLFELKQSQFCLAVQEGSLVLLYDFGAGLKKAVPL 3014
Db 2876 SFEKQFSNTKRFQDELRLVSYNGIIFELKQESQFCLAVQEGILVLFYDFGSLKKADPL 2935
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Db 2936 QPPQALTAASKAIQVFLLAGNRKRLVVRVERATVSVDDQNMLEWADAYYLGVPPEQLP 2995
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Db 2996 LSLRQLFPSSGSGVRCIKIGIKALGYVDLKRNLTTGISFGCTADLLVGRMTTFHGHGFLP 3055
QY 3135 LALSNVAPLTGNVYSGFGFHSQAQDSALLYRASPDGLCQVLSQGRVSLQLLRTEVKTOA 3194
Db 3056 LALPDVAPITEVVYSGFGFRGTQDNNLLYRTSPDGPYQVSLREGHVTLRFMNQEVETQR 3115
QY 3195 GFADGAPHYVAFYSNATGVWLYVDDQLQOMKPHRGPPPELQPOPEGPRLLLGGLPESGT 3254
Db 3116 VFADGAPHYVAFYSNVTGVWLYVDDQLQVKSHERTTPMLQLQPEBSRLLLGGLPVSQT 3175
QY 3255 IYNFSGCISNVFQRLGPQRVFDLQNLGNSVNVSTGCAPALQATPGLGPRGLQATARK 3314
Db 3176 FHNFGCISNVFQRLGPQRVFDLQHNMGNSVNVSVGCTPAQLIETS-----RATAQK 3228
QY 3315 ASRRSRQPARHPACMLPPHLRTTRDSYQFGSLSHLEFVGILARHNRNWPSSLMHVLP- 3373
Db 3229 VSRRSRQPSQDLACTTPWLPGTIQDAYQFGGPLPSYLOFVGISPSHRNRLHLSMLVRPHA 3288
QY 3374 SSRGLLLFTARLRPGSPSLALFLSNHGFVAQMEGLGTRLRRAQSRQSRPGRWHKVSVRWE 3433
Db 3289 ASQGLLLSTAPMSGRSPSLVFLNHHGFVAQTEGPPRLQVQSRQHSRAGQWHRVSVRWG 3348
QY 3434 KNRILLVTDGARAWSQEGPHRQHQGAEPHQPHTLFGVGLPASSHSSKLPVTVGFSGCVKR 3493
Db 3349 MQQIQLVWDGSGQTSQKALHHRVPRAPRQPVTLSVGGLPASSYSSKLPVSVGFSGCLKK 3408
QY 3494 LRLHGRPLGAPTRMAGVTPCILGPLEAGLFFPGSGGVTILDLPGATLPDVGLELEVRPLA 3553
Db 3409 LQLDKQPLRTPTQMVGVTPCVSGPLEDGLFFPGSEGVVTLLEPKAMPYVVSLEMRPLA 3468
QY 3554 VTGLIFHLGOARTPPYLOQVTEKQVLLRADDDGAGEFSTSVTRPSVLCDGQWHRLAMVKS 3613
Db 3469 AAGLIFHLGOALATPYMQLKVLTEQVLLQANDGAGEFSTWVTYPK-LCDGRWHRVAVIMG 3527

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Qy	2835	RTLQFGHMSVTVVERQMIQETKGTAVAPGAEGLLNLNRDDDFVYVGGYPSFTPTPLLRFP	2894
Db	2756	RTLQFGHMSVTVVEKQMVHEIKGDTVAPGSEGLLNLHPDDDFVYVGGYPSNFTTPEPLRFP	2815
Qy	2895	GYRGCIEMDTLNEEVVSLYNFERTFQDLTAVDRPCARSKSTGDPWLTDGSLDGTGFARI	2954
Db	2816	GYLGCIEMETLNEEVVSLYNFEQTFMLDTAVDKPCARSKATGDPWLTDGSLDGSGFARI	2875
Qy	2955	SPDSQISTTKRFEQELRLVSYSGVLFFFLKQSQFCLAVQEGSLVLLYDFGAGLKKAAPVL	3014
Db	2876	SFEKQFSNTKRFQDELRLVSYNGIIFFLKQESQFCLAVQEGTLVLFYDFGSLKKADPL	2935
Qy	3015	QPPPLTASAKAIQVFLGGRKRVLRVERATVYSVEQDNDELEADAYILGVSPPDQLP	3074
Db	2936	QPPQALTAASKAIQVFLLAGNRKRVLRVERATVFSVDQDNMLEMADAYILGVPPEQLP	2995
Qy	3075	PSLRWLFPPTGGSVRGCVKGIKALGKYVDLKLRLNTTGVSAAGCTADLLVGRAMTFHGHGFLR	3134
Db	2996	LSLRQLFPPSGSVRGCVKGIKALGKYVDLKLRLNTTGISFGCTADLLVGRMTTFHGHGFLP	3055
Qy	3135	LALSNVAPLTGNVYSGFGFHSAQDSALLYRASPDGLCQVSLQQGRVSLQLLRTTEVKTQA	3194
Db	3056	LALPDVAPITEVVYSGFGFRGTQDNLLYYRTSPDGPYQVSLREGHVTLRFVWQVEVETQR	3115
Qy	3195	GFADGAPHYVAFYSNATGVWLYYDDQLQCMQKPHRGPPPELOPOEGPPRLILGGLPESGT	3254
Db	3116	VFADGAPHYVAFYSNVTGVWLYYDDQLQLVKSHERTTPTMLQLQPEEPSRLILGGLPVSQT	3175
Qy	3255	IYNFSGCISNVFVORLLGPORVFDLQONLGSVNVSTGCAPALQAQTPGLGPRGLQATARK	3314
Db	3176	FHNFSGCISNVFVORLRGPORVFDLHQNMGSVNVSVGCTPAQLIETS-----RATAQK	3288
Qy	3315	ASRRSRQPARHPACMLPPHLRTTRDSYQFGGSLSSHLEFVVGILARHRNWPSLSMHVLP-	3373
Db	3229	VSRSRQPSQDLACTTTPWLPGTIQDAYQFGGPLPSYLQFVGISPSHRNRLHLSMLVRPHA	3288
Qy	3374	SSRGLLFTARLRPGSPSLALFLSNGHFVAQMEGLGTRLRAQSRQSRPGRWHKVSVRWE	3433
Db	3289	ASQGLLLSTAPMSGRSPSLVFLNHHGHFVAQTEGPGPRLOVQSRQHSRAGQWHVSVRWG	3348
Qy	3434	KNRILLVTDGARAWSQEGPHRQHQGAHPHPTLFGGLPASSHSSKLPVTTVGFSGCVKR	3493
Db	3349	MQQIQLVVDGSQTWSQKALHHRVPRAEPRQPYTLISVGGLPASSYSKLPVSVGSGCLKX	3408
Qy	3494	LRLHGRPLCAPTRMAGVTPCILGLEAGLFFPGSGGVITLDPGATLPDVGLELEVRPLA	3553
Db	3409	LQLDKQPLRTPTQMVGVTPCVSGPLEDGLFFPGSEGVVTLLELPKAKMPYVLSLEEMRPLA	3468
Qy	3554	VTGLIFHLGQARTPPYLQLOVTEKQVLLRADDDGAGEFSTSVTRPSVLCDGQWHRILAVMKS	3613
Db	3469	AAGLIFHLGQALATPYMQLVTEQVLLQANDGAGEFSTWVTYPK-LCDGRWHRVAVIMG	3527
Qy	3614	GNVLRLEVDAQSNHTVGPLLAAAAGAPALYLGLGLPEPMAVQPPPAYCGCMRRILAVNRS	3673
Db	3528	RDTLRLEVDTSNHTTGRLPESLAGSPALLHLGSLPKSSTARPELPAYRGCLRLKLLINGA	3587
Qy	3674	PVAMTRSVEVHGAVGASGCPA	3694
Db	3588	PVNVTASVOIQGAVGMRGCP	3608

RESULT 11
US-10-037-182-36
; Sequence 36, Application US/10037182
; Publication No. US2003004899A1
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Doi, Masayuki
; APPLICANT: Thyboll, Jill
; TITLE OF INVENTION: Recombinant Laminin 10

FILE REFERENCE: 99-274-F
CURRENT APPLICATION NUMBER: US/10/037,182
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/257,449
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/279,282
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 36
LENGTH: 2743
TYPE: PRT
ORGANISM: Homo sapiens
US-10-037-182-36

Query Match 75.2%; Score 15120; DB 14; Length 2743;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2743; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKRLCAGSALCVRGPRGPAPLLVLGLALLGAARAREEAGGFSLHPPYFNLAEGARIAA 60
DB 1 MAKRLCAGSALCVRGPRGPAPLLVLGLALLGAARAREEAGGFSLHPPYFNLAEGARIAA 60

QY 61 SATCGEEAPARGSPRPTELDYCKLVGGPVAGGDPNQTIRGOYCDICTAANSNKAHPASNA 120
DB 61 SATCGEEAPARGSPRPTELDYCKLVGGPVAGGDPNQTIRGOYCDICTAANSNKAHPASNA 120

QY 121 IDGTERWWQSPPLSRGLEYNENVTLDLGOVHVAYVLIKPAANSRPRDLWTLERSMDFGR 180
DB 121 IDGTERWWQSPPLSRGLEYNENVTLDLGOVHVAYVLIKPAANSRPRDLWTLERSMDFGR 180

QY 181 TYQPWQFFASSKRDCLERFGPQILERTDAAICTEYSRIVPLENGEIVVSLVNGRPG 240
DB 181 TYQPWQFFASSKRDCLERFGPQILERTDAAICTEYSRIVPLENGEIVVSLVNGRPG 240

QY 241 AMNFSYSPILLREFTKATNVLRLFLRTNTLLGLHMGKALRDPVTTRYYYSIKDISIGGRC 300
DB 241 AMNFSYSPILLREFTKATNVLRLFLRTNTLLGLHMGKALRDPVTTRYYYSIKDISIGGRC 300

QY 301 VCHGHADACDAKDPDPRFLOCTCOHNTCGGTCDCRCPCGFNQPKPATANSANECQSCN 360
DB 301 VCHGHADACDAKDPDPRFLOCTCOHNTCGGTCDCRCPCGFNQPKPATANSANECQSCN 360

QY 361 CYGHATDCYDPEVDRRRASQSLDGTQGGVCIDCQHHTAGVNCERCLPGFYRSPNHPL 420
DB 361 CYGHATDCYDPEVDRRRASQSLDGTQGGVCIDCQHHTAGVNCERCLPGFYRSPNHPL 420

QY 421 DSPHVCRRNCESDFTDGTCEDLTGRCYCRPNFSGRCDVCAEGFTGFPSCYPTPSSND 480
DB 421 DSPHVCRRNCESDFTDGTCEDLTGRCYCRPNFSGRCDVCAEGFTGFPSCYPTPSSND 480

QY 481 TREQVLPAGIIVNCDCSAAGTQGNACRKPVRGRCCLKPNFQTHCELCAFGYGPQCQ 540
DB 481 TREQVLPAGIIVNCDCSAAGTQGNACRKPVRGRCCLKPNFQTHCELCAFGYGPQCQ 540

QY 541 CQCSSPGVADDDCDPDTGQCRCRVGFEGATCDRCAPGYFHFPLCQLCGSPAGTLPBGCD 600
DB 541 CQCSSPGVADDDCDPDTGQCRCRVGFEGATCDRCAPGYFHFPLCQLCGSPAGTLPBGCD 600

QY 601 EAGRCLCOPEFAGPHCDRCRPGYHGFPCNCACTCDPRGALDQLCGAGGICRCRPGYTGT 660
DB 601 EAGRCLCOPEFAGPHCDRCRPGYHGFPCNCACTCDPRGALDQLCGAGGICRCRPGYTGT 660

QY 661 CQECSPGFHGFPPSCVPHCSAEGSLHAACDPRSGQSCSRPRVTGLRCDTCVPGAYNFPYC 720
DB 661 CQECSPGFHGFPPSCVPHCSAEGSLHAACDPRSGQSCSRPRVTGLRCDTCVPGAYNFPYC 720

QY 721 EAGSCHPAGLAPVDPALPEAQVPCMCRAHVEGPSDCRCKPGFWGLSPSNPEGCTRCSCDL 780
DB 721 EAGSCHPAGLAPVDPALPEAQVPCMCRAHVEGPSDCRCKPGFWGLSPSNPEGCTRCSCDL 780

QY 781 RGTLLGVAECQPGTGQCFCKPHVCGQACASCKDFFGLDQADYFGFGRSCRCDIGGALQS 840
DB 781 RGTLLGVAECQPGTGQCFCKPHVCGQACASCKDFFGLDQADYFGFGRSCRCDIGGALQS 840

DB 781 RGTLLGVAECQPGTGQCFCKPHVCGQACASCKDFFGLDQADYFGFGRSCRCDIGGALQS 840
QY 841 CEPRTGVCRCRPNTGPTCSEPARDHVLPDLHLHLRLLELEEAATPEGHAVRFGFNPLEFEN 900
DB 841 CEPRTGVCRCRPNTGPTCSEPARDHVLPDLHLHLRLLELEEAATPEGHAVRFGFNPLEFEN 900

QY 901 FSWRGYAQMAYQPRIVARLNLTSPLFVFRVYVNRGAMSVSGVSVREGRSAACANC 960
DB 901 FSWRGYAQMAYQPRIVARLNLTSPLFVFRVYVNRGAMSVSGVSVREGRSAACANC 960

QY 961 TAQSQPVAFPPSTEPAFITVPORGFGEPEFVLPNGTALRVEAEGVLLDYVWLLPSAYVEA 1020
DB 961 TAQSQPVAFPPSTEPAFITVPORGFGEPEFVLPNGTALRVEAEGVLLDYVWLLPSAYVEA 1020

QY 1021 ALLQLRVTEACTVPSAQSGDNCLLYTHLPDGFPSAAGLEALCRQDNLSPRCPTEQL 1080
DB 1021 ALLQLRVTEACTVPSAQSGDNCLLYTHLPDGFPSAAGLEALCRQDNLSPRCPTEQL 1080

QY 1081 SPSHPPLITCTGSDVDVQLQVAVPOPGRYALVVEYANEDARQEVGVAVHTPQRAPOQGLL 1140
DB 1081 SPSHPPLITCTGSDVDVQLQVAVPOPGRYALVVEYANEDARQEVGVAVHTPQRAPOQGLL 1140

QY 1141 SLHPCLYSTLCRGPTARDTQDHLAVFHLDSASVRLTAEOARFPLHGVTLVPIEFSPEFV 1200
DB 1141 SLHPCLYSTLCRGPTARDTQDHLAVFHLDSASVRLTAEOARFPLHGVTLVPIEFSPEFV 1200

QY 1201 EPRVSCISSHGAFGPNNSAACLPSPRFPKPPQPIILRDCQVILPPLPGLPLTHAQDLTPATSP 1260
DB 1201 EPRVSCISSHGAFGPNNSAACLPSPRFPKPPQPIILRDCQVILPPLPGLPLTHAQDLTPATSP 1260

QY 1261 AGPRPRPPTAVDPPDAEPTLLREPOATVVFTTHVPTLGRYAFLLHGYQPAHPTFPVEVLIN 1320
DB 1261 AGPRPRPPTAVDPPDAEPTLLREPOATVVFTTHVPTLGRYAFLLHGYQPAHPTFPVEVLIN 1320

QY 1321 AGRVWQGHANASFCPHGYGCRITLVVCEGQALLDVTHSELTVTVRVEGRWLWLDYVVLVVP 1380
DB 1321 AGRVWQGHANASFCPHGYGCRITLVVCEGQALLDVTHSELTVTVRVEGRWLWLDYVVLVVP 1380

QY 1381 ENVYSFGLYLRREEPLDKSYDFISHCAAQGYHISPSSSSLFCORNAASLSLFYNNGARPCGC 1440
DB 1381 ENVYSFGLYLRREEPLDKSYDFISHCAAQGYHISPSSSSLFCORNAASLSLFYNNGARPCGC 1440

QY 1441 HEVGATGPTCEPFGGQCPCHAHVIGRDCSRCATGYWGFPCNCRPCDCGARLCELTGQCIC 1500
DB 1441 HEVGATGPTCEPFGGQCPCHAHVIGRDCSRCATGYWGFPCNCRPCDCGARLCELTGQCIC 1500

QY 1501 PPRTIPDCLLCQPTQTFGCHPLVGCCECNCSGPGIQELTDTCTDSGQCKCRNVTGRR 1560
DB 1501 PPRTIPDCLLCQPTQTFGCHPLVGCCECNCSGPGIQELTDTCTDSGQCKCRNVTGRR 1560

QY 1561 CDTCSGPHGYPRCPCDCHEAGTAPGVCDPLTGQCYCKENVQKCDQCSLGTFSLDAA 1620
DB 1561 CDTCSGPHGYPRCPCDCHEAGTAPGVCDPLTGQCYCKENVQKCDQCSLGTFSLDAA 1620

QY 1621 NPKGCTRCFCFGATERCRSSSYTRQEFVDMEGWVLLSTDRQVVPHERQPGTEMLRADLRH 1680
DB 1621 NPKGCTRCFCFGATERCRSSSYTRQEFVDMEGWVLLSTDRQVVPHERQPGTEMLRADLRH 1680

QY 1681 VPEAVPEAFPELYWQAPPSYLGDRVSSYGGTLRYELHSETQRGDVFPVPMESRDPVVLQGN 1740
DB 1681 VPEAVPEAFPELYWQAPPSYLGDRVSSYGGTLRYELHSETQRGDVFPVPMESRDPVVLQGN 1740

QY 1741 QMSITFLEPAYTPGHVHRGQLQVVEGNFRHTTETRTNVSREELMMVLASLEQLIRALFS 1800
DB 1741 QMSITFLEPAYTPGHVHRGQLQVVEGNFRHTTETRTNVSREELMMVLASLEQLIRALFS 1800

QY 1801 QISSAVSLRRVALEVASPAGQALASNVLELCLCPASVYRGDSQCECAPGFYRDYKGLFLGR 1860
DB 1801 QISSAVSLRRVALEVASPAGQALASNVLELCLCPASVYRGDSQCECAPGFYRDYKGLFLGR 1860

QY 1861 CVPCQCHGHSRCLPLPGSGVVCDCQHNTEGAHRCERCOAGFMSSRDDPSAPCVSCPCPLSVP 1920
DB 1861 CVPCQCHGHSRCLPLPGSGVVCDCQHNTEGAHRCERCOAGFMSSRDDPSAPCVSCPCPLSVP 1920

QY 1921 SNNFAEGCVLRGGRTQCLCKPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSNGDPNLL 1980
Db 1921 SNNFAEGCVLRGGRTQCLCKPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSNGDPNLL 1980
QY 1981 FSDCDPLTGACRGCLRHHTTGPCEICAPGFYGNALLPGNCTRCDCCTPCGTEACDPHSGHC 2040
Db 1981 FSDCDPLTGACRGCLRHHTTGPCEICAPGFYGNALLPGNCTRCDCCTPCGTEACDPHSGHC 2040
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Db 2041 LCKAGVTGRRCDRCQEGHFGNGCGGCRPCACGPAAGSECHPQSGQCHCRPPTMGPOCR 2100
QY 2101 ECAPGYWGLPEQGCRRRCQEGHFGNGCGGCRPCACGPAAGSECHPQSGQCHCRPPTMGPOCR 2160
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QY 2161 SIHCEVCDHCVLLDDLERAGALLPAIHEQLRGINASSMAWARLHRLNASIADLQSQLR 2220
Db 2161 SIHCEVCDHCVLLDDLERAGALLPAIHEQLRGINASSMAWARLHRLNASIADLQSQLR 2220
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QY 2641 DTATRVQSQLQAMQENVERWQGEGLRGQDLGQAVLDAGHSVSTLEKTLPLQALLAKLSIL 2700
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Db 2701 ENRGVHNASLALSASIGRVRELIAQARGAASKVKVPMKFNGRS 2743

APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Zhiwei
TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and
TITLE OF INVENTION: Secreted Polypeptides
FILE REFERENCE: 805A
CURRENT APPLICATION NUMBER: US/10/112,944
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: US 09/515,126
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: US 09/519,705
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 09/552,929
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: US 09/577,408
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 924
SOFTWARE: pt FL_genes Version 5.0
SEQ ID NO 801
LENGTH: 1677
TYPE: PRT
ORGANISM: Homo sapiens
US-10-112-944-801

Query Match 42.3%; Score 8504.5; DB 12; Length 1677;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1642; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
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Db 1 CDRCEGHGFGNGCGCRPCACGPAAGSECHPQSGQCHCRPPTMGPOCRECAPGYWGLP 60
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Db 61 EQCRRRCQCGGCRDPHTGRCNCPPLSGERCDCSCQHQVVPVGGPVGSHICEVCDHC 120
QY 2171 VVLLDDLERAGALLPAIHEQLRGINASSMAWARLHRLNASIADLQSQLRSPGPRHETA 2230
Db 121 VVLLDDLERAGALLPAIHEQLRGINASSMAWARLHRLNASIADLQSQLRSPGPRHETA 180
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Db 181 QQLEVEQOSTSLGQDARRLGQAVGTRDQASQLLAGTEATLGHAKTLAAIRAVIDRTLS 240
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QY 2351 RVQEQSLSSLWENQALATQTRDRLAQHEAGLMDLREALNRAVDATREAEELNSRNQERLE 2410
Db 301 RVQEQSLSSLWENQALATQTRDRLAQHEAGLMDLREALNRAVDATREAEELNSRNQERLE 360
QY 2411 EALQKQELSRDNATLQATLHAARDTLASVFRLLHSLDQAKEELERLAASLDGARTPLLQ 2470
Db 361 EALQKQELSRDNATLQATLHAARDTLASVFRLLHSLDQAKEELERLAASLDGARTPLLQ 420
QY 2471 RMQTFSPAGSKLRLVEAAEAHAQQQLGQALNLSIIILDVNQDRLTQRAIEASNAYSRILO 2530
Db 421 RMQTFSPAGSKLRLVEAAEAHAQQQLGQALNLSIIILDVNQDRLTQRAIEASNAYSRILO 480
QY 2531 AVQAAEDAAGQALQADHTWATVVRQGLVDRAQQLLANSTALEEAMLEQOQRLGLVMAAL 2590
Db 481 AVQAAEDAAGQALQADHTWATVVRQGLVDRAQQLLANSTALEEAMLEQOQRLGLVMAAL 540
QY 2591 QGARTQLRDVRAKDDQLEAHIQAAQAMLANDTDETSKKIAHAKAVAAEAQDTATRVQSQL 2650

RESULT 12
US-10-112-944-801
Sequence 801, Application US/10112944
Publication No. US20040048249A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Yang, Yonghong
APPLICANT: Weng, Gezhi
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Xue, Aidong J.
APPLICANT: Wang, Jian-Rui
APPLICANT: Wehrman, Tom
APPLICANT: Ghosh, Malabika
APPLICANT: wang, Dunrui

Db 541 QGARTQLRDVRAKKDQLEAHIAQAQAMLAAMDTEDESKIAHAKAVAAEAQDTATRVQSQL 600

Qy 2651 QAMQENVERWQGYEGLRGQDLGQAVLDAGHSVSTLEKTLPLLAKLSILENRGVHNASL 2710

Db 601 QAMQENVERWQGYEGLRGQDLGQAVLDAGHSVSTLEKTLPLLAKLSILENRGVHNASL 660

Qy 2711 ALSASIGRVRELIQAARGAASKVKVPMKFNRSVQLRTRDRLADLAAYTALKFYLGPE 2770

Db 661 ALSASIGRVRELIQAARGAASKVKVPMKFNRSVQLRTRDRLADLAAYTALKFYLGPE 720

Qy 2771 PEPGQGTEDRFVYMNGSRQATGDYMGVSLRDKKVVHVVYQLGEAGPAVLSDIDEGEFAA 2830

Db 721 PEPGQGTEDRFVYMNGSRQATGDYMGVSLRDKKVVHVVYQLGEAGPAVLSDIDEGEFAA 780

Qy 2831 VSLDRTLQFGHMSVTVRQMIQETKGDIVAPGAEGLLNLRDDDFVYVGGYPTFTPPPL 2890

Db 781 VSLDRTLQFGHMSVTVRQMIQETKGDIVAPGAEGLLNLRDDDFVYVGGYPTFTPPPL 840

Qy 2891 LRFPYRGCIEMDTLNEEVVSLYNFERTFQDLTAVDRPCARSKSTGDPWLTGSDYLDGTG 2950

Db 841 LRFPYRGCIEMDTLNEEVVSLYNFERTFQDLTAVDRPCARSKSTGDPWLTGSDYLDGTG 900

Qy 2951 FARISFDSQISTTKRFEQELRLVSVSGVLFLLKQSQFLCLAVQEGSLVLLYDFGAGLKK 3010

Db 901 FARISFDSQISTTKRFEQELRLVSVSGVLFLLKQSQFLCLAVQEGSLVLLYDFGAGLKK 960

Qy 3011 AVPLQPPPLTSASKAIQVFLGGSRKRVLRVERATVYSVEQDNDLELADAYILGGVPP 3070

Db 961 AVPLQPPPLTSASKAIQVFLGGSRKRVLRVERATVYSVEQDNDLELADAYILGGVPP 1020

Qy 3071 DQLPPSLRWLFPITGSGVRGCVKGIKALGKYVDLKRNTTGVSAAGTADLLVGRAMTFHGH 3130

Db 1021 DQLPPSLRWLFPITGSGVRGCVKGIKALGKYVDLKRNTTGVSAAGTADLLVGRAMTFHGH 1080

Qy 3131 GFRLRLALSNVAPLTGNVYSGFGFHSQDSALLYRASPDGLCQVSLQGRVSLQLLRTEV 3190

Db 1081 GFRLRLALSNVAPLTGNVYSGFGFHSQDSALLYRASPDGLCQVSLQGRVSLQLLRTEV 1140

Qy 3191 KTOAGFADGAPHYVAFYSNATGVWLVYDDQLQOMKPHRGPPPELOPOEGPRLLLGLLP 3250

Db 1141 KTOAGFADGAPHYVAFYSNATGVWLVYDDQLQOMKPHRGPPPELOPOEGPRLLLGLLP 1200

Qy 3251 ESGTIYNFSGCISNVFVQRLLPQVFDLQONLGSVNVSTGCAPALQATPGLGPRGLQA 3310

Db 1201 ESGTIYNFSGCISNVFVQRLLPQVFDLQONLGSVNVSTGCAPALQATPGLGPRGLQA 1260

Qy 3311 TARKASRRSRQARHPACMLPPHLRTRDSYQFGGSLSHLEFVGILARHNWPSLSMHV 3370

Db 1261 TARKASRRSRQARHPACMLPPHLRTRDSYQFGGSLSHLEFVGILARHNWPSLSMHV 1320

Qy 3371 LPRSSRGLLLFTARLRPGSPSLALFLSNHGFVAQMEGLGTRLRASQRQRSRPRGWHKVS 3430

Db 1321 LPRSSRGLLLFTARLRPGSPSLALFLSNHGFVAQMEGLGTRLRASQRQRSRPRGWHKVS 1380

Qy 3431 RWEKNRILLVTDGARAWSQEGPHRQHGAEHPQPHTLFVGGLPASSHSSKLPVTVGFSGC 3490

Db 1381 RWEKNRILLVTDGARAWSQEGPHRQHGAEHPQPHTLFVGGLPASSHSSKLPVTVGFSGC 1440

Qy 3491 VKRLRLHGRPLGAPTRMAGVTPCILGLEAGLFFPGSGGVITLDLPGATLPDVGLELEVR 3550

Db 1441 VKRLRLHGRPLGAPTRMAGVTPCILGLEAGLFFPGSGGVITLDLPGATLPDVGLELEVR 1500

Qy 3551 PLAVTGLIFHLGQARTPPYLQVTEKQVLLRADDGAGERSTSVTRPSVLCGQWHRLAV 3610

Db 1501 PLAVTGLIFHLGQARTPPYLQVTEKQVLLRADDGAGERSTSVTRPSVLCGQWHRLAV 1560

Qy 3611 MKSGNVLRLEVDQAQSNHTVGPLLAAACAPAPLYLGLLPPMAVQPPWPAYCGCMRRLAV 3670

Db 1561 MKSGNVLRLEVDQAQSNHTVGPLLAAACAPAPLYLGLLPPMAVQPPWPAYCGCMRRLAV 1620

Qy 3671 NRS-PVAMTRSRVEHGAAGASGCPA 3694

Db 1621 NRSPPVAMTRSRVEHGAAGASGCPD 1645

RESULT 13

US-10-037-417-8

; Sequence 8, Application US/10037417

; Publication No. US20040052806A1

; GENERAL INFORMATION:

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Alsobrook II, John P

; APPLICANT: Tchernev, Velizar T

; APPLICANT: Liu, Xiaohong

; APPLICANT: Spytek, Kimberly A

; APPLICANT: Patturajan, Meera

; APPLICANT: Grosse, William M

; APPLICANT: Lepley, Denise M

; APPLICANT: Burgess, Catherine E

; APPLICANT: Vernet, Corine A.M.

; APPLICANT: Li, Li

; APPLICANT: Gorman, Linda

; APPLICANT: Edinger, Shlomit R

; APPLICANT: Sciore, Paul

; APPLICANT: Ellerman, Karen

; APPLICANT: Malyankar, Uriel M

; APPLICANT: Rothenberg, Mark

; APPLICANT: Stone, David J

; APPLICANT: Boldog, Ferenc L

; APPLICANT: Guo, Xiaojia

; APPLICANT: Shenoy, Suresh G

; APPLICANT: Anderson, David W

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Taupier Jr, Raymond J

; APPLICANT: Miller, Charles E

; APPLICANT: Eisen, Andrew J

; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-235

; CURRENT APPLICATION NUMBER: US/10/037,417

; CURRENT FILING DATE: 2002-09-20

; PRIOR APPLICATION NUMBER: 60/260,018

; PRIOR FILING DATE: 2001-01-05

; PRIOR APPLICATION NUMBER: 60/260,360

; PRIOR FILING DATE: 2001-01-08

; PRIOR APPLICATION NUMBER: 60/272,411

; PRIOR FILING DATE: 2001-02-28

; PRIOR APPLICATION NUMBER: 60/272,817

; PRIOR FILING DATE: 2001-03-02

; PRIOR APPLICATION NUMBER: 60/291,186

; PRIOR FILING DATE: 2001-05-15

; PRIOR APPLICATION NUMBER: 60/303,231

; PRIOR FILING DATE: 2001-07-05

; PRIOR APPLICATION NUMBER: 60/305,060

; PRIOR FILING DATE: 2001-07-12

; PRIOR APPLICATION NUMBER: 60/318,405

; PRIOR FILING DATE: 2001-09-10

; PRIOR APPLICATION NUMBER: 60/318,700

; PRIOR FILING DATE: 2001-09-12

; NUMBER OF SEQ ID NOS: 227

; SOFTWARE: Patent in Ver. 2.1

; SEQ ID NO 8

; LENGTH: 1640

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-037-417-8

Query Match 42.2%; Score 8499.5; DB 12; Length 1640;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 1640; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

Qy 2051 CDRCEGHFGFNGCGGCRPCACGPAABGSECHPQSGQCHCRPCTMGPGQRCRCAPGYWGLP 2110

Db 1 CDRCEGHFGFNGCGGCRPCACGPAABGSECHPQSGQCHCRPCTMGPGQRCRCAPGYWGLP 60

Qy 2111 EQGCRRCQCPGGRCDPHTGRCNCPPLSGRCDTCSQQHQVVPFGVGHSHCEVCDHC 2170

Db 61 EQCRRCCQPGRCDPHTGRCNCPPGLSGBRCDTCSQQHQVVPVPGSPVGHSHCEVCDHC 120

QY 2171 VVLLDDDLERAGALLPAIHEQLRGINASSMAWARLHRLNASIADLQSLRSPGLPRHETA 2230

Db 121 VVLLDDDLERAGALLPAIHEQLRGINASSMAWARLHRLNASIADLQSLRSPGLPRHETA 180

QY 2231 QOLEVLEQQSTSLGQDARRLLGGQAVGTRDQASQLLAGTEATLGHAKTLLAAIRAVDRTLS 2290

Db 181 QOLEVLEQQSTSLGQDARRLLGGQAVGTRDQASQLLAGTEATLGHAKTLLAAIRAVDRTLS 240

QY 2291 ELMSQTHLGLANASPSGEQLLRTLAEVERLLWEMWARDLGAPOAAAEAEELAAQORLLA 2350

Db 241 ELMSQTHLGLANASPSGEQLLRTLAEVERLLWEMWARDLGAPOAAAEAEELAAQORLLA 300

QY 2351 RVQEQLSSLWEENQALATQTRDRLAQHEAGLMDLREALNRAVDATREAOELNSRNOERLE 2410

Db 301 RVQEQLSSLWEENQALATQTRDRLAQHEAGLMDLREALNRAVDATREAOELNSRNOERLE 360

QY 2411 EALQRKQELSRDNATLQATLHAARDTLASVFRLLHSLDOAKEELERLARASLDGARTPLIQ 2470

Db 361 EALQRKQELSRDNATLQATLHAARDTLASVFRLLHSLDOAKEELERLARASLDGARTPLIQ 420

QY 2471 RMQTFSPAGSKRLRVEAAEAAHAQOLGOLALNLSSIIDVNQDRLTQRAIEASNAYSRILO 2530

Db 421 RMQTFSPAGSKRLRVEAAEAAHAQOLGOLALNLSSIIDVNQDRLTQRAIEASNAYSRILO 480

QY 2531 AVQAAEDAAGQALQQADHTWATVVRQGLVDRAQQLLANSTALEEAMLOEQORLGLVWAAL 2590

Db 481 AVQAAEDAAGQALQQADHTWATVVRQGLVDRAQQLLANSTALEEAMLOEQORLGLVWAAL 540

QY 2591 QGARTQLRDVRAKDDQLEAHTQAAQAMLAMDTDETSKKIAHAKAVAAEAQDTATRVQSOL 2650

Db 541 QGARTQLRDVRAKDDQLEAHTQAAQAMLAMDTDETSKKIAHAKAVAAEAQDTATRVQSOL 600

QY 2651 QAMQENVERWQGYEGLRGQDLGOAVLDAGHSVSTLEKTLPLLAKLSILENRGVHNASL 2710

Db 601 QAMQENVERWQGYEGLRGQDLGOAVLDAGHSVSTLEKTLPLLAKLSILENRGVHNASL 660

QY 2711 ALSASIGRVRELIAQARGAASKVKVPMKFNRSVQVLRTPRDLADLAAYTALKFYLGQPE 2770

Db 661 ALSASIGRVRELIAQARGAASKVKVPMKFNRSVQVLRTPRDLADLAAYTALKFYLGQPE 720

QY 2771 PEPGQGTEDRFVMYMGSRQATGYMGVSLRDKKVHVYVQJGEAGPAVLSIDEDICEQFAA 2830

Db 721 PEPGQGTEDRFVMYMGSRQATGYMGVSLRDKKVHVYVQJGEAGPAVLSIDEDICEQFAA 780

QY 2831 VSLDRTLQFGHMSVTVVERQMIQETKGDTVAPGAEGLLNLRPDDFVYVGGYPSFTPPPL 2890

Db 781 VSLDRTLQFGHMSVTVVERQMIQETKGDTVAPGAEGLLNLRPDDFVYVGGYPSFTPPPL 840

QY 2891 LRFPGYRGCIEMDTLNEEVVSLNPFERTFQDPTAVDRPCARSKSTGDPWLTDGSLYLDGTG 2950

Db 841 LRFPGYRGCIEMDTLNEEVVSLNPFERTFQDPTAVDRPCARSKSTGDPWLTDGSLYLDGTG 900

QY 2951 FARISFDSQISTTKRFEQELRLVSYSGVLFFFLKQSQOFLCLAVQEGSLVLLYDFGAGLKK 3010

Db 901 FARISFDSQISTTKRFEQELRLVSYSGVLFFFLKQSQOFLCLAVQEGSLVLLYDFGAGLKK 960

QY 3011 AVPLQPPPLTSASKAIQVFLGGSRKRVLRVERATVYSVEQDNDLELADAYYLGGVPP 3070

Db 961 AVPLQPPPLTSASKAIQVFLGGSRKRVLRVERATVYSVEQDNDLELADAYYLGGVPP 1020

QY 3071 DQLPPSLRWLPPTGGSVRGCVKGIKALGKYVDLKLRLNTTGVSACTADLLVGRAMTFHG 3130

Db 1021 DQLPPSLRWLPPTGGSVRGCVKGIKALGKYVDLKLRLNTTGVSACTADLLVGRAMTFHG 1080

QY 3131 GFLRLALSNVAPLTGNVYSGFGFHSADQSALLYRASPDGLCQVSLQQGRVSLQLLRTEV 3190

Db 1081 GFLRLALSNVAPLTGNVYSGFGFHSADQSALLYRASPDGLCQVSLQQGRVSLQLLRTEV 1140

QY 3191 KTOAGFADGAPHYVAFYSNATGVWLYVDDQLQOMKPHRGPPPELOQPQEGPRLLLGGLP 3250

Db 1141 KTOAGFADGAPHYVAFYSNATGVWLYVDDQLQOMKPHRGPPPELOQPQEGPRLLLGGLP 1200

QY 3251 ESGTIYNFSGCISNVFVQRLGLGPQRFVFDLQONLGSVNVSTGCPALQAQTPGLGPRGLQA 3310

Db 1201 ESGTIYNFSGCISNVFVQRLGLGPQRFVFDLQONLGSVNVSTGCPALQAQTPGLGPRGLQA 1260

QY 3311 TARKASRRSRQPARHPACMLPPHLRTRTDSYQFGGSLSSHLEFVGILARHNWPSLSMHV 3370

Db 1261 TARKASRRSRQPARHPACMLPPHLRTRTDSYQFGGSLSSHLEFVGILARHNWPSLSMHV 1320

QY 3371 LPRSSRGLLLFTARLRPGSPSLALFLSNHGFVAQMEGLGTRLRAQSRQRSPGRWHKVSU 3430

Db 1321 LPRSSRGLLLFTARLRPGSPSLALFLSNHGFVAQMEGLGTRLRAQSRQRSPGRWHKVSU 1380

QY 3431 RWEKNRILLVTDGARAWSOEGPHRQHQAEPHQPHTLFGGGLPASSHSSKLPVTVGFSGC 3490

Db 1381 RWEKNRILLVTDGARAWSOEGPHRQHQAEPHQPHTLFGGGLPASSHSSKLPVTVGFSGC 1440

QY 3491 VKRLRHLGRPLGAPTRMAGVTTPCILGPLEAGLFFPGSGGVITLDLPGATLPDVGLELEVR 3550

Db 1441 VKRLRHLGRPLGAPTRMAGVTTPCILGPLEAGLFFPGSGGVITLDLPGATLPDVGLELEVR 1500

QY 3551 PLAVTGLIFHLGQARTPPVLIQVTEKQVLLRADDDGAGEFSTSVTRPSVLCDGOWHRLAV 3610

Db 1501 PLAVTGLIFHLGQARTPPVLIQVTEKQVLLRADDDGAGEFSTSVTRPSVLCDGOWHRLAV 1555

QY 3611 MKSGNVLRLEVDAQSNHTVGPBLLAAAAGAPAPLYLGGIPEPMAVQPPPAYCGCMRRLAV 3670

Db 1556 MKSGNVLRLEVDAQSNHTVGPBLLAAAAGAPAPLYLGGIPEPMAVQPPPAYCGCMRRLAV 1615

QY 3671 NRSPVAMTRSVFVHGAAGVSGCPAA 3695

Db 1616 NRSPVAMTRSVFVHGAAGVSGCPAA 1640

RESULT 14

US-10-037-417-49

; Sequence 49, Application US/10037417

; Publication No. US20040052806A1

; GENERAL INFORMATION:

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Alsobrook II, John P

; APPLICANT: Tchernev, Velizar T

; APPLICANT: Liu, Xiaohong

; APPLICANT: Spytek, Kimberly A

; APPLICANT: Patturajan, Meera

; APPLICANT: Grosse, William M

; APPLICANT: Lepley, Denise M

; APPLICANT: Burgess, Catherine E

; APPLICANT: Vernet, Corine A.M.

; APPLICANT: Li, Li

; APPLICANT: Gorman, Linda

; APPLICANT: Edinger, Shlomit R

; APPLICANT: Sciore, Paul

; APPLICANT: Ellerman, Karen

; APPLICANT: Malyankar, Uriel M

; APPLICANT: Rothenberg, Mark

; APPLICANT: Stone, David J

; APPLICANT: Boldog, Ferenc L

; APPLICANT: Guo, Xiaojia

; APPLICANT: Shenoy, Suresh G

; APPLICANT: Anderson, David W

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Taupier Jr, Raymond J

; APPLICANT: Miller, Charles E

; APPLICANT: Eisen, Andrew J

; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-235

; CURRENT APPLICATION NUMBER: US/10/037,417

; CURRENT FILING DATE: 2002-09-20

; PRIOR APPLICATION NUMBER: 60/260,018

; PRIOR FILING DATE: 2001-01-05

; PRIOR APPLICATION NUMBER: 60/260,360

; PRIOR FILING DATE: 2001-01-08

; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 49
; LENGTH: 1634
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-037-417-49

Query Match 38.8%; Score 7804.5; DB 12; Length 1634;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1533; Conservative 1; Mismatches 5; Indels 13; Gaps 1;

QY 2157 PVGHSIHC-----EVCDCVLLDDLLERAGALLPAIHEQLRGINASSMAWA 2203
Db 83 PAASSIRCLFAGLWATASTVKVCDHCVVLLDDLLERAGALLPAIHEQLRGINASSMAWA 142

QY 2204 RLHRLNASIADLQSLRSLPLGPRHETAQQLVLEQQSTSLGQDARRLGGQAVGTRDQASQ 2263
Db 143 RLHRLNASIADLQSLRSLPLGPRHETAQQLVLEQQSTSLGQDARRLGGQAVGTRDQASQ 202

QY 2264 LLAGTEATLGHAKTLLAAIRAVDRTLSELMSQTGHLGLANASAPSGEQLRLTAEVERLL 2323
Db 203 LLAGTEATLGHAKTLLAAIRAVDRTLSELMSQTGHLGLANASAPSGEQLRLTAEVERLL 262

QY 2324 WEMRARDLGAPOAAAEAEALAAQRLARVQEQSLSSWEENQALATQTRDRLAQHEAGLMD 2383
Db 263 WEMRARDLGAPOAAAEAEALAAQRLARVQEQSLSSWEENQALATQTRDRLAQHEAGLMD 322

QY 2384 LREALNRAVDATREAOELNSRNOERLEALQKQELSRDNATLQATLHAARDTLASVRL 2443
Db 323 LREALNRAVDATREAOELNSRNOERLEALQKQELSRDNATLQATLHAARDTLASVRL 382

QY 2444 LHSLDQAKEELERLAASLDGARTPLLQRMQTFSPAGSKRLRVEAAEAHAQQLGQALNLS 2503
Db 383 LHSLDQAKEELERLAASLDGARTPLLQRMQTFSPAGSKRLRVEAAEAHAQQLGQALNLS 442

QY 2504 SIILDVNQDRLTORAIEASNAYSRILOAVQAAEDAAQALQADHTWATVVRQGLVDRAQ 2563
Db 443 SIILDVNQDRLTORAIEASNAYSRILOAVQAAEDAAQALQADHTWATVVRQGLVDRAQ 502

QY 2564 QLLANSTALEEAMLOEQORLGLVWAAALQAGARTQLRDVRAKQDQLEAHIQAAQAMLMDTD 2623
Db 503 QLLANSTALEEAMLOEQORLGLVWAAALQAGARTQLRDVRAKQDQLEAHIQAAQAMLMDTD 562

QY 2624 ETSKKIAHAKAVAAEAQDTATRVQSQLOAQENVERWQOQYEGRLRGQDLGQAVLDAGHSV 2683
Db 563 ETSKKIAHAKAVAAEAQDTATRVQSQLOAQENVERWQOQYEGRLRGQDLGQAVLDAGHSV 622

QY 2684 STLEKTLPLQAKLSILENRGVHNASIALSASIGRVRELIAQARGAASKVKVPMKFNRS 2743
Db 623 STLEKTLPLQAKLSILENRGVHNASIALSASIGRVRELIAQARGAASKVKVPMKFNRS 682

QY 2744 GVQLRTPRDLADLAAYTALKFYLOQPEPEPGQGTEDRFVMYMGSRQATGDMVSVLRDKK 2803
Db 683 GVQLRTPRDLADLAAYTALKFYLOQPEPEPGQGTEDRFVMYMGSRQATGDMVSVLRDKK 742

QY 2804 VHWYQOLGEAGPAVLSDIDEDIGEQAFAVSLDRTLQFGHMSVTVERQMIQETKGDITVAPGA 2863
Db 743 VHWYQOLGEAGPAVLSDIDEDIGEQAFAVSLDRTLQFGHMSVTVERQMIQETKGDITVAPGA 802

QY 2864 EGLNLRPDDFVYVGGYPSTFTPPPLRFPYRGCIEMDTLNEBVVSLYNFERTFQDLD 2923
Db 803 EGLNLRPDDFVYVGGYPSTFTPPPLRFPYRGCIEMDTLNEBVVSLYNFERTFQDLD 862

QY 2924 AVDRPCARSKSTGDPWLTDGSLDGTGFARISFDSQISTTKRFEQELRLVSYSGVLFELK 2983
Db 863 AVDRPCARSKSTGDPWLTDGSLDGTGFARISFDSQISTTKRFEQELRLVSYSGVLFELK 922

QY 2984 QOSQFLCLAVQEGSLVLLYDFGAGLKKAVPLQPPPLTSASKAIQVFLLLGGSRKRVLRV 3043
Db 923 QOSQFLCLAVQEGSLVLLYDFGAGLKKAVPLQPPPLTSASKAIQVFLLLGGSRKRVLRV 982

QY 3044 ERATVYSVEQNDLELADAYLGGVPPDQPPSLRWLFPPTGGSVRGCVKGIKALGKYVDL 3103
Db 983 ERATVYSVEQNDLELADAYLGGVPPDQPPSLRWLFPPTGGSVRGCVKGIKALGKYVDL 1042

QY 3104 KRLNTTGVSAAGTADLLVGRAMTFHGHGFLRLALSNAVPLTGNVYSGFGFHSQAQDSALLY 3163
Db 1043 KRLNTTGVSAAGTADLLVGRAMTFHGHGFLRLALSNAVPLTGNVYSGFGFHSQAQDSALLY 1102

QY 3164 YRASPDGLCQVSLQOGRVSLQLLRTVEVKTQAGFADGAPHYVAFYSNATGVWLYVDDQLQ 3223
Db 1103 YRASPDGLCQVSLQOGRVSLQLLRTVEVKTQAGFADGAPHYVAFYSNATGVWLYVDDQLQ 1162

QY 3224 MKPHRGPPPELQPEGPRLLLGGLPESGTIYNFSGCISNVFQRLLPQRFVDFDLOQNL 3283
Db 1163 MKPHRGPPPELQPEGPRLLLGGLPESGTIYNFSGCISNVFQRLLPQRFVDFDLOQNL 1222

QY 3284 GSVNVSTGCAPALQAQTPGLGPRGLQATARKASRRSRQPARHPACMLPPLHRTTRDSYQF 3343
Db 1223 GSVNVSTGCAPALQAQTPGLGPRGLQATARKASRRSRQPARHPACMLPPLHRTTRDSYQF 1282

QY 3344 GGSLSHLEFVGILARHNPWPSLSMHVLPSSRGLLLFTARLRPGSPSLALFLSNGHFVA 3403
Db 1283 GGSLSHLEFVGILARHNPWPSLSMHVLPSSRGLLLFTARLRPGSPSLALFLSNGHFVA 1342

QY 3404 QMEGLGTRLRQSRQSRPGRWHKVSVRWEKNRILLVTDGARAWSQEGPHRQHQAEPHQ 3463
Db 1343 QMEGLGTRLRQSRQSRPGRWHKVSVRWEKNRILLVTDGARAWSQEGPHRQHQAEPHQ 1402

QY 3464 PHTLVGGLPASSHSSKLPVTGVFGSGVKRLRLHGRPLGAPTRMAGVTPCILGLEAGLF 3523
Db 1403 PHTLVGGLPASSHSSKLPVTGVFGSGVKRLRLHGRPLGAPTRMAGVTPCILGLEAGLF 1462

QY 3524 FPGSGGVITLDPGATLPDVGLELEVRPLAVTGLIFHLGQARTPPYLQVTEKQVLLRA 3583
Db 1463 FPGSGGVITLDPGATLPDVGLELEVRPLAVTGLIFHLGQARTPPYLQVTEKQVLLRA 1522

QY 3584 DDGAGEFSTVTRPSVLCGQWHRLAVMKSNGVLRLEVDASQNHVTGVLAAAAGAPAPL 3643
Db 1523 DDGAGEFSTVTRPSVLCGQWHRLAVMKSNGVLRLEVDASQNHVTGVLAAAAGAPAPL 1582

QY 3644 YLGGLPEPMAVQPPPAYCGCMRRLAVNRSFVAMTRSVVEHGAAGVSGCPAA 3695
Db 1583 YLGGLPEPMAVQPPPAYCGCMRRLAVNRSFVAMTRSVVEHGAAGVSGCPAA 1634

RESULT 15
US-10-037-417-48
; Sequence 48, Application US/10037417
; Publication No. US20040052806A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vernet, Corine A.M.

```

; APPLICANT: Li, Li
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; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/10/037,417
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 3712
; TYPE: PRN
; ORGANISM: Drosophila melanogaster
US-10-037-417-48

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Query Match      25.3%; Score 5097; DB 12; Length 3712;
Best Local Similarity 31.7%; Pred. No. 2.4e-288;
Matches 1248; Conservative 609; Mismatches 1541; Indels 540; Gaps 122;

QY 45 LHPYFNLAEGARIAASATCGEEAPARGSPRTEDLYCKLVGGPVAGGDPN-QTIRGQYC 103
Db 24 LTPYFNLAATGRKIYATATCG---PDTDGP---ELYCKLVGANTHHDHIDYSVIQGVQC 76

QY 104 DICTAANSNKAPASNAIDGTERWWSPPPLSRGLEYNVNVNLTDLGQVFFHVAYLIKFN 163
Db 77 DYCDPTVPERNHPENAIIDGTEAWWSPPPLSRGMKFNENLTINFEQEFHVAYLIFIRMG 136

QY 164 SPRPDLWVLSRMDFGRTYQWPQFFASSKRDCLERFGPQTLERITRDDAAICTEYSRIV 223
Db 137 SPRPGLWTLKSTDYGKTWTWPQHFSPTADCEYFGKDYKPKITRDDDDVICTEYSKIV 196

QY 224 PLENGEIVVSLVNGRPGAMNFSYSPLLREFTKATNVRLRFLRTNTLLGLHLMGKALRDPTV 283
Db 197 PLENGEIVPMLNRPSSSTNYFNSTVQLQEWTRATNVRIALLRTKNLLGLHLSVARQDPTV 256

QY 284 TRYYYSIKDISIGRCVCHGHADACADKPTDPR-LQCTCQHTCGGTCCRCPPGFNQ 342
Db 257 TRRYFYSIKDISIGRCMCHGHADTCVDPKSPVRIACRCQHTCGIQCNECCPGFEQ 316

QY 343 QPWKPATANSANECQSCNCGHATDCYDPEVDRRRASOSLDGTYYGGGVCIQCQHTAG 402
Db 317 KWRQNTNARPNCEPCNCHGSHNECKYDEVNRLKGLSLDIHGYDGGVGCQCHQNTVG 376

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QY 403 VNCERCLFGRSPNHPDLDSHVCRRCNCESDFTDGTCTEDLTGRCYCRNFSGERCDVCA 462
Db 377 INCNKCRPKYRPRKGMWNETDVCSPQCQDYFFSTGHCEETGNCERAAAFQPPSCDSCA 436
QY 463 EGFTGFPSCYPTPSSSNDTRQVLPAGQIVNCDASAAGTQGNACRKPDRVGRCLCKPNFQ 522
Db 437 YGYGYGPNC-----RE-----CECNLNGTNGYHCEAESG-QQCPCKINFA 475
QY 523 GTHCELCAFGFYG-PGQCPQCSCSSPGVADDDRDPTGQCRVGVGEGATCDRCAPGYFHF 581
Db 476 GAYCKQCAEGYGFPECKACBCKNIGSITNDNCNVTGECCKLTNFGGDNCEBCKKHGFNY 535
QY 582 PLCQLCCGSPAGTLPPEGCD-SAGRCLCQPEFAGFAGHCDRCRPGYHGFNCACTCDPRGAL 640
Db 536 PTCSYCDNDNQTESEICNKQSGQICREGFGGPRCDQCLPGFYNYPDCKPCNCSSTGSS 595
QY 641 DQLCGAGGLCRCPGYGTGTACQECSPGFHGFPPSCVPHCHCSAEGSLHAACDPRSGQCSCR 700
Db 596 AITCDNTGKCNLNNFAGKQCTLTCTAGYYSYPCDLPCHCDSHSGQVSCN-SDGQCLCQP 654
QY 701 RVTGLRCDTCTVPGAYNFPYCEAGSCHPAGLAPVDPALPEAQP-----CMCRAHVEG 756
Db 655 NFDGRQDSCKEGFYNFPSCEDCNDPAGV--IDKFAAGCGSVPVGELCKCKERVITGRICN 712
QY 757 RCXPGFWGLSPSPNEGCTRCSCDLRGLTGLGVAECPQGTGQCFCCKPHVCGQACASCKDGF 816
Db 713 ECKPLYWNLNISNTEGCEICDCTDGTISALDCTCTSKSGQCPCKPHTQGRRCQECRDGT 772
QY 817 GLDQADYFGCRSCRCRDIGGALGQSCBPRTVGCRCPNTQGTCTCEPARDHYLPDLHLRL 876
Db 773 DLDSASLFGCKDCSDVGGSWQSCDKISGQCKCHPRITGLACTQELTHFFPTLHQFY 832
QY 877 ELEBAATPEGHAVRFGFNPLEFENFWSRGYQAQMAPVQPRIVARLNLTPDLFWLVFVYN 936
Db 833 EYEDGSLPSGTQVRYDYDEAAPPFGSSKGYVVFNAIONDVNRNVNFKSSLYRIVLYVN 892
QY 937 RGMSVSGRVSVREEGRSAAACANCTAQSQPVAFPPSTPEAFITV--PQGFGEFFVLPNG 994
Db 893 PNAENVTATISVTSNDPLE-----VDQHVKVLLOPTSEPQFVTVAGPLGVKPSAIVLDPG 947
QY 995 TWALRVEA-EGVLLDYVLLPSAYYEAALLQLRVTEACTYRPSAQSGDNCNLLYTHLPLD 1053
Db 948 RYVFTTKANKVMLDYFVLLPAAAYEAGILTRHISNPCEL-----GNMELCRHYKYASVE 1002
QY 1054 GFPSAAGLEALCRQDNLSPRCPTQELSPSHPLIT-----CTGSDVDVQLQVAVPQP 1106
Db 1003 VESPA--TPFVIGENSKPTNPVETYTDEHLQIVSHVGDIPVLSGSQNELHYIVDVPRS 1060
QY 1107 GRYALVVEY-ANEDARQEVGAVHTPQRAPOQGLLSLHPCLYSTLCRGRTARDTQDHLAVF 1165
Db 1061 GRYIFVIDYISDRNFPDSYINLKLKNDPDSSETSVLLYPCLYSTICR-TSVNEDGMEKSF 1119
QY 1166 HLDSE--ASVRLTA---EQARFELHGVTLVPIBEFSPFVEPRVSCISSHGAFGPNAAAC 1220
Db 1120 YINKEDLOPVIISADIEDGSRFPIISVTAIPVDQWSIDYINPSPVCI-----HDQOC 1172
QY 1221 LPSRFPKPPQPIILRDCQVPLPPGLPLTHAQDLTPATSPAGPRPPPTAVDPDAEPTLL 1280
Db 1173 ATPKFRSVP-----DSKKIEFE-----TDHEDRIATNKP-----PYASLDERVKLVHL 1215
QY 1281 -REPOATVFTTHV-----PTLGRYAFLLHGYQPAHPTFPPEVLINAGR-VWQGHANASFC 1334
Db 1216 DSQNEATIVIESKVDATKPNL--FVILVKYQPSHPKYQVYITLTAGKNQYDGKFDIQHC 1273
QY 1335 PHGYGCRTLVVCQGAALLDVTHSELTVTVRVEPGRWLWLDVYLVVENVVSYFGYLREEPL 1394
Db 1274 PSSSGCRGVIRPAGESGFEI-DDEFKFTITTDRSQSVWLDYLVVPLKQYNDLLVEETF 1332
QY 1395 DKSDFISHCAAQGYHISPSSSSLFCRNAASLSLFYNNGARPCGCHVEGATGPTCEPFG 1454
Db 1333 DQTKEFIQNGHDFHITHNASD-FCKKSVFSLTADYNSGALPCNCDYAGSTSFECHEPFG 1391

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QY 1455 GQCPCHAVIGRDCSRCATGYWFPNCRPCDC-GARLCDELTCGICPPRTIPDCLLQ 1513
Db 1392 GQCKQKPNVIERTCGRCSRXYGFPDCKPKCKPCNSAMCEPTTGECMCPNVIDLCEKCA 1451
QY 1514 POTFGHPLVGBECNCSGPGIGELTDPTCDTDSGQCKRPNVTGRRCDTCSGFGHYPR 1573
Db 1452 PNTYGFHQVIGCEECACNPMGIAN-GNSQCDLFGNGTCECRQNIIEGRACDVCSNGYFNFPH 1510
QY 1574 CRPCDCHAGTAPGVCDPLTGCYCKENVQGPCKDCQSLGTFSLDAANPKGCTRCFCFGA 1633
Db 1511 CEQCSCHKPGTELEVCDKIDGACFCCKNVVGRDCDQVGTYNLQESNPDGCTTCFCFGK 1570
QY 1634 TERCSSSYTRQEFVDMEGWVLLSTDRQVVPHERQ-----PGTEM-----LRAD-- 1677
Db 1571 TSRC-DSAYLRVNVVSLKHVSITTFEF---HEESIKFDMWPVPADEILLNETTLKADFT 1626
QY 1678 LRHVPRAVPEAFPELYWQAPPSYL---GDRVSSYGGTFLRYELHSETQRGDVFPVPMESRPD 1734
Db 1627 LREVNDERPAYFGVL-----DYLLNQNNHISAYGGDLAYTLHFTSGFGDKYI---VAPD 1677
QY 1735 VVLQGNQMSITFLEPAYPTPGHVHRGQLQLVNEGFRHTETRTNTVSRREELMMVLASLEQLQ 1794
Db 1678 VILFSEHNALVHTSYEQPSRNEBPFTNRVNIVESNQ-TISGKPVSRADFMVLRDLKVIF 1736
QY 1795 IRALFSQISSAVSLRRVALEVASPAGQGA-----LASNVELCLCPASVYRGDSQCECAPGF 1849
Db 1737 IRANYWEQTLVTHLSDVYTLADEDADGTGEYQFLA--VERCSCPFGYSGHSCDECAPGY 1794
QY 1850 YRDVXGLFLGRVCPQCCHGSHDRCLPGSGVVCVDCOHNTEGAHCERCOAGFM-SSRDDPSA 1908
Db 1795 YRDPSPGYGGYCIPECNCGHSETCDATGICSKCHGTEGDHCHERCVCVSGYGNATNGTPG 1854
QY 1909 PCVSCPCPLSVPSNNFAEGCVL--RGGRTQCLCKPGYAGASCERCAPGFFGNPLVLGSSC 1966
Db 1855 DCMICACPLPFDNNFATSCISESGDQIHCECKPGYTGPCECANGFYGEPEISIGVC 1914
QY 1967 QPCDCSGNDPNLLFSDCDPLTGACRGCLRHTTGPRCEICAPGYGNALLPFGNCTRCDC 2026
Db 1915 KPCCSGNINPEDQGS-CDRTTGECLRLNNTFGAACNLCPAGFYGDAIKLKNQCSCDCD 1973
QY 2027 PCGTEACDPHSGHCLCKAGVTGRRCDRCQEGHFGNGCGGCRPCACGPAAGSECHPQSG 2086
Db 1974 DLGTQCTDPFVGVCTCHENVIGDRCDRCCKPDHYGFSVGVCRACDCAASNSTQCDDPHG 2033
QY 2087 QCHCRPGTMGPQCRECAPGYWGLPEQGCRRCCQCPGG-----RCDPHGTGRNCPPGLSGER 2141
Db 2034 HCAKSGVTGRQCDRCVADHWKYEKDGCTPCNQCNGYSRGFGCNPNTGKCQCLPGVIGDR 2093
QY 2142 CDTCSQQRQVVPVGGPVGHSIHCEVCDHCVVLLDDLERAGALLPAIHEQLRGINASSVA 2201
Db 2094 CDACPNRWVLIKOE-----CQECNNCHALLDVTDRMYQIDSV---LEDFNSVTLA 2143
QY 2202 WARLHRLN-----ASIALQSLRSPPLGPRHET-AQOL 2233
Db 2144 FFTSQKLYYDQLADELPKVKLLDPNSVDLSPSKCANSELESDAKSYAKQVNOQLANAF 2203
QY 2234 EVLEQQSTSLGQDARLGGQAVGTRDQASQLLAGTEATLGHAKTL-LAAIRAVDRTLSEL 2292
Db 2204 DIRERSSTTLG-NITVAYDEAVKSADQAKEATASVEAL---SKNLEAAASTKIDAALBOA 2259
QY 2293 MSQTGHLGLANASAPSGEQLLRTLAEVERLLWEMRARDLGAPQAAAEAEIAAQAORLARV 2352
Db 2260 QHILGQINGTSIELTPNEQVL-----EKARKLYE-EVNTLVLPKAKQNSLNALKNDIGEF 2314
QY 2353 QEQLSLWEEENOALATQTRDRRLAQHEAGLMDLREALN-RAVDATREAQELNSRNQERLEE 2411
Db 2315 SDHLEDLFNWSEASQAKSAD-----VERRNVANQKAFD-----NSKFDTVSEQ 2357
QY 2412 ALQKQKQEL-SRDNATLQATLHAARDTLASVFRLLHSLDQAKEELERLAASLDGARTPLIQ 2470
Db 2358 KLQAEKNIKADAGNFLNGDL-----TLNQINQKLDNLRDALNELNSFNKNVD-EELPVRE 2411
QY 2471 RMQTFSPAGSKLRLVEABABAHAAQQLQGLALNLSSIIILDVNQDRLTQRAEASNAYSRIQ 2530

Db 2412 DQKHEAD-----LTDQAEQKAAELAIAQDLAAQYTDWTAS--AEPAIKATAYSGIVE 2464
QY 2531 AVQAAEDAAGQALQOQADHTWATVVRQGLVDRAQQILLANSTALEEAMLEQQ----- 2581
Db 2465 AVEAAQKLSQDAISAAGN--ATDKTDGIEERAHLAHDITGSDLLQARQSLQKVQDDLEPR 2522
QY 2582 -----RLGLVWAAALQARTQLRDVRAKQDQLEAHIOA-----AQAMLMDTDDETSKK 2628
Db 2523 LNASAGKVQKISAVNNATEHQKLDINKLIDQLPAESQDRMWNKSNANASDALEILKNVLE 2582
QY 2629 IAHAKAVAAEAQ-DTATRVQSLOQAMQENVERWQGVYEGRLGQDLGOAVLDACHSVSTLE 2687
Db 2583 ILEPVSVQTPKELEKAGINRDLDTNKDVSOANKQLDDVEG-----SVSKLN 2630
QY 2688 KTLPOLLAKLSILENRGVHNASLASASIGRVRELIAQARGAASKVKVPMKFNERSGVOL 2747
Db 2631 E-----LAEDIEEQOHRVGSQSRQLGQEIENLKAQVEAARQLANSIKVGVNFKPSTILEL 2685
QY 2748 RTPRDLADLAAYTALKFYLOQPEPEPGQGTEDRFVVMYG-----SRQATGDMGVSLRDKK 2803
Db 2686 KTEPKTKLLATRTNLSTYFRITTEP-----SGFLYLGNDNKTAOKNDFVAIVEVNGY 2738
QY 2804 VHWYQIGEAGPAVLSIDEDI--GEQFAAVSLDRTLOFGHMSVTVERQMIQETKGDTV-- 2859
Db 2739 PILTIDLGN-GPERITSDKYVADGRWYQAV-VDR--MGNPAKLTIREEL---PNGDVVEH 2791
QY 2860 -----APGAEGLLNLRPDDFVFYVGGYP--STFTPPPLLRFPGYRGCIEMDTLNEEVVSL 2912
Db 2792 SKSGYLEGSQNLHVHDKNSRLF-VGGYPGISDFNAPDPLTTNSFSGDIEDLKIGDESGL 2850
QY 2913 YNF-----ERTFQDLTAVDRPCARSKSTGDPWLTGSLYDGTGFARISFDSQIS 2961
Db 2851 WNFVYGGDDNDQAGARERDVLEKKKPVTLGLRFKNGVYQNLNATSLNKSRSSTQPSFKADK 2910
QY 2962 TTKRFEQELRLVSYSGVLFFLKQSQSFLCLAVQEGSLVLLYDFGAGLKKAVLPQPPPLT 3021
Db 2911 TS-----NGLFFYGRDKHYSIEMIDGAFENISLGE----- 2944
QY 3022 SASKAIQVFLIGGSRKRV-----LVRVER-----ATVYSVEQDNDLELA 3060
Db 2945 ---GGVQ-----SGSQDRYNDNQHWKVQAEARENNGLLKVDDIVISRTNAFLADLELPLK 2997
QY 3061 DAYLGGVPPDQPLPSLRWLFTGGSVRGCVKGIKALGYVDLKLRLNT-TGVSAGCTADL 3119
Db 2998 RRLYFGG-HPRRLNTSIS-LQP---NFDGCIDNVVINGQVVDLTYVTGGGVEEGCSAKF 3052
QY 3120 LVGRAMTFHGHGFLRLALSNAVPLTGNVYSGFGFHSADQSALLYYRASPD--GLCQVSLQ 3177
Db 3053 STVVSYPAPHEYGFLR--MNNVSS-DNNLHVVLHFXTQPNGVLFYAAHNDQSSSTIGLSLQ 3109
QY 3178 QGRVSLQLLRT-EVKTQAGFADGAPHYVAFYSNATGVWLVDLQLOQMKHRGPPPELQ 3236
Db 3110 DGLLKLNSMGSQLVIDDRILNDGEDHVVTVQHTQBELRLTVDDVDNKRGLG-----SP 3161
QY 3237 QP---EGPRLLLGLLPES-----GTIYNFSGCISNVFVQRLLLGPQRFVDL---QQ 3281
Db 3162 QPLILEGSD-IPFAGLPDNTVTPRNALASLAYFVGCISDVTN-----EELINFANSAEK 3215
QY 3282 NLGSVNVSTGCAPALQAOPTGLGP----- 3305
Db 3216 KNGNIN---GCPPHVLAYEPSLVPSYPSGDNVESPSWNADTLPLPKDDIESTLPPPTT 3272
QY 3306 -----RGLQATARKASRRSRQPAR-----HPA 3327
Db 3273 TTTTTTTTTTTTTTTTTTTPSPDIVIDEKEIEAKTPQKILTRPPAKNLNLPDSER 3332
QY 3328 CMLPPH-----LRTTRDSYQFGGSLSSHLEFVGLIARHNWPSLSMHLPRSSRGLLLFTA 3383
Db 3333 CKLPEQNFEDVDFTTEAGYFVGLREQRLQINSLPVKVRHHDIGISFTRFPNGLLIY-A 3391
QY 3384 RLRPGSPSLALFLSNHGFVAQMEGLGTRLRAQ--SRQSRPRGRHWKVSVRWEKNRILLVT 3441

Db 3392 GSKQRDDFIAYVLLDGRVTYER-VGAQLQAKITTEAELNDGTWHTVEVVRTQKVSLLI 3450

QY 3442 DGARAWSQEGPHRQHQAEHPQP-----HTLFVGGI-----PASSHSSKLPVTVGF 3487

Db 3451 D-----KLEQPGSVDLNAERSAPVLAVELPIYLGGVNKFLESEVKNLTDFKTEVPY---F 3502

QY 3488 SGCVXRRLRHGRPLGAPTRMAGVTPCIIIGLEAGLFFPGSGGVTILDLPGATLPDVGLEL 3547

Db 3503 NGCLKNIKFDAMDLETPPEEFGVVP-SEQVERGLFFNNQKAFVKI-----FDHFDVGTGM 3557

QY 3548 EV---RPLAVTGLIFHLGQARTPPYLQVTEKQVLLRADDGAGEESTSVTRPS--VLC 3601

Db 3558 KISFDFRPRDPNGLFVSVHGKNSYAILL-VDNTLYFTVKTDLKNIVSTNYKLPNNESFC 3616

QY 3602 DGQWHRRLAVMKSQNVLRLEVD-AQSNHTVGPLLAAAAAGAPAPLYLGGLPEPMAVQWP-- 3658

Db 3617 DGKTRNVQAIKSKFVINIAVDFISSNPGVGNESVITRTNRPLFLGG---HVAFQRAPGI 3673

QY 3659 ---PAYCGCMRRRLAVNRSVPVAMTRSVEVHGAVGASGCP 3693

Db 3674 KTKSKFGKCISKVEVNOQRMNITPNMVV-GDIWQGYCP 3710

Search completed: May 18, 2004, 15:41:36
Job time : 133.004 secs

OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:28 ; Search time 100.235 Seconds
(without alignment)

Title: US-10-037-182-2
Perfect score: 20118
Sequence: 1 MAKRLCAGSALCVGRGPA.....AMTRSEVHGAVGASGCPAA 3695

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 25:

- 1: sp_archaea:
- 2: sp_bacteria:
- 3: sp_fungi:
- 4: sp_human:
- 5: sp_invertebrate:
- 6: sp_mammal:
- 7: sp_mhc:
- 8: sp_organelle:
- 9: sp_phage:
- 10: sp_plant:
- 11: sp_rodent:
- 12: sp_virus:
- 13: sp_vertebrate:
- 14: sp_unclassified:
- 15: sp_rvirus:
- 16: sp_bacteriap:
- 17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20118	100.0	3695	4 Q8TDF8	Q8tdf8 homo sapien
2	5093	25.3	3712	5 Q9VRW0	Q9vrv0 drosophila
3	4964	24.7	3704	5 P91904	P91904 caenorhabdi
4	4010	19.9	1486	4 O14637	O14637 homo sapien
5	3360.5	16.7	670	4 Q9BTT3	Q9btt3 homo sapien
6	2715.5	13.5	794	11 Q8R3Y7	Q8r3y7 mus musculu
7	2601	12.9	3102	5 Q45614	Q45614 caenorhabdi
8	2566	12.8	1806	4 Q96TG0	Q96tg0 homo sapien
9	2467.5	12.3	3375	5 Q8IP51	Q8ip51 drosophila
10	2438.5	12.1	3367	5 Q9XZC9	Q9xzc9 drosophila
11	2302	11.4	1725	6 Q867A1	Q867a1 canis fami
12	2249	11.2	1725	11 P70570	P70570 rattus norv
13	2160.5	10.7	2731	5 Q9VJT5	Q9vjt5 drosophila
14	1630.5	8.1	1792	13 O57484	O57484 gallus gall
15	1624	8.1	1799	11 Q8R0Y0	Q8r0y0 mus musculu
16	1556.5	7.7	1761	4 Q86XN2	Q86xn2 homo sapien

RESULT 1

ID	Q8TDF8	PRELIMINARY;	PRT;	3695 AA.
AC	Q8TDF8;			
DT	01-JUN-2002 (TRENBLrel. 21, Created)			
DT	01-JUN-2002 (TRENBLrel. 21, Last sequence update)			
DT	01-OCT-2003 (TRENBLrel. 25, Last annotation update)			
DE	Laminin alpha5 chain precursor.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21935381; PubMed=11821406;			
RA	Doi M., Thyboll J., Kortessmaa J., Jansson K., Iivanainen A.,			
RA	Parvardeh M., Timpi R., Hedin U., Swedenborg J., Tryggvason K.;			
RT	"Recombinant Human Laminin-10 (alpha5beta1gamma1). Production,			
RT	Purification, and Migration-Promoting Activity on Vascular Endothelial			
RT	Cells."			
RL	J. Biol. Chem. 277:12741-12748(2002)."			
DR	EMBL; AF443072; AAM12527.1; -			
DR	GO; GO:0005578; C:extracellular matrix; IEA.			
DR	GO; GO:00030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.			
DR	GO; GO:0004872; F:receptor activity; IEA.			
DR	GO; GO:0005198; F:structural molecule activity; IEA.			
DR	GO; GO:0003743; F:translation initiation factor activity; IEA.			
DR	GO; GO:0005215; F:transporter activity; IEA.			
DR	GO; GO:0006413; P:translational initiation; IEA.			
DR	GO; GO:0006810; P:transport; IEA.			
DR	InterPro; IPR008985; ConA like lec_gl.			
DR	InterPro; IPR006209; EGF like.			
DR	InterPro; IPR000034; Laminin_B.			
DR	InterPro; IPR002049; Laminin_EGF.			
DR	InterPro; IPR001791; Laminin_G.			
DR	InterPro; IPR008211; LamNT.			
DR	InterPro; IPR008212; Lam_N2.			
DR	InterPro; IPR001638; SBP_bac_3.			
DR	InterPro; IPR001950; TIF_SUII.			

ALIGNMENTS

DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00052; laminin_B; 1.
DR Pfam; PF00053; laminin_EGF; 18.
DR Pfam; PF00054; laminin_G; 2.
DR Pfam; PF00055; laminin_Nterm; 1.
DR PRINTS; PR00011; EGF_LAMININ.
DR ProDom; PD003031; Laminin_B; 1.
DR ProDom; PD002082; Lam_N2; 1.
DR SMART; SM00180; EGF_Lam; 20.
DR SMART; SM00281; LamB; 1.
DR SMART; SM00282; LamG; 5.
DR SMART; SM00136; LamNT; 1.
DR PROSITE; PS00022; EGF_1; 19.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 19.
DR PROSITE; PS50025; LAM_G_DOMAIN; 5.
DR PROSITE; PS01039; SBP_BACTERIAL_3; 1.
DR PROSITE; PS01118; SUII_1; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
KW Laminin EGF-like domain; Signal.
FT SIGNAL 1 35 POTENTIAL.
FT CHAIN 36 3695 LAMININ ALPHA5 CHAIN.
SQ SEQUENCE 3695 AA; 399642 MW; 69703B52536EFOA3 CRC64;

Query Match 100.0%; Score 20118; DB 4; Length 3695;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKRLCAGSALCVRGPRGAPLLVGLALLGAARAREBAGGFSLHPPYFNLAEGARIAA 60
Db 1 MAKRLCAGSALCVRGPRGAPLLVGLALLGAARAREBAGGFSLHPPYFNLAEGARIAA 60

QY 61 SATCGEEAPARGSPRPTELDYCKLVGGPVAGGDPNQITRGQYCDICTAANSNKAHPASNA 120
Db 61 SATCGEEAPARGSPRPTELDYCKLVGGPVAGGDPNQITRGQYCDICTAANSNKAHPASNA 120

QY 121 IDGTERWQSPPLSRGLEYNVNTLDLQGVHVAIVLIKFANSRPDLWVLEERSMDFGR 180
Db 121 IDGTERWQSPPLSRGLEYNVNTLDLQGVHVAIVLIKFANSRPDLWVLEERSMDFGR 180

QY 181 TYQPWFQFASSKRDCLERFGPQTLERITRDDAAICTTEYSRIIVPLENGEIVVSLVNGRPG 240
Db 181 TYQPWFQFASSKRDCLERFGPQTLERITRDDAAICTTEYSRIIVPLENGEIVVSLVNGRPG 240

QY 241 AMNFSYSPLLREFTKATNVRLRLRTNTLLGLHMGKALRDPVTVRRYVYSIKDISIGGRC 300
Db 241 AMNFSYSPLLREFTKATNVRLRLRTNTLLGLHMGKALRDPVTVRRYVYSIKDISIGGRC 300

QY 301 VCHGHADACDAKDPDTPFLQCTCQHTNCTGGTCDCRCPGFNQPKPATANSANECQSCN 360
Db 301 VCHGHADACDAKDPDTPFLQCTCQHTNCTGGTCDCRCPGFNQPKPATANSANECQSCN 360

QY 361 CYGHATDCYDPEVDRRRRASQSLDGTQYGGGVCIDCQHHTAGVNCERCLPGFYRSPNHPL 420
Db 361 CYGHATDCYDPEVDRRRRASQSLDGTQYGGGVCIDCQHHTAGVNCERCLPGFYRSPNHPL 420

QY 421 DSPHVCRRNCESDFTDGTCEDLTGRCYCRPNFSGRCDVCAEGFTGFPSCYPTPSSSND 480
Db 421 DSPHVCRRNCESDFTDGTCEDLTGRCYCRPNFSGRCDVCAEGFTGFPSCYPTPSSSND 480

QY 481 TREQVLPAGQIVNCDCSAAGTQGNACRKPDRVGRCLCKPNFQTHCELCAPEGFYGPGCQ 540
Db 481 TREQVLPAGQIVNCDCSAAGTQGNACRKPDRVGRCLCKPNFQTHCELCAPEGFYGPGCQ 540

QY 541 CQCSSPGVADDRCDPDTGQCRVGFEGATCDRCAPGYFHFPLCQLCGCSPAGTLPFGCD 600
Db 541 CQCSSPGVADDRCDPDTGQCRVGFEGATCDRCAPGYFHFPLCQLCGCSPAGTLPFGCD 600

QY 601 EAGRCLQPEFAGPHCHDRCPGYHGFNQCQACTCDPRGALDQLCGAGGICRCRPGYTGT 660
Db 601 EAGRCLQPEFAGPHCHDRCPGYHGFNQCQACTCDPRGALDQLCGAGGICRCRPGYTGT 660

QY 661 COECSPGFHGFSPSCVPCCHSAEGSLHAACDPRSGQSCRPRTVTLGLRCDTCVPGAYNFPYC 720
Db 661 COECSPGFHGFSPSCVPCCHSAEGSLHAACDPRSGQSCRPRTVTLGLRCDTCVPGAYNFPYC 720

QY 721 EAGSCHPAGLAPVDPALPEAQVPCMCRAHVGBSPSCDRCKPGFWGLSPSNPEGCTRCSCDL 780
Db 721 EAGSCHPAGLAPVDPALPEAQVPCMCRAHVGBSPSCDRCKPGFWGLSPSNPEGCTRCSCDL 780

QY 781 RGTLLGGVAECQPGTGQCFCKPHVCGQACASCKDGGFFGLDQADYFGCRSCRCIDIGGALQGS 840
Db 781 RGTLLGGVAECQPGTGQCFCKPHVCGQACASCKDGGFFGLDQADYFGCRSCRCIDIGGALQGS 840

QY 841 CEPRTGVCRCRNPNTQGTCTSEPARDHYLPDLHLHLRLELEAAATPEGHAVRFGFNPLEFEN 900
Db 841 CEPRTGVCRCRNPNTQGTCTSEPARDHYLPDLHLHLRLELEAAATPEGHAVRFGFNPLEFEN 900

QY 901 FSWRGYAQMAMPVQPRIVARLNLTSPLDFWLVFRYVNRGAMSVSGRVSVREGRSAACANC 960
Db 901 FSWRGYAQMAMPVQPRIVARLNLTSPLDFWLVFRYVNRGAMSVSGRVSVREGRSAACANC 960

QY 961 TAQSQPVAFPPSTPAFITVPQRFGEPPFVLPNGTWARVBAEGLLDYVWLLPSAYYEA 1020
Db 961 TAQSQPVAFPPSTPAFITVPQRFGEPPFVLPNGTWARVBAEGLLDYVWLLPSAYYEA 1020

QY 1021 ALLQLRVTEACTYRPSAQSGDNCLLYTHPLDGFPSAAGLEALCRQDNLSPRCPTEQL 1080
Db 1021 ALLQLRVTEACTYRPSAQSGDNCLLYTHPLDGFPSAAGLEALCRQDNLSPRCPTEQL 1080

QY 1081 SPSPPLITCTGSDVDVQLOQAVPOPGRYALVWEYANEDARQEVGVAVHTPQAPQOGLL 1140
Db 1081 SPSPPLITCTGSDVDVQLOQAVPOPGRYALVWEYANEDARQEVGVAVHTPQAPQOGLL 1140

QY 1141 SLHPCLYSTLCRGRTARDTQDLHAFVHLDSEASVRLTAEOARFPLHGVTLVPIEFSPEFV 1200
Db 1141 SLHPCLYSTLCRGRTARDTQDLHAFVHLDSEASVRLTAEOARFPLHGVTLVPIEFSPEFV 1200

QY 1201 EPRVSCISSHGAFGPNNSAACLPSPRFKPPQPIILRDCQVILPPLPGLPLTHAQDLTPATSP 1260
Db 1201 EPRVSCISSHGAFGPNNSAACLPSPRFKPPQPIILRDCQVILPPLPGLPLTHAQDLTPATSP 1260

QY 1261 AGPRPRPPTAVDPDAEPTLLREPOATVFTTHVPTLGRYAFLLHGYQPAHPTFPVEVLIN 1320
Db 1261 AGPRPRPPTAVDPDAEPTLLREPOATVFTTHVPTLGRYAFLLHGYQPAHPTFPVEVLIN 1320

QY 1321 AGRVWQHGHANASFCPHGYGCRTLVVCEGQALLDVTHSELTVTVRVPEGRWLWLDYVLVVP 1380
Db 1321 AGRVWQHGHANASFCPHGYGCRTLVVCEGQALLDVTHSELTVTVRVPEGRWLWLDYVLVVP 1380

QY 1381 ENVYSGYLREBPLDKSYDFISHCAAQGYHISPSSSSLFCRNAAAASLSLFYNNGARPCGC 1440
Db 1381 ENVYSGYLREBPLDKSYDFISHCAAQGYHISPSSSSLFCRNAAAASLSLFYNNGARPCGC 1440

QY 1441 HEVGATGPTCEPFGGQCPCHAHVIGRDCSRCATGYWGFNCRPCDCGARLCELTGQCIC 1500
Db 1441 HEVGATGPTCEPFGGQCPCHAHVIGRDCSRCATGYWGFNCRPCDCGARLCELTGQCIC 1500

QY 1501 PPRTIPPDCLLCQPTFGCHPLVGCCEECNCSGPGIQELTDPTCDTDSGQCKCRPNVTGRR 1560
Db 1501 PPRTIPPDCLLCQPTFGCHPLVGCCEECNCSGPGIQELTDPTCDTDSGQCKCRPNVTGRR 1560

QY 1561 CDTCSPGFHGYPRCPCDCHEAGTAPGVCDPLTGQCYCKENVQPKCDQCSLGTFSLDAA 1620
Db 1561 CDTCSPGFHGYPRCPCDCHEAGTAPGVCDPLTGQCYCKENVQPKCDQCSLGTFSLDAA 1620

QY 1621 NPKGCTRCFCFGATERCRSSSYTRQEFVDMEGWVLLSTDRQVVPHERQPGTGNLRADLRH 1680
Db 1621 NPKGCTRCFCFGATERCRSSSYTRQEFVDMEGWVLLSTDRQVVPHERQPGTGNLRADLRH 1680

QY 1681 VPEAVPEAPPPELYWQAPPSSYLGDVSSYGGTTLRYELHSETQRGDVFPVMEGRPDVVLQGN 1740
Db 1681 VPEAVPEAPPPELYWQAPPSSYLGDVSSYGGTTLRYELHSETQRGDVFPVMEGRPDVVLQGN 1740

QY 1741 QMSITFLEPAYPTPGHVHRGQLQLVEGNFRHTETRTNTVSRREELMMVLASLEQLQIRALFS 1800

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:25:32 ; Search time 100.235 Seconds
(without alignments)
10415.614 Million cell updates/sec

Title: US-10-037-182-2
Perfect score: 20118
Sequence: 1 MAKRLCAGSALCVGRGPA.....AMTRSVEVHGAVGAGCPAA 3695

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20118	100.0	3695	5	ABB81588
2	20060.5	99.7	3696	5	AAE17310
3	20030	99.6	3705	5	AAE17309
4	18254.5	90.7	3600	5	ABB09501
5	18231	90.6	3597	5	ABB09503
6	15839	78.7	3635	5	ABB81589
7	15839	78.7	3635	5	AAM50357
8	15120	75.2	2743	5	ABB81598
9	8499.5	42.2	1640	5	ABB09504
10	8255	41.0	1601	4	AAM39009
11	6916	34.4	3332	7	ADE08094
12	5093	25.3	3712	4	ABB64954
13	5002	24.9	953	5	AAM50358
14	4756.5	23.6	908	5	ABB09502
15	4058	20.2	1486	7	ADE09114
16	3141.5	15.6	3106	3	AAB19795
17	3141.5	15.6	3106	7	ADE61792
18	3133.5	15.6	3084	3	AAB19796
19	3123.5	15.5	3122	7	ADE61794
20	3103.5	15.4	3110	2	AAR71730
21	3103.5	15.4	3110	2	AAY15460
22	3103.5	15.4	3110	3	AAB19793
23	3103.5	15.4	3110	5	AAU84345
24	3101.5	15.4	3110	3	AAB19791
25	3099.5	15.4	3088	3	AAB19794

26	3097.5	15.4	3089	3	AAB19792	Aab19792 Human lam
27	3069.5	15.3	3070	5	AAO17359	Aao17359 Human lam
28	2998	14.9	3150	4	ABG20414	Abg20414 Novel hum
29	2933	14.6	3084	4	AAE11215	Aae11215 Mouse lam
30	2923	14.5	3084	2	AAW50891	Aaw50891 Mouse lam
31	2854	14.2	3075	2	AAW50892	Aaw50892 Human lam
32	2598	12.9	2901	4	ABG09763	Abg09763 Novel hum
33	2342.5	11.6	3319	4	ABB70376	Abb70376 Drosophil
34	2260.5	11.2	1693	3	AAB48459	Aab48459 Human lam
35	2260.5	11.2	1693	3	AAB48457	Aab48457 Human lam
36	2260.5	11.2	1713	3	AAB48458	Aab48458 Human lam
37	2260.5	11.2	1713	6	ABR92102	AbR92102 Human cer
38	2260.5	11.2	1713	7	ADD29904	Add29904 Human lam
39	2260.5	11.2	1724	3	AAB48456	Aab48456 Human lam
40	2249	11.2	1694	3	AAB48461	Aab48461 Rat lamin
41	2249	11.2	1725	3	AAB48460	Aab48460 Rat lamin
42	2228.5	11.1	1713	2	AAR70148	Aar70148 Deduced s
43	2155.5	10.7	3084	1	AAP94758	Aap94758 Sequence
44	2153.5	10.7	1816	7	ADC01879	Adc01879 Human lam
45	2149	10.7	1823	5	ABP63020	Abp63020 Human pol

ALIGNMENTS

RESULT 1
ABB81588
ID ABB81588 standard; protein; 3695 AA.
XX
AC ABB81588;
XX
DT 19-SEP-2002 (first entry)
XX
DE Human laminin alpha 5 protein SEQ ID NO:2.
XX

Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;
tissue repair development; laminin; healing; vascular tissue;
re-endothelialisation; vascular injury; cell attachment; cell stasis;
proliferation; migration.

XX Homo sapiens.

XX
FH Key Location/Qualifiers
FT Peptide 1..35
FT Protein 36..3695
FT /label= laminin_alpha_5

XX WO200250111-A2.

XX 27-JUN-2002.

XX 21-DEC-2001; 2001WO-US051035.

XX 21-DEC-2000; 2000US-0257449P.

XX 28-MAR-2001; 2001US-0279282P.

XX 13-NOV-2001; 2001US-00279282.

XX (BIOS-) BIOSTRATUM INC.

XX Tryggvason K, Doi M, Thyboll J;

XX WPI; 2002-557650/59.

XX N-PSDB; ABQ72906.

XX New human laminin-10 proteins, useful for accelerating the healing of
vascular tissue, improving the biocompatibility of grafts, or for
promoting re-endothelialization at the site of vascular injuries.

XX Claim 5; Page 68-79; 231pp; English.

XX The present sequence represents human laminin alpha 5. Also described is
an isolated laminin 10. Laminin 10 has vulnerary activity. Laminins are

CC useful in maintaining cell/tissue phenotype as well as promoting cell
CC growth and differentiation in tissue repair development. Specifically,
CC laminin 10 can be used for accelerating the healing injuries of vascular
CC tissue, improving the biocompatibility of grafts useful for treating such
CC injuries, for promoting re-endothelialisation at the site of vascular
CC injuries, and promote cell attachment and subsequent cell stasis,
CC proliferation, differentiation, and/or migration
XX
SQ Sequence 3695 AA;

Query Match 100.0%; Score 20118; DB 5; Length 3695;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MAKRLCAGSALCVRGPRGAPAPLLLVGLALLGAARAREEAGGGFSLHPPYFNLAEGARIAA	60
Db	1	MAKRLCAGSALCVRGPRGAPAPLLLVGLALLGAARAREEAGGGFSLHPPYFNLAEGARIAA	60
QY	61	SATCGEAPARGSPRPTELDYCKLVGGPVAGGDPNQTIRGQYCDICTAANSNKAHPASNA	120
Db	61	SATCGEAPARGSPRPTELDYCKLVGGPVAGGDPNQTIRGQYCDICTAANSNKAHPASNA	120
QY	121	IDGTERWQSPPLSRGLEYNVNTLDLQGVFHVAYVLKFNANSPRDLVWLSRMDGFR	180
Db	121	IDGTERWQSPPLSRGLEYNVNTLDLQGVFHVAYVLKFNANSPRDLVWLSRMDGFR	180
QY	181	TYQWQFPAASSKRDCLERFGQTLERITRDAAICTEYSRIVPLENGEIIWVSLVNGRPG	240
Db	181	TYQWQFPAASSKRDCLERFGQTLERITRDAAICTEYSRIVPLENGEIIWVSLVNGRPG	240
QY	241	AMNFSYSPLLREFTKATNVRLRFLRNTLLGHLGKALRDPVTVRRYYYSIKDISIGRC	300
Db	241	AMNFSYSPLLREFTKATNVRLRFLRNTLLGHLGKALRDPVTVRRYYYSIKDISIGRC	300
QY	301	VCHGHADACDAKDPDTPFRLOCTCQHNCTCGTCRCCPGFNQKPWKATANSANECQSCN	360
Db	301	VCHGHADACDAKDPDTPFRLOCTCQHNCTCGTCRCCPGFNQKPWKATANSANECQSCN	360
QY	361	CYGHATDCYYDPEVDRRRASQSLDGTYYQGGVVCIDCQHHTAGVNCERCLPGFYRSPNHPL	420
Db	361	CYGHATDCYYDPEVDRRRASQSLDGTYYQGGVVCIDCQHHTAGVNCERCLPGFYRSPNHPL	420
QY	421	DSPHVRRNCESDFTDGTCEDLTGRCYCRPNFSGERCDVCAEGTGFPPSCYPTPSSND	480
Db	421	DSPHVRRNCESDFTDGTCEDLTGRCYCRPNFSGERCDVCAEGTGFPPSCYPTPSSND	480
QY	481	TREQVLPAQIVNCDCSAAGTQGNACRKPVRGRCLCKPNFQGTGTHCLCAPGYGPGCQ	540
Db	481	TREQVLPAQIVNCDCSAAGTQGNACRKPVRGRCLCKPNFQGTGTHCLCAPGYGPGCQ	540
QY	541	CQCSFPGVADRDCTDGTGCRVGFEGATCDRCAPGYFHFPLCQLCGCSPAGTLPEGCD	600
Db	541	CQCSFPGVADRDCTDGTGCRVGFEGATCDRCAPGYFHFPLCQLCGCSPAGTLPEGCD	600
QY	601	EAGRLCQPEFAGPHCDRCRPGYHGFNPNCACTDPRGALDQLCGAGGLCRCPGYTGTA	660
Db	601	EAGRLCQPEFAGPHCDRCRPGYHGFNPNCACTDPRGALDQLCGAGGLCRCPGYTGTA	660
QY	661	CQCSFPGHGFPPSCVPCCHCSAEGSLHAACDPRSGQSCRRPRVTGLRCDTCVPGAYNFPYC	720
Db	661	CQCSFPGHGFPPSCVPCCHCSAEGSLHAACDPRSGQSCRRPRVTGLRCDTCVPGAYNFPYC	720
QY	721	EAGSHPAGLAPVDPALPEAQVPCMCRAHVEGSCDRCKPGFGLSPSNPEGCTRCSCDL	780
Db	721	EAGSHPAGLAPVDPALPEAQVPCMCRAHVEGSCDRCKPGFGLSPSNPEGCTRCSCDL	780
QY	781	RGTLLGVAECQPGTGQCFCCKPHVCGQACASCKDGGFFGLDQADYFGCRSQRCDIGGALGQS	840
Db	781	RGTLLGVAECQPGTGQCFCCKPHVCGQACASCKDGGFFGLDQADYFGCRSQRCDIGGALGQS	840
QY	841	CEPRTGVCRCRNPNTQGTCTSEPARDHYLPDLHLRLLELEEAATPEGHAVRFGFNPLEFEN	900
Db	841	CEPRTGVCRCRNPNTQGTCTSEPARDHYLPDLHLRLLELEEAATPEGHAVRFGFNPLEFEN	900

QY	901	FSWRGYAQMVPQPRIVARLNLTSBDFLFWLVFRYVNRGAMSVGRVSVREGRSAACANC	960
Db	901	FSWRGYAQMVPQPRIVARLNLTSBDFLFWLVFRYVNRGAMSVGRVSVREGRSAACANC	960
QY	961	TAQSQVAFPPSTPEAFITVPQGFGEFFVLNPGTWARVEAGVLLDYVVLPSAYYEA	1020
Db	961	TAQSQVAFPPSTPEAFITVPQGFGEFFVLNPGTWARVEAGVLLDYVVLPSAYYEA	1020
QY	1021	ALLQLRVTEACTYRPSAQSGDNCLLYTHLPLDGFPSAAGLEALCRQDNLSPRCPTEQL	1080
Db	1021	ALLQLRVTEACTYRPSAQSGDNCLLYTHLPLDGFPSAAGLEALCRQDNLSPRCPTEQL	1080
QY	1081	SPSHPLITCTGSDVDVQLQVAVPQPGRYALVVEYANEDARQEVGVAVHTPQAPQOGLL	1140
Db	1081	SPSHPLITCTGSDVDVQLQVAVPQPGRYALVVEYANEDARQEVGVAVHTPQAPQOGLL	1140
QY	1141	SLHPCLYSTLCRGRTARDTQDHLAVFHLDSASVRLTABQARFLLHGVTLVPIEESPEFV	1200
Db	1141	SLHPCLYSTLCRGRTARDTQDHLAVFHLDSASVRLTABQARFLLHGVTLVPIEESPEFV	1200
QY	1201	EPRVSCISSHGAAGPNSAACLSRFPKPPQPIIILRDCQVILPPLPGLPLTHAQDLTPATSP	1260
Db	1201	EPRVSCISSHGAAGPNSAACLSRFPKPPQPIIILRDCQVILPPLPGLPLTHAQDLTPATSP	1260
QY	1261	AGPRPRPTAVDPAEPTLLREBQATVFTTHVPTLGRYAFLLHGYQPAHPTFPVEVLIN	1320
Db	1261	AGPRPRPTAVDPAEPTLLREBQATVFTTHVPTLGRYAFLLHGYQPAHPTFPVEVLIN	1320
QY	1321	AGRVWQHANASFCPHGYGCRITLVVCEGQALLDVTHSELTVTVRVPGEGRWLWDYVLVVP	1380
Db	1321	AGRVWQHANASFCPHGYGCRITLVVCEGQALLDVTHSELTVTVRVPGEGRWLWDYVLVVP	1380
QY	1381	ENVYSGYLREEPLDKSYDFISHCAAQYHISPSSSLFCRNAAASLSLFYNGARPCGC	1440
Db	1381	ENVYSGYLREEPLDKSYDFISHCAAQYHISPSSSLFCRNAAASLSLFYNGARPCGC	1440
QY	1441	HEVGATGPTCEPFGGQCPCHAHVIGRDCSRCATGTVGFPNCRPCDCGARLDELDTGCIC	1500
Db	1441	HEVGATGPTCEPFGGQCPCHAHVIGRDCSRCATGTVGFPNCRPCDCGARLDELDTGCIC	1500
QY	1501	PPRTIPDCLLCQPTQFCHPLVGCCECNCSPGIGIQLDPTCDTDSGQCKCRPNVTGRR	1560
Db	1501	PPRTIPDCLLCQPTQFCHPLVGCCECNCSPGIGIQLDPTCDTDSGQCKCRPNVTGRR	1560
QY	1561	CDTCSFGHGYPRCPCDCHEAGTAPGVCDPLTGQYCKENVOGPKDCQCSLGTSLDAA	1620
Db	1561	CDTCSFGHGYPRCPCDCHEAGTAPGVCDPLTGQYCKENVOGPKDCQCSLGTSLDAA	1620
QY	1621	NPKGCTRCFCFGATERCRSSSYTRQEFVDMEGVLLSTDRQVPHERQPGTEMLRADLRH	1680
Db	1621	NPKGCTRCFCFGATERCRSSSYTRQEFVDMEGVLLSTDRQVPHERQPGTEMLRADLRH	1680
QY	1681	VPEAVPEAFPELYWQAPPSYLGDRVSSYGGTLRYELHSETQRGDVFPVMESERPDVVLQGN	1740
Db	1681	VPEAVPEAFPELYWQAPPSYLGDRVSSYGGTLRYELHSETQRGDVFPVMESERPDVVLQGN	1740
QY	1741	QMSITFLEPAYPTPGHVHRGQQLQOLVEGNFRHTETRTVSRRELMVLALEQLQIRALFS	1800
Db	1741	QMSITFLEPAYPTPGHVHRGQQLQOLVEGNFRHTETRTVSRRELMVLALEQLQIRALFS	1800
QY	1801	QISSAVSLRRVALEVASPACQAGALASNVLCPCASVYRSDSCQECAPGFYRDVKGLFLGR	1860
Db	1801	QISSAVSLRRVALEVASPACQAGALASNVLCPCASVYRSDSCQECAPGFYRDVKGLFLGR	1860
QY	1861	CVPCQCHGHSRCLPLGSGVGVDCQHNTEGAHCHERCQAGFMSSRDDPSAPCVSCPCPLSVP	1920
Db	1861	CVPCQCHGHSRCLPLGSGVGVDCQHNTEGAHCHERCQAGFMSSRDDPSAPCVSCPCPLSVP	1920
QY	1921	SNNFAEGCVLRGGRTQCLCKPGYAGASCERCAPFFGNPLVLGSSCQPCDCSNGDPNLL	1980
Db	1921	SNNFAEGCVLRGGRTQCLCKPGYAGASCERCAPFFGNPLVLGSSCQPCDCSNGDPNLL	1980

QY	1981	FSDCDLTGACRGCLRHTTGPRCEICAPGFYGNALLPGNCTRCDCCTPCGTEACDPHSGHC	2040
Db	1981		
QY	2041	LCKAGVTGRRCDRCQEGHGFNGCGGCRPCACGPAEGBECHPQSGQCHCRPGTGMFPQCR	2100
Db	2041		
QY	2101	ECAPGYWGLPEQGCRRQCPCGGRCDPHTGRCNCPPLSGERCDTCSQQHQVPVPGPVGH	2160
Db	2101		
QY	2161	SIHCEVCDHCVVLLDDLERAGALLPAIHEQLRGINASSMAWARLHRLNASIADLOSQLR	2220
Db	2161		
QY	2221	SPLGPRHETAQQLVLEQQSTSLGQDARRLGGQAVGTRDQASQLLAGTEATLGHAKTLLA	2280
Db	2221		
QY	2281	AIRAVDRTLSELMSTQTHGLLANASAPSGEQLLRTLAEVERLLWEMRARDLGAPQAAAEA	2340
Db	2281		
QY	2341	ELAAAQORLLARVQEQSLSSLWEEHQALATQTRDRLAQHEAGLMDLREALNRAVDATREAQE	2400
Db	2341		
QY	2401	LNSRNOERLEALQKQELS RDNATLOATLHAARDTLASVFRLLHSLDQAKEELERLAAS	2460
Db	2401		
QY	2461	LDGARTPLLQRMQTFSPAGSKLRLVEAAABAHAQQLGOLALNLSSTILDVNQDRLTQRAIE	2520
Db	2461		
QY	2521	ASNAYSRILOAVQAAEDAAGALQQADHTWATVVRQGLVDRAQQLLANSTALEAMLQEQ	2580
Db	2521		
QY	2581	QRLGLVWAALQGARTQLRDVRAKKDQLEAHIQAAQAAMLAMDTDETSKKIAHAKAVAAEAQ	2640
Db	2581		
QY	2641	DTATRVQSOLQAMOENVERWQGYEGLRGQDLGQAVLDAGHSVSTLEKTLPLLAKLSIL	2700
Db	2641		
QY	2701	ENRGVHNASLALSASIGRVRELIAQARGAASKVKVPMKFNRSRGVQLRTPRDLADLAAYT	2760
Db	2701		
QY	2761	ALKFYLOQPEPEPGQGTEDRFVVMYMGSRQATGDMYGVSLRDKKVVHWVYQLGEAGPAVLSI	2820
Db	2761		
QY	2821	DEDIGEQFAAVSLDRTLQFGHMSVTVERQMIQETKGDTPVAPGAEGLNLRPDDFVIFYVG	2880
Db	2821		
QY	2881	YPSTFTPPPLLRFPGYRGCTIEMDTLNEEVVSLYNPRTFQDLTAVDRPCARSKSTGDPWL	2940
Db	2881		
QY	2941	TDGSYLDGTGFARISFDSQISTTKRFEQELRLVSYSGVLFFLKQSQSFLCLAVQEGSLVL	3000
Db	2941		
QY	3001	LYDFGAGLKKAVPLQPPPLTSASKAIQVFLLGSRKRVLVRVERATVYSVEQDNDLELA	3060
Db	3001		
QY	3061	DAYYLGVPDPQLPPSLRWLFPPTGGSVRGCVKGIKALGKYVDLKRLNTTGVSAAGCTADLL	3120

Db	3061	DAYYLGVPDPQLPPSLRWLFPPTGGSVRGCVKGIKALGKYVDLKRLNTTGVSAAGCTADLL	3120
QY	3121	VGRAMTFHGHGFLRLALSNVAPLTGNVYSGFGFHSQAQDSALLYRASPDGLCQVSLQOQR	3180
Db	3121		
QY	3181	VSLQLLRTEVKTQAGFADGAPHYVAFYSNATGVWLIVDDQLQOMKPHRGPPPELQPOPEG	3240
Db	3181		
QY	3241	PPRLLLGGLPESGCTIYNFSGCISNVFQORLLGPORVFDLQONLGSNVNSTGCAPALQAO	3300
Db	3241		
QY	3301	PGLGPRGLQATARKASRRSRQPARHPACMLPPHLRTRTRDSYQFGGSLSSHLEFVFGILARH	3360
Db	3301		
QY	3361	RNWPSLSMHVLPSSRGLLLFTARLRPGSPSLALFLSNGHFVAQMEGLGTRLRAQSRORS	3420
Db	3361		
QY	3421	RPGRWHKVSVRWEKNRILLVTDGARAWSQEGPHRQHOGAHPQHTLFFVGGLPASSHSSK	3480
Db	3421		
QY	3481	LPVTGVFGSGCVKRLRLHGRPLGAPTRMAGVTPCILGPLEAGLFFPGSGGVITLDLPGATL	3540
Db	3481		
QY	3541	PDVGLELEVRPLAVTGLIFHLGQARTPPYLQVTEKQVLLRADDGAGEFSTSVTRPSVL	3600
Db	3541		
QY	3601	CDGQWHLAVMKSQNVLRLEVDQAQSNHTVGPLLAAAAGAPAPLYLGLPEPMAVQWPWPPA	3660
Db	3601		
QY	3661	YCGCMRRLAVNRSVPVAMTRSVEVHGAVGASGCPAA	3695
Db	3661		

RESULT 2
AAE17310
ID AAE17310 standard; protein; 3696 AA.
XX
AC AAE17310;
XX
DT 18-APR-2002 (first entry)
XX
DE Human laminin alpha protein, sbg417005LAMININ_ALPHA #2.
XX
KW Human; therapy; wound healing disorder; vaccine; cancer; infection;
KW autoimmune disorder; haematopoietic disorder; inflammation; arthritis;
KW parkinson's disease; Huntington's chorea; schizophrania; antiarrhythmic;
KW multiple sclerosis; Alzheimer's disease; analgesic; cardiant; asthma;
KW ischaemia; stroke; AIDS; bone disease; atherosclerosis; brain disorder;
KW depression; cardiovascular disease; myocardial infarction; renal failure;
KW respiratory disease; liver disorder; Fanconi's syndrome; spleen disorder;
KW type II diabetes mellitus; skeletal muscle disorder; immunosuppressive;
KW hypersplenism; renal disease; hypoglycaemia; gastrointestinal disease;
KW neutropenic; cirrhosis; Hodgkin's disease; neuroleptic; antiinflammatory;
KW haemostatic; vulnery; anticonvulsant; antirheumatic; neuroprotective;
KW nephrotropic; hypotensive; vasotropic; cytostatic; cerebroprotective;
XX allergy; laminin alpha protein.

OS Homo sapiens.
XX
FN WO200198342-A1.
XX
PD 27-DEC-2001.

XX 22-JUN-2001; 2001WO-US019929.
PF
XX 22-JUN-2000; 2000US-0213156P.
PR
22-JUN-2000; 2000US-0213161P.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
XX
PI Agarwal P, Cogswell JP, Kabnic KS, Lai Y, Martensen SA;
PI Murdock PR, Smith RF, Strum JC, Xiang Z, Xie Q, Rizni SK;
XX WPI; 2002-139783/18.
DR N-PSDB; AAD27805.
XX
PT Novel secreted and membrane-associated polypeptides and polynucleotides
PT useful for preventing, ameliorating or correcting dysfunction or disease
PT including diabetes, cancer, hypertension and growth abnormalities.
XX
PS Claim 1; Page 115-122; 138pp; English.
XX
CC The invention relates to secreted and membrane-associated polypeptides
CC and polynucleotides. The sequences of the invention are useful in
CC diagnostic assays for detecting diseases associated with inappropriate
CC activity or levels of these polynucleotides, and in identifying their
CC agonists and antagonists that are potentially useful in therapy. The
CC sequences of the invention are useful as vaccines for inducing
CC immunological response. The sequences of the invention are useful for
CC treating cancers, infections, autoimmune disorders, haematopoietic
CC disorders, wound healing disorders, cholesterol ester storage disease,
CC inflammation, congenital muscular dystrophy, junctional epidermolysis
CC bullosa, Parkinson's disease, Huntington's chorea, multiple sclerosis,
CC viral and bacterial infections, Alzheimer's disease, asthma, arthritis,
CC allergies, schizophrenia, sbg442445PROA-associated disorders,
CC septicemia, psoriasis, inflammatory bowel disease, transplant rejection,
CC graft versus host disease, ischaemia, stroke, acute respiratory disease
CC syndrome, restenosis, brain injury, AIDS, bone diseases, atherosclerosis,
CC brain disorders including parasupranuclear palsy, myotonic dystrophy,
CC depression, anxiety disorders and sleep disorders, cardiovascular
CC diseases including congestive heart failure and myocardial infarction,
CC respiratory diseases including chronic obstructive pulmonary disease,
CC acute bronchitis and adult respiratory distress syndrome, liver disorders
CC including hypercholesterolaemia, hypertriglyceridaemia, cirrhosis, viral
CC and non-viral hepatitis, type II diabetes mellitus, renal disease
CC including acute and chronic renal failure, glomerulonephritis, Fanconi's
CC syndrome, cystinuria, skeletal muscle disorders including hypoglycaemia
CC and tendinitis, gastrointestinal diseases including intestinal
CC obstruction and tropical sprue, spleen disorders including hypersplenism,
CC Hodgkin's disease and malignant lymphoma, testicular cancer, male
CC reproductive diseases including low testosterone and male infertility.
CC The present sequence is human laminin alpha protein
XX
SQ Sequence 3696 AA;

Query Match 99.7%; Score 20060.5; DB 5; Length 3696;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3687; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 1 MAKRLCAGSALCVRGPRGPAPLLLVGLLGAARAREEAGGFSLHPPYFNLAEGARIAA 60
DB 1 MAKRLCAGSALCVRGPRGPAPLLLVGLLGAARAREEAGGFSLHPPYFNLAEGARIAA 60
QY 61 SATCGEEAPARGSPRPTEDLYCKLVGGPVAGDPNQTIRGOYCDICTAANSNKAHPASNA 120
DB 61 SATCGEEAPARGSPRPTEDLYCKLVGGPVAGDPNQTIRGOYCDICTAANSNKAHPASNA 120
QY 121 IDGTERWQSPPLSRGLEYNVNVTLIDQGVHVAAYVLIKAFANSRPDLWILERSMDFGR 180
DB 121 IDGTERWQSPPLSRGLEYNVNVTLIDQGVHVAAYVLIKAFANSRPDLWILERSMDFGR 180
QY 181 TYQPWFQFASSKRDCLERFGPQTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRPG 240
DB

Db 181 TYQPWFQFASSKRDCLERFGPQTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRPG 240
QY 241 AMNFSYSPLLREFTKATNVRLRFLRTNTLLGLMKGALRDPVTTRRYYSIKDISIGGRC 300
Db 241 AMNFSYSPLLREFTKATNVRLRFLRTNTLLGLMKGALRDPVTTRRYYSIKDISIGGRC 300
QY 301 VCHGHADACDAKDPDTPFRLOCTCOHNTCGGTCDRCPCPGNQPKPATANSANECQSCN 360
Db 301 VCHGHADACDAKDPDTPFRLOCTCOHNTCGGTCDRCPCPGNQPKPATANSANECQSCN 360
QY 361 CYGHATDCYYDPEVDRRRASQSLDGTYYGGGVCIDCQHHTAGVNCERCLPGFYRSPNHPL 420
Db 361 CYGHATDCYYDPEVDRRRASQSLDGTYYGGGVCIDCQHHTAGVNCERCLPGFYRSPNHPL 420
QY 421 DSPHVCHRCNCESDFTDGTCEDLTGRCYCRPNFSGRCDVCAEGFTGFPSCYPTPSSND 480
Db 421 DSPHVCHRCNCESDFTDGTCEDLTGRCYCRPNFSGRCDVCAEGFTGFPSCYPTPSSND 480
QY 481 TREQVLPAGQIVNCDCSAAGTQGNACRDKPRVGRCLCKPNFQGTGTHCELCAFGYGGCQP 540
Db 481 TREQVLPAGQIVNCDCSAAGTQGNACRDKPRVGRCLCKPNFQGTGTHCELCAFGYGGCQP 540
QY 541 CQSSPGVADDDCDPDTGQCRVGFEGATCDRCAPGYFHFPLCQLCGCSPAGTLPEGCD 600
Db 541 CQSSPGVADDDCDPDTGQCRVGFEGATCDRCAPGYFHFPLCQLCGCSPAGTLPEGCD 600
QY 601 EAGRCLCQPEFAGPHCDRCRPGYHGFNCOACTCDPRGALDQLCGAGGLCRCPGYTGTA 660
Db 601 EAGRCLCQPEFAGPHCDRCRPGYHGFNCOACTCDPRGALDQLCGAGGLCRCPGYTGTA 660
QY 661 COECSGPFHGFPPSCVPCCHSAEGLHAACDPRSGQCSRCRPRVTGLRCDTQVPGAYNFPYC 720
Db 661 COECSGPFHGFPPSCVPCCHSAEGLHAACDPRSGQCSRCRPRVTGLRCDTQVPGAYNFPYC 720
QY 721 EAGSCHPAGLAPVDPALPEAQVPCMCRAHVEGSPCDRCCKPGFWGLSPNPEGTRCSCDL 780
Db 721 EAGSCHPAGLAPVDPALPEAQVPCMCRAHVEGSPCDRCCKPGFWGLSPNPEGTRCSCDL 780
QY 781 RGTILGVAECQPGTGQCFCKPHVCGQACASCKDGFGLDQADYFGCRSCRCIDIGGALQS 840
Db 781 RGTILGVAECQPGTGQCFCKPHVCGQACASCKDGFGLDQADYFGCRSCRCIDIGGALQS 840
QY 841 CEPRTGVCRCRNPNTQGTCTSEPARDHYLPDLHLRLLELEAAATPEGHAVRFGNPLEFEN 900
Db 841 CEPRTGVCRCRNPNTQGTCTSEPARDHYLPDLHLRLLELEAAATPEGHAVRFGNPLEFEN 900
QY 901 FSWRGYAQMAPPVQPRIVARLNLTSPLDLFWLVRYVNRGAMSVSRVREGRSAACANC 960
Db 901 FSWRGYAQMAPPVQPRIVARLNLTSPLDLFWLVRYVNRGAMSVSRVREGRSAACANC 960
QY 961 TAQSQPVAFPPSTEPAFITVPQRGFGEPPFVLPNGTVALRVEAGVLLDYVLLPSAYYEA 1020
Db 961 TAQSQPVAFPPSTEPAFITVPQRGFGEPPFVLPNGTVALRVEAGVLLDYVLLPSAYYEA 1020
QY 1021 ALLQLRVTEACTYRPSAQSGDNCLLYTHPLDGFPPSAAGLEALCRQDNLPRPCPTEQL 1080
Db 1021 ALLQLRVTEACTYRPSAQSGDNCLLYTHPLDGFPPSAAGLEALCRQDNLPRPCPTEQL 1080
QY 1081 SPSHPPLITCTGSDVDVQLQVAVPQGRYALVVEYANEDARQEVGVAVHTPQAPQOGLL 1140
Db 1081 SPSHPPLITCTGSDVDVQLQVAVPQGRYALVVEYANEDARQEVGVAVHTPQAPQOGLL 1140
QY 1141 SLHPCLYSTLCRGFARDTQDHLAVFHLDSASVRLTAEQARFLLHGVTLPVIEEFSPEFV 1200
Db 1141 SLHPCLYSTLCRGFARDTQDHLAVFHLDSASVRLTAEQARFLLHGVTLPVIEEFSPEFV 1200
QY 1201 EPRVSCISSHGAFGNSAACLPSPRFPKPPQPIILRDCQVILPPLGLPLTHAODLTPTATSP 1260
Db 1201 EPRVSCISSHGAFGNSAACLPSPRFPKPPQPIILRDCQVILPPLGLPLTHAODLTPTATSP 1260
QY 1261 AGPRPRPPTAVDPDAEPTLLREPOATVFTTHVPTLGRYAFLLHGYQPAHPTFFPVEVLIN 1320
Db 1261 AGPRPRPPTAVDPDAEPTLLREPOATVFTTHVPTLGRYAFLLHGYQPAHPTFFPVEVLIN 1320

QY 1321 AGRVWQGHANASFCPHGYGCRTLVVCBQALLDVTHSELVTTVRVPEGRWLWLDYVLVVP 1380
Db 1321 AGRVWQGHANASFCPHGYGCRTLVVCBQALLDVTHSELVTTVRVPKGRWLWLDYVLVVP 1380
QY 1381 ENVYSFGYLREBPLDKSYDFISHCAAQGYHISPSSSFLCRNAAASLSLFYNNGARPCGC 1440
Db 1381 ENVYSFGYLREBPLDKSYDFISHCAAQGYHISPSSSFLCRNAAASLSLFYNNGARPCGC 1440
QY 1441 HEVGATGPTCEPFGQCPCHAHVIGRDCSRCATGYWGFNCRPCDCGARLDELGTQCIC 1500
Db 1441 HEVGATGPTCEPFGQCPCHAHVIGRDCSRCATGYWGFNCRPCDCGARLDELGTQCIC 1500
QY 1501 PPRITPPDCLLCOPQTFGCHPLVGCCEECNCSGPGIQELTDPTCDTDSGQCKCRPNVTGRR 1560
Db 1501 PPRITPPDCLLCOPQTFGCHPLVGCCEECNCSGPGIQELTDPTCDTDSGQCKCRPNVTGRR 1560
QY 1561 CDTCSPGFHGYPRCPCDCHEAGTAPGVCDPLTGQCYCKENVQPKCDQCSLGTFSLDAA 1620
Db 1561 CDTCSPGFHGYPRCPCDCHEAGTAPGVCDPLTGQCYCKENVQPKCDQCSLGTFSLDAA 1620
QY 1621 NPKGCTRCFCFGATERCRSSSYTROEFFVDMEGVLLSTDQVVPHERQPGTEMLRADLRH 1680
Db 1621 NPKGCTRCFCFGATERCRSSSYTROEFFVDMEGVLLSTDQVVPHERQPGTEMLRADLRH 1680
QY 1681 VPEAVPEAFPELYWQAPPSYLGDRVSSYGGLLYELHSETQRGDVFVPMESRPDVVLQGN 1740
Db 1681 VPEAVPEAFPELYWQAPPSYLGDRVSSYGGLLYELHSETQRGDVFVPMESRPDVVLQGN 1740
QY 1741 QMSITFLEPAYPTPGHVHRGQLQLVEGNFRHTETRTNTVSREELMMVLASLEQLQIRALFS 1800
Db 1741 QMSITFLEPAYPTPGHVHRGQLQLVEGNFRHTETRTNTVSREELMMVLASLEQLQIRALFS 1800
QY 1801 QISSAVSLRRVALEVASPAGQALASNVLCPCASYRGDSCQECAPGYRDVKGLFLGR 1860
Db 1801 QISSAVFLRRVALEVASPAGQALASNVLCPCASYRGDSCQECAPGYRDVKGLFLGR 1860
QY 1861 CVPCQCHGHSRCLPGSGVCVDCQHNTGAHCERCOAGFMSSRDDPSAPCVSCPCPLSVP 1920
Db 1861 CVPCQCHGHSRCLPGSGVCVDCQHNTGAHCERCOAGFVSSRDDPSAPCVSCPCPLSVP 1920
QY 1921 SNNFAEGCVLRGGRTQCLCKPGYAGASCERCAPGFGNPLVLGSSCQPCDCSGNDPNLL 1980
Db 1921 SNNFAEGCVLRGGRTQCLCKPGYAGASCERCAPGFGNPLVLGSSCQPCDCSGNDPNLL 1980
QY 1981 FSDCDPLTGACRGCLRHTTGPRCEICAPGYGNALLPGNCTRCDCTPCGTEACDPHSGHC 2040
Db 1981 FSDCDPLTGACRGCLRHTTGPRCEICAPGYGNALLPGNCTRCDCTPCGTEACDPHSGHC 2040
QY 2041 LCKAGVTGRRCDRCQEGHFGGCGGCRPCACGPAAGSECHPQSGQCHCRPGTMGPQCR 2100
Db 2041 LCKAGVTGRRCDRCQEGHFGGCGGCRPCACGPAAGSECHPQSGQCHCRPGTMGPQCR 2100
QY 2101 ECAPGYWGLPEQGCRRCCQPGRCDPHTGRCNCPPGLSGERCDTCSQQHQVVPVPGPVGH 2160
Db 2101 ECAPGYWGLPEQGCRRCCQPGRCDPHTGRCNCPPGLSGERCDTCSQQHQVVPVPGPVGH 2160
QY 2161 SIHCEVCDHCVVLLDDLERAGALLPAIHEQLRGINASSMAWARLHRLNASIADLQSQLR 2220
Db 2161 SIHCEVCDHCVVLLDDLERAGALLPAIHEQLRGINASSMAWARLHRLNASIADLQSQLR 2220
QY 2221 SPLGPRHETAQOQLEVLQOQSTSLGQDARRLGGQ-AVGTFDQASQLLAGTEATLGHAKTLL 2279
Db 2221 SPLGPRHETAQOQLEVLQOQSTSLGQDARRLGGQAVGTFDQASQLLAGTEATLGHAKTLL 2280
QY 2280 AAIRAVDRTLSELMSQTGHLGLANASAPSGEQLLRTILAEVERLLWEMRARDILGAPQAAAE 2339
Db 2281 AAIRAVDRTLSELMSQTGHLGLANASAPSGEQLLRTILAEVERLLWEMRARDILGAPQAAAE 2340
QY 2340 AELAAQORLLARVQEQQLSSLWEEENQALATQTRDRLAQHEAGLMDLREALNRAVDATREAO 2399
Db 2341 AELAAQORLLARVQEQQLSSLWEEENQALATQTRDRLAQHEAGLMDLREALNRAVDATREAO 2400

QY 2400 ELNSRNQERLEALQKQELSRDNATLQATLHAARDTLASVFRLLHSLDQAKEELERLAA 2459
Db 2401 ELNSRNQERLEALQKQELSRDNATLQATLHAARDTLASVFRLLHSLDQAKEELERLAA 2460
QY 2460 SLDGARTPLLRMQTFSPAGSKRLRVEABAAHQQLGOLALNLSSIILDVNQDRLTORAI 2519
Db 2461 SLDGARTPLLRMQTFSPAGSKRLRVEABAAHQQLGOLALNLSSIILDVNQDRLTORAI 2520
QY 2520 EASNAYSRILOAVQAAEDAAGQALQQADHTWATVVRQGLVDRAQQLLANSTALEEAMLOE 2579
Db 2521 EASNAYSRILOAVQAAEDAAGQALQQADHTWATVVRQGLVDRAQQLLANSTALEEAMLOE 2580
QY 2580 QORLGLVWAALQAGARTQLRDVRAKKDQLEAHIQAAQAMLAMDTDETSKKIAHAKAVAAEA 2639
Db 2581 QORLGLVWAALQAGARTQLRDVRAKKDQLEAHIQAAQAMLAMDTDETSKKIAHAKAVAAEA 2640
QY 2640 QDTATRVQSQLQAMQENVERWQGYEGRLRGDGLGQAVLDAGHSVSTLEKTLFQLLAKLSI 2699
Db 2641 QDTATRVQSQLQAMQENVERWQGYEGRLRGDGLGQAVLDAGHSVSTLEKTLFQLLAKLSI 2700
QY 2700 LENRGVHNASLALSASIGRVRELIAQARGAASKVKVPMKFNRSVQVQLRTPRDLADLAAY 2759
Db 2701 LENRGVHNASLALSASIGRVRELIAQARGAASKVKVPMKFNRSVQVQLRTPRDLADLAAY 2760
QY 2760 TALKFYLOGPEPEPGQGTEDRFVMYMGSRQATGDMGVSLRDKKVHVYQOLGEAGPAVLS 2819
Db 2761 TALKFYLOGPEPEPGQGTEDRFVMYMGSRQATGDMGVSLRDKKVHVYQOLGEAGPAVLS 2820
QY 2820 IDEDIGEQAFAAVSLDRTLOFGHMSVTVERQMIQETKGDTVAPGAEGLLNLRPDDVFYVVG 2879
Db 2821 IDEDIGEQAFAAVSLDRTLOFGHMSVTVERQMIQETKGDTVAPGAEGLLNLRPDDVFYVVG 2880
QY 2880 GYPSTFTPPPLLRFPFGYRGCIEMDTLNEEVVSLYNFERTFQDITAVDRPCARSKSTGDPW 2939
Db 2881 GYPSTFTPPPLLRFPFGYRGCIEMDTLNEEVVSLYNFERTFQDITAVDRPCARSKSTGDPW 2940
QY 2940 LTDGSYLDGTGFARISFDSQISITTKRFEQELRLVSYSGVLFFLKQOQSOFCLAVQEGSLV 2999
Db 2941 LTDGSYLDGTGFARISFDSQISITTKRFEQELRLVSYSGVLFFLKQOQSOFCLAVQEGSLV 3000
QY 3000 LLYDFGAGLKKAVPLQPPPLTSSASKAIQVFLGGSRKRVLRVERATVYSVEQDNDLEL 3059
Db 3001 LLYDFGAGLKKAVPLQPPPLTSSASKAIQVFLGGSRKRVLRVERATVYSVEQDNDLEL 3060
QY 3060 ADAYILGGVPPDQLPPSLRWLPPTGGSVRGCVKGIKALGKYVDLKLRLNTTGVSACTADL 3119
Db 3061 ADAYILGGVPPDQLPPSLRWLPPTGGSVRGCVKGIKALGKYVDLKLRLNTTGVSACTADL 3120
QY 3120 LVGRAMTFHGHGFLRLALSINVAPLTGNVSYSGFGFHSQDSALLYRASPDGLCQVSLQOQ 3179
Db 3121 LVGRAMTFHGHGFLRLALSINVAPLTGNVSYSGFGFHSQDSALLYRASPDGLCQVSLQOQ 3180
QY 3180 RVSLQLLRTEVKTQAGFADGAPHYVAFYSNATGVWLYVDDQLQOMKPHRGPPELOQPOE 3239
Db 3181 RVSLQLLRTEVKTQAGFADGAPHYVAFYSNATGVWLYVDDQLQOMKPHRGPPELOQPOE 3240
QY 3240 GPPRILLGGLPESGTIYNFSGCISNVFVQRLLGQORVFDLQONLGSVNVSTGCAPALQAO 3299
Db 3241 GPPRILLGGLPESGTIYNFSGCISNVFVQRLLGQORVFDLQONLGSVNVSTGCAPALQAO 3300
QY 3300 TPGLGPRGLQATARKASRRSRPARHPACMLPPLHRTTRDSYQFGGSLSSHLEFVGILAR 3359
Db 3301 TPGLGPRGLQATARKASRRSRPARHPACMLPPLHRTTRDSYQFGGSLSSHLEFVGILAR 3360
QY 3360 HRNWPISLMSHVLPRSSRGLLFTARLRPGSPSLALFLSNHGFVAQMEGLGTRLRAQSRQR 3419
Db 3361 HRNWPISLMSHVLPRSSRGLLFTARLRPGSPSLALFLSNHGFVAQMEGLGTRLRAQSRQR 3420
QY 3420 SRPGRWHKVSVRWEKNRILLVTDGARAWSQEGPHRQHQAHEHPQPHTLFVGGLPASSHSS 3479
Db 3421 SRPGRWHKVSVRWEKNRILLVTDGARAWSQEGPHRQHQAHEHPQPHTLFVGGLPASSHSS 3480
QY 3480 KLPVTVGFSGCVKRLRLHGRPLGAPTRMAGVTPCILGPLEAGLFFPGSGGVITLDFPGAT 3539

Db 3481 KLPVTVGFSGVCKRLRLHGRPLCAPTRMAGVTPCIIGLPLEAGLFFPGSGGVITLDLPAT 3540
QY 3540 LPDVGLEVRPLAVTGLIFHLGQARTPPYLQVTEKQVLLRADGAGERFSTSVTRPSV 3599
Db 3541 LPDVGLEVRPLAVTGLIFHLGQARTPPYLQVTEKQVLLRADGAGERFSTSVTRPSV 3600
QY 3600 LCDGQMRHLAVMKSGNVLRLVDAQSNHTVGPLLAAAGAPAPLYLGLGLPEPMVQWPWP 3659
Db 3601 LCDGQMRHLAVMKSGNVLRLVDAQSNHTVGPLLAAAGAPAPLYLGLGLPEPMVQWPWP 3660
QY 3660 AYCGCMRRLAVNRSPVAMTRSRVEVHGAVGASGCPAA 3695
Db 3661 AYCGCMRRLAVNRSPVAMTRSRVEVHGAVGASGCPAA 3696

RESULT 3

AAE17309
ID AAE17309 standard; protein; 3705 AA.

XX AC AAE17309;

XX DT 18-APR-2002 (first entry)

XX DE Human laminin alpha protein, sbg417005LAMININ_ALPHA #1.

XX KW Human; therapy; wound healing disorder; vaccine; cancer; infection;
KW autoimmune disorder; haematopoietic disorder; inflammation; arthritis;
KW Parkinson's disease; Huntington's chorea; schizophrania; antiarrhythmic;
KW multiple sclerosis; Alzheimer's disease; analgesic; cardiac; asthma;
KW ischaemia; stroke; AIDS; bone disease; atherosclerosis; brain disorder;
KW depression; cardiovascular disease; myocardial infarction; renal failure;
KW respiratory disease; liver disorder; Fanconi's syndrome; spleen disorder;
KW type II diabetes mellitus; skeletal muscle disorder; immunosuppressive;
KW hypersplenism; renal disease; hypoglycaemia; gastrointestinal disease;
KW neutropenic; cirrhosis; Hodgkin's disease; neuroleptic; antiinflammatory;
KW haemostatic; vulnary; anticonvulsant; antirheumatic; neuroprotective;
KW nephrotropic; hypotensive; vasotropic; cytostatic; cerebroprotective;
KW allergy; laminin alpha protein.

XX OS Homo sapiens.

XX PN WO200198342-A1.

XX PD 27-DEC-2001.

XX PF 22-JUN-2001; 2001WO-US019929.

XX PR 22-JUN-2000; 2000US-0213156P.

XX PR 22-JUN-2000; 2000US-0213161P.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX PA (SMIK) SMITHKLINE BEECHAM PLC.

XX PA (GLAX) GLAXO GROUP LTD.

XX PI Agarwal P, Cogswell JP, Kabnic KS, Lai Y, Martensen SA;

XX PI Murdock PR, Smith RF, Strum JC, Xiang Z, Xie Q, Rizni SK;

XX DR WPI; 2002-139783/18.

XX DR N-PSDB; AAD27804.

XX PT Novel secreted and membrane-associated polypeptides and polynucleotides
XX PT useful for preventing, ameliorating or correcting dysfunction or disease
XX PT including diabetes, cancer, hypertension and growth abnormalities.

XX PS Claim 1; Page 107-114; 138pp; English.

XX CC The invention relates to secreted and membrane-associated polypeptides
XX CC and polynucleotides. The sequences of the invention are useful in
XX CC diagnostic assays for detecting diseases associated with inappropriate
XX CC activity or levels of these polynucleotides, and in identifying their
XX CC agonists and antagonists that are potentially useful in therapy. The
XX CC sequences of the invention are useful as vaccines for inducing

CC immunological response. The sequences of the invention are useful for
CC treating cancers, infections, autoimmune disorders, haematopoietic
CC disorders, wound healing disorders, cholesteryl ester storage disease,
CC inflammation, congenital muscular dystrophy, junctional epidermolysis
CC bullosa, Parkinson's disease, Huntington's chorea, multiple sclerosis,
CC viral and bacterial infections, Alzheimer's disease, asthma, arthritis,
CC allergies, schizophrenia, sbg42445PROA-associated disorders,
CC septicemia, psoriasis, inflammatory bowel disease, transplant rejection,
CC graft versus host disease, ischaemia, stroke, acute respiratory disease
CC syndrome, restenosis, brain injury, AIDS, bone diseases, atherosclerosis,
CC brain disorders including parasupranuclear palsy, myotonic dystrophy,
CC depression, anxiety disorders and sleep disorders, cardiovascular
CC diseases including congestive heart failure and myocardial infarction,
CC respiratory diseases including chronic obstructive pulmonary disease,
CC acute bronchitis and adult respiratory distress syndrome, liver disorders
CC including hypercholesterolaemia, hypertriglyceridaemia, cirrhosis, viral
CC and non-viral hepatitis, type II diabetes mellitus, renal disease
CC including acute and chronic renal failure, glomerulonephritis, Fanconi's
CC syndrome, cystinuria, skeletal muscle disorders including intestinal
CC and tendinitis, gastrointestinal diseases including intestinal
CC obstruction and tropical sprue, spleen disorders including hypersplenism,
CC Hodgkin's disease and malignant lymphoma, testicular cancer, male
CC reproductive diseases including low testosterone and male infertility.
CC The present sequence is human laminin alpha protein

XX SQ Sequence 3705 AA;

Query Match 99.6%; Score 20030; DB 5; Length 3705;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 3683; Conservative 3; Mismatches 9; Indels 10; Gaps 1;

QY 1 MAKRLCAGSALCVGRGPPAPLLVGLALLGAARAREEAGGGFSLHPPYFNLAEGARIAA 60

Db 1 MAKRLCAGSALCVGRGPPAPLLVGLALLGAARAREEAGGGFSLHPPYFNLAEGARIAA 60

QY 61 SATCGEAPARGSPRPTELYCKLVGGPVAGDPNQTIRGQYCDICTAANSNKAHPASNA 120

Db 61 SATCGEAPARGSPRPTELYCKLVGGPVAGDPNQTIRGQYCDICTAANSNKAHPASNA 120

QY 121 IDGTERWQSPPLSRGLEYNVNTLDLQGVFHVAYLIKFNANPRPDLWVLSRMDFG 180

Db 121 IDGTERWQSPPLSRGLEYNVNTLDLQGVFHVAYLIKFNANPRPDLWVLSRMDFG 180

QY 181 TYQPWFQFASSKRDCLERFGPQTLERITRDDAAICTEYSRIVPLENGEIVVSLVNGRPG 240

Db 181 TYQPWFQFASSKRDCLERFGPQTLERITRDDAAICTEYSRIVPLENGEIVVSLVNGRPG 240

QY 241 AMNFSYPLLRFTKATNVRFLRLTNTLLHLMGKALRDPVTTRRYYSIKDISIGGR 300

Db 241 AMNFSYPLLRFTKATNVRFLRLTNTLLHLMGKALRDPVTTRRYYSIKDISIGGR 300

QY 301 VCHGHADACDAKDPDPFRLQCTCQHTCGGTCDRCPCGPNQPKPATANSANECQSCN 360

Db 301 VCHGHADACDAKDPDPFRLQCTCQHTCGGTCDRCPCGPNQPKPATANSANECQSCN 360

QY 361 CYGHATDCYDPEVDRRRASQSLDGTQGGVVCIDCQHHTAGVNCERCLPGFYRSPNHPL 420

Db 361 CYGHATDCYDPEVDRRRASQSLDGTQGGVVCIDCQHHTAGVNCERCLPGFYRSPNHPL 420

QY 421 DSPHVCRRNCESDFTDGTCEBTLTGRCYCRPNFSGERCDCVCAEGTGFPPSSND 480

Db 421 DSPHVCRRNCESDFTDGTCEBTLTGRCYCRPNFSGERCDCVCAEGTGFPPSSND 480

QY 481 TREQVLEAGQIVNCDSCAAGTQGNACRKPVRVGRCLCKPNFQGTHTCELCAFGYGPCCQP 540

Db 481 TREQVLEAGQIVNCDSCAAGTQGNACRKPVRVGRCLCKPNFQGTHTCELCAFGYGPCCQP 540

QY 541 CQSSPGVADDCDPDTGQCRVRVFEAGATCDRCAPGYFHFPLCQLCGSPAGTLPEGCD 600

Db 541 CQSSPGVADDCDPDTGQCRVRVFEAGATCDRCAPGYFHFPLCQLCGSPAGTLPEGCD 600

QY 601 EAGRCLQPEFAGPHCDRCRPGYHGFNCPQACTCDPRGALDQLCGAGGLCRCPGYTGTA 660

Db 601 EAGRCLQPEFAGPHCDRCRPGYHGFNCPQACTCDPRGALDQLCGAGGLCRCPGYTGTA 660

Db 601 EAGRLCOPEAFAGHCDRCRFGYHGFNFCQACTCDPRGALDQLCGAGGLCRCRPGYTGT 660
QY 661 CQECSPGFHGFSPCVCHCSAEGSLHAAACDPRSGQCSRRVTLGLRCDTCVPGAYNFPYC 720
Db 661 CQECSPGFHGFSPCVCHCSAEGSLHAAACDPRSGQCSRRVTLGLRCDTCVPGAYNFPYC 720
QY 721 EAGSCHPAGLAPVDPALPEAQVPCMCRAHVEGSPCDRCCKPFGWGLSPSNPEGCTRCSCDL 780
Db 721 EAGSCHPAGLAPVDPALPEAQVPCMCRAHVEGSPCDRCCKPFGWGLSPSNPEGCTRCSCDL 780
QY 781 RGTGGVAECQGTGQCFCKPHVCGQACASCKDGFGLDQADYFGCRSCRDICGALGQS 840
Db 781 RGTGGVAECQGTGQCFCKPHVCGQACASCKDGFGLDQADYFGCRSCRDICGALGQS 840
QY 841 CEPRTGVCRCPNTQGPTCSEPARDHYLPDLHLRLLELEAATPEGHAVRFGNPLEFEN 900
Db 841 CEPRTGVCRCPNTQGPTCSEPARDHYLPDLHLRLLELEAATPEGHAVRFGNPLEFEN 900
QY 901 FSWRGYAQMVPQPRIVARLNLTSPDLFWLVFRYVNRGAMSVGRVSVREEGSAAACANC 960
Db 901 FSWRGYAQMVPQPRIVARLNLTSPDLFWLVFRYVNRGAMSVGRVSVREEGSAAACANC 960
QY 961 TAQSQPVAFPPSTEPAFITVPQGEFEPVLPNPGTWARVEAEGVLLDYVVLPSAYYEA 1020
Db 961 TAQSQPVAFPPSTEPAFITVPQGEFEPVLPNPGTWARVEAEGVLLDYVVLPSAYYEA 1020
QY 1021 ALLQLRVTEACTYRPSAQSGDNCLLYTHLPLDGFPSAAGLEALCRQDNLSLPRCPTEQL 1080
Db 1021 ALLQLRVTEACTYRPSAQSGDNCLLYTHLPLDGFPSAAGLEALCRQDNLSLPRCPTEQL 1080
QY 1081 SPSHPPLTCTGSDVDVQLQVAVPQGRYALVVEYANEDARQEVGVAHTPORAPQQGLL 1140
Db 1081 SPSHPPLTCTGSDVDVQLQVAVPQGRYALVVEYANEDARQEVGVAHTPORAPQQGLL 1140
QY 1141 SLHPCLYSTLCRGRTARDTQDHLAVFHLDSASVRLTAQARFLLHGVTLPVEEFSPEFV 1200
Db 1141 SLHPCLYSTLCRGRTARDTQDHLAVFHLDSASVRLTAQARFLLHGVTLPVEEFSPEFV 1200
QY 1201 EPRVSCISSHGAFGPNNSAACLPSPKPPQPIIILRDCQVPLPPGLPLTHAQDLTPATSP 1260
Db 1201 EPRVSCISSHGAFGPNNSAACLPSPKPPQPIIILRDCQVPLPPGLPLTHAQDLTPAMSP 1260
QY 1261 AGPRPRPTAVDPDAEPTLLREPOATVFTTHVPTLGRYAFLLHGYPAPHTFPVEVLIN 1320
Db 1261 AGPRPRPTAVDPDAEPTLLREPOATVFTTHVPTLGRYAFLLHGYPAPHTFPVEVLIN 1320
QY 1321 AGRVWQHGANASFCPHGYGCRILVCEGOALLDVTHSELTVTVRVPEGRWLWLDYVLVVP 1380
Db 1321 AGRVWQHGANASFCPHGYGCRILVCEGOALLDVTHSELTVTVRVPEGRWLWLDYVLVVP 1380
QY 1381 ENVYSGYLREEPLDKSYDFISHCAAQGYHISPSSSLFCRNAAASLSLFYNNGARPCGC 1440
Db 1381 ENVYSGYLREEPLDKSYDFISHCAAQGYHISPSSSLFCRNAAASLSLFYNNGARPCGC 1440
QY 1441 HEVGATGPTCEPFGGQCPCHAHVIGRDCSRCATGYWGFNCRPCDCGARLDELTCQCIC 1500
Db 1441 HEVGATGPTCEPFGGQCPCHAHVIGRDCSRCATGYWGFNCRPCDCGARLDELTCQCIC 1500
QY 1501 PPRTIPDCLLCQPQTFGCHPLVGCCEECNCSGPGIQELTDPTCDTDSGCKCRPNVTGRR 1560
Db 1501 PPRTIPDCLLCQPQTFGCHPLVGCCEECNCSGPGIQELTDPTCDTDSGCKCRPNVTGRR 1560
QY 1561 CDTCSGPHGYPRCPCDCHAGTAPGVCDPLTGOCYCKENVQPKCDQCSLGTFSLDAA 1620
Db 1561 CDTCSGPHGYPRCPCDCHAGTAPGVCDPLTGOCYCKENVQPKCDQCSLGTFSLDAA 1620
QY 1621 NPKGTRCFCFGATERCRSSSYTRQEFVDMEGWVLLSTDRQVVPHERQPGTEMLRADLRH 1680
Db 1621 NPKGTRCFCFGATERCRSSSYTRQEFVDMEGWVLLSTDRQVVPHERQPGTEMLRADLRH 1680
QY 1681 VPEAVPEAFPELYWQAPPSYLGDRVSSYGGTLRYELHSETQRGDVFPVPMESRPDVVLQGN 1740
Db 1681 VPEAVPEAFPELYWQAPPSYLGDRVSSYGGTLRYELHSETQRGDVFPVPMESRPDVVLQGN 1740

QY 1741 QMSITFLEPAYTPGPHRGQLQOLVEGNFRHTETRTNTVSREELMMVLASLEQLQIRALFS 1800
Db 1741 QMSITFLEPAYTPGPHRGQLQOLVEGNFRHTETRTNTVSREELMMVLASLEQLQIRALFS 1800
QY 1801 QISSAVSLRRVALEVASPAGQALASNVELCLCPAS YRGDS CQECAPGFYRDVKGLFLGR 1860
Db 1801 QISSAVFLRRVALEVASPAGQALASNVELCLCPAS YRGDS CQECAPGFYRDVKGLFLGR 1860
QY 1861 CVPCQCHGHSRCLPGSGVCVDQHNTEGAHCERCQAGFMSSRRDPSAPCVSCPCPLSVP 1920
Db 1861 CVPCQCHGHSRCLPGSGVCVDQHNTEGAHCERCQAGFVSSRRDPSAPCVSCPCPLSVP 1920
QY 1921 SNNFAEGCVLRGGRTQCLCKPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSNGDNNLL 1980
Db 1921 SNNFAEGCVLRGGRTQCLCKPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSNGDNNLL 1980
QY 1981 FSDCDPLTGACRGCLRHHTTGPRCEICAPGFGVGNALLPGNCTRCDCCTPCGTEACDPHSGHC 2040
Db 1981 FSDCDPLTGACRGCLRHHTTGPRCEICAPGFGVGNALLPGNCTRCDCCTPCGTEACDPHSGHC 2040
QY 2041 LCKAGVTGRRCDRCQEGHFGFNGCGGCRPCACGPAAGSECHPSQSQCHQCHRPMTGPOCR 2100
Db 2041 LCKAGVTGRRCDRCQEGHFGFNGCGGCRPCACGPAAGSECHPSQSQCHQCHRPMTGPOCR 2100
QY 2101 ECAPGYWGLPEQGCRCRCQPCGRCDPHTGRCNCPPLSGERCDCSCQHQHVPPVGGPVGH 2160
Db 2101 ECAPGYWGLPEQGCRCRCQPCGRCDPHTGRCNCPPLSGERCDCSCQHQHVPPVGGPVGH 2160
QY 2161 SIHCEVCDHCVVLLDDLERAGALLPAIHEQLRGINASSMAWARLHRLNASIADLQSLR 2220
Db 2161 SIHCEVCDHCVVLLDDLERAGALLPAIHEQLRGINASSMAWARLHRLNASIADLQSLR 2220
QY 2221 SPLGPRHETAQOLEVLEEQOSTSLGQDARRLGQAVGTRD-----QASQLLAGTEA 2270
Db 2221 SPLGPRHETAQOLEVLEEQOSTSLGQDARRLGQAGAPRPPRAPGFFHLYQASQLLAGTEA 2280
QY 2271 TLGHAKTLLAAIRAVDRTLSELMSQTHGLGLANASAPSGEQLLRTLAEVERLLWEMRAD 2330
Db 2271 TLGHAKTLLAAIRAVDRTLSELMSQTHGLGLANASAPSGEQLLRTLAEVERLLWEMRAD 2330
QY 2281 TLGHAKTLLAAIRAVDRTLSELMSQTHGLGLANASAPSGEQLLRTLAEVERLLWEMRAD 2340
Db 2281 TLGHAKTLLAAIRAVDRTLSELMSQTHGLGLANASAPSGEQLLRTLAEVERLLWEMRAD 2340
QY 2331 LGAPQAAAEAEELAAQORLLARVQEQSLSLWEENOALATQTRDLAQHEAGLMDLREALNR 2390
Db 2331 LGAPQAAAEAEELAAQORLLARVQEQSLSLWEENOALATQTRDLAQHEAGLMDLREALNR 2390
QY 2341 LGAPQAAAEAEELAAQORLLARVQEQSLSLWEENOALATQTRDLAQHEAGLMDLREALNR 2400
Db 2341 LGAPQAAAEAEELAAQORLLARVQEQSLSLWEENOALATQTRDLAQHEAGLMDLREALNR 2400
QY 2391 AVDATREAOELNSRQERLEALQKQELSRDNATLQATLHAARDTLASVFRLLHSLDQA 2450
Db 2391 AVDATREAOELNSRQERLEALQKQELSRDNATLQATLHAARDTLASVFRLLHSLDQA 2450
QY 2401 AVDATREAOELNSRQERLEALQKQELSRDNATLQATLHAARDTLASVFRLLHSLDQA 2460
Db 2401 AVDATREAOELNSRQERLEALQKQELSRDNATLQATLHAARDTLASVFRLLHSLDQA 2460
QY 2451 KEELERLAAASLDGARTPLQORMOTFSPAGSKRLVEAAEAHAQQLGOLALNLSIIILDVN 2510
Db 2451 KEELERLAAASLDGARTPLQORMOTFSPAGSKRLVEAAEAHAQQLGOLALNLSIIILDVN 2510
QY 2461 KEELERLAAASLDGARTPLQORMOTFSPAGSKRLVEAAEAHAQQLGOLALNLSIIILDVN 2520
Db 2461 KEELERLAAASLDGARTPLQORMOTFSPAGSKRLVEAAEAHAQQLGOLALNLSIIILDVN 2520
QY 2511 QDRLTORAIENASNAYSRILOAVQAAEDAAGQALQOQADHTWATVVRQGLVDRAQQLLANST 2570
Db 2511 QDRLTORAIENASNAYSRILOAVQAAEDAAGQALQOQADHTWATVVRQGLVDRAQQLLANST 2570
QY 2521 QDRLTORAIENASNAYSRILOAVQAAEDAAGQALQOQADHTWATVVRQGLVDRAQQLLANST 2580
Db 2521 QDRLTORAIENASNAYSRILOAVQAAEDAAGQALQOQADHTWATVVRQGLVDRAQQLLANST 2580
QY 2571 ALEEAMLOEQORLGLVWAAALQARTQLRDVRAKKDQLEAHIQAAQAMLMDTDETSKIA 2630
Db 2571 ALEEAMLOEQORLGLVWAAALQARTQLRDVRAKKDQLEAHIQAAQAMLMDTDETSKIA 2630
QY 2581 ALEEAMLOEQORLGLVWAAALQARTQLRDVRAKKDQLEAHIQAAQAMLMDTDETSKIA 2640
Db 2581 ALEEAMLOEQORLGLVWAAALQARTQLRDVRAKKDQLEAHIQAAQAMLMDTDETSKIA 2640
QY 2631 HAKAVAAEAQDTATRVQSOLOQAMQENVERWQOYEGRLRGQDLGOAVLDAGHSVSTLEKTL 2690
Db 2631 HAKAVAAEAQDTATRVQSOLOQAMQENVERWQOYEGRLRGQDLGOAVLDAGHSVSTLEKTL 2690
QY 2641 HAKAVAAEAQDTATRVQSOLOQAMQENVERWQOYEGRLRGQDLGOAVLDAGHSVSTLEKTL 2700
Db 2641 HAKAVAAEAQDTATRVQSOLOQAMQENVERWQOYEGRLRGQDLGOAVLDAGHSVSTLEKTL 2700
QY 2691 POLLAKLSILENRGVHNASLALSASIGRVRRELIAQARGAASKVKVPMKFNNGRSGVQLRTP 2750
Db 2691 POLLAKLSILENRGVHNASLALSASIGRVRRELIAQARGAASKVKVPMKFNNGRSGVQLRTP 2750
QY 2701 POLLAKLSILENRGVHNASLALSASIGRVRRELIAQARGAASKVKVPMKFNNGRSGVQLRTP 2760
Db 2701 POLLAKLSILENRGVHNASLALSASIGRVRRELIAQARGAASKVKVPMKFNNGRSGVQLRTP 2760
QY 2751 RDLADLAAAYTALKFYLOQPEPEPGQGTEDRFVVMYMGSRQATGDYMGVSLRDKKVVHVVYQL 2810
Db 2751 RDLADLAAAYTALKFYLOQPEPEPGQGTEDRFVVMYMGSRQATGDYMGVSLRDKKVVHVVYQL 2810
QY 2761 RDLADLAAAYTALKFYLOQPEPEPGQGTEDRFVVMYMGSRQATGDYMGVSLRDKKVVHVVYQL 2820
Db 2761 RDLADLAAAYTALKFYLOQPEPEPGQGTEDRFVVMYMGSRQATGDYMGVSLRDKKVVHVVYQL 2820

CC atherosclerosis, cell signal processing-related disorders and disorders
CC of metabolic pathway regulation. NOVX nucleic acids and polypeptides may
CC be used to identify cellular receptors or downstream effectors which
CC binds to a NOVX protein, and are also useful as targets for the
CC identification of small molecules that modulate or inhibit processes such
CC as neurogenesis, cell differentiation, cell motility, cellular
CC proliferation, haematopoiesis, wound healing and angiogenesis. NOVX
CC nucleic acid sequences can be used to identify a cell or tissue type and
CC are useful as a source of primers or probes for forensic biology and for
CC identifying and cloning NOVX homologues in other cell types. Cells
CC comprising NOVX nucleic acids are useful for producing non-human
CC transgenic animals which are useful for studying the function and
CC activity of NOVX proteins and for identifying and evaluating modulators
CC of NOVX activity. The present sequence represents the laminin alpha-5-
CC like protein NOV1a. The gene encoding NOV1a is located on chromosome 20
XX
SQ Sequence 3600 AA;

Query Match 90.7%; Score 18254.5; DB 5; Length 3600;
Best Local Similarity 91.8%; Pred. No. 0;
Matches 3433; Conservative 18; Mismatches 103; Indels 187; Gaps 23;

QY	1	MAKRLCAGSALCVRGPRGAPLL	LLVGLALLGAARAREEAGGFSLHPPYFNLAEGARIAA	60
Db	1	MAKRLCAGSALCVRGPRGAPLL	-----LHPPYFNLAEGARIAA	39
QY	61	SATCGEEAPARGSPRPTELDYCKLVGGPVAGDPNQITIRGOYCDICTAANSNKAHPASNA	120	
Db	40	SATCGEEAPARGSPRPTELDYCKLVGGPVAGDPNQITIRGOYCDICTAANSNKAHPASNA	99	
QY	121	IDGTERWQSPPLSRGLEYNVNTLDLGOVHVAYVLIKFANSRPDLWVLSMDFGR	180	
Db	100	IDGTERWQSPPLSRGLEYNVNTLDLGOVHVAYVLIKFANSRPDLWVLSMDFGR	159	
QY	181	TYQPWQFFASSKRDCLERFGPQTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRPG	240	
Db	160	TYQPWQFFAASKRDCLERFGPQTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRPG	219	
QY	241	AMNFSYSPLLREFTKATVRLRFLRNTLLGLMGLKALRDPVTRRYYSIKDISIGGRC	300	
Db	220	AMNFSYSPLLREFTKATVRLRFLRNTLLGLMGLKALRDPVTRRYYSIKDISIGGRC	279	
QY	301	VCHGHADACDAKDPDPRLOCTCOHNTCGGTCDRCPCGFNQOPWKPATANSANECQSCN	360	
Db	280	VCHGHADACDAKDPDPRLOCTCOHNTCGGTCDRCPCGFNQOPWKPATANSANECQ-CE	338	
QY	361	CYGHATDCYDPEVDRRRASQSLDGTYYGGGVCIDCOHHTAGVNCERCCLPGFYRSPNHPL	420	
Db	339	CYGHATDCYDPEVDRRRASQSLDGTYYGGGVCIDCOHHTAGVNCERCCLPGFYRSPNHPL	398	
QY	421	DSPHVCRRCNCESDFTDGTCEDLTGRCYCRPNFSGERCDCVCAEGFTGFPSCYPTPSSND	480	
Db	399	DSPHVCRGCNCESDFTDGTCEDLTGRCYCRPNFSGERCDCVCAEGFTGFPSCYREHLPND	458	
QY	481	TREQVLPAGQIVNDCSAACTQGNACRKDPVGRCLCKPNFQGTCHCELCAFGYGGCQP	540	
Db	459	TREQVLPAGQIVSCDCSAACTQGNACRKDPVGRCLCKPNFQGTCHCELCAFGYGGC-P	517	
QY	541	CQCSS---PGVADDRCDPDTGQCRVGFEGATCDRCAPGYF-----HFPLCQLCGCSP	591	
Db	518	ASVPALWPMPTAVTLTQASAG---AEWASRGPHVIAVPPATFTSLASHPURSACVCGCSP	574	
QY	592	AGTLPEGCDEAGRCCLCQPEFAGPHCDRCRPGYHGFNCQACTCDPRGALDQLCGAGGLCR	651	
Db	575	AGTLPEGCDEAGRCCLCQPEFAGPHCDRCRPGYHGFNCQACTCDPRGALDQLCGAGGLCR	634	
QY	652	CRPGYGTACQECSPGFHGFSPCVPHCSAEGSLHAAC---DPRSQCSCR-P-RVTGLR	706	
Db	635	CRPGYGTACQECSPGFHGFPS-----CPATALLKAPCTQVTPVGVGSAAGPVRCGCVT	689	
QY	707	--CDTCVPGAYNFFPYCEAGSCHPAGLAPVDPALPEAQVPCMCRAHVEGPSCDCKPGFWG	764	
Db	690	HVCPVPTTSPTAKPLFTAGSCHPAGLAPVDPALPEVSPPCMCRAHVEGPSCDCKPGFWG	749	

QY	765	LSPSNPEGCTRCSDLRGTLGGVAECQPTGQCFCCKPHVCGQACASCKDGFGLDQADYF	824
Db	750	LSPSNPEGCTRCSDLRGTLGGVAECQ-GTGQCFCCKPHVCGQACASCKDGFGLDQADYF	808
QY	825	GCRSCRCDIGGALQSCSEPRTGVCRCRPNTOGPTCSEPARDHYPDLHLRLLEEAATP	884
Db	809	GCRSCRCDIGGALQSCSEPRTGVCRCRPNTOGPTCSEPARDHYPDLHLRLLEEAATP	868
QY	885	EGHAVRFGFNPLEFENFSWRGYAQMAYQVQPRIVARLNLTSPLDFWLVRVYVNRGAMSVSG	944
Db	869	EGHAVRFGFNPLEFENFSWRGYAQMAYQVQPRIVARLNLTSPLDFWLVRVYVNRGAMSVSG	928
QY	945	RVSREGRSAACANCTAQSQPVAFPPSTEPARITVPORGEGEPFVLNPGTVALRVEAEG	1004
Db	929	RVSREGRSATCANCTAQSQPVAFPPSTEPARITVPORGEGEPFVLNPGTVALRVEAEG	988
QY	1005	VLLDYVWLLPSAYYEALQLRVTEACTYRPSAQSGDNCLLYTHLPDGFPSAAGLEAL	1064
Db	989	VLLDYVWLLPSAYYEALQLRVTEACTYRPSAQSGDNCLLYTHLPDGFPSAAGLEAL	1048
QY	1065	CRQDNSLPRPCPTQQLSPSHPLITCTGSDVDVQLQVAVPQPGRYALVVEYANEDARQEV	1124
Db	1049	CRQDNSLPRPCPTQQLSPSHPLITCTGSDVDVQLQVAVPQPGRYALVVEYANEDARQEV	1108
QY	1125	GVAVHTPQRAPOQQLSLHPCLYSTLCRGRTARTQDHLAVFHLDSVASVRLTAEQARFFL	1184
Db	1109	GVAVHTPQRAPOQQLSLHPCLYSTLCRGRTARTQDHLAVFHLDSVASVRLTAEQARFFL	1168
QY	1185	HGVTLPVPIEEFSPEFVEPRVSCISSHGAFGPNAAACLPSPFPKPPQPIILRDCQVPLPP	1244
Db	1169	HGVTLPVPIEEFSPEFVEPRVSCISSHGAFGPNAAACLPSPFPKPPQPIILRDCQVPLPP	1228
QY	1245	GLPLTHAQDLTPATSPAGPRPRPTAVDPAEPTLLREPOATVFTTHVPTLGRYAFLLH	1304
Db	1229	GLPLTHAQDLTPAMSPAGPRPRPTAVDPAEPTLLREPOATVFTTHVPTLGRYAFLLH	1288
QY	1305	GYQPAHPTFPVEVLINAGRVWQGHANASFCPHGYGCTLVVCEGQALLDVTHSELTVTVR	1364
Db	1289	GYQPAHPTFPVEVLINAGRVWQGHANASFCPHGYGCTLVVCEGQALLDVTHSELTVTVR	1348
QY	1365	VPEGRWLWDYVLVVPENYVSFGYLREEPLDKSYDFISHCAAQGYHISPSSSSLFCRNAA	1424
Db	1349	VPEGRWLWDYVLVVPENYVSFGYLREEPLDKSYDFISHCAAQGYHISPSSSSLFCRNAA	1408
QY	1425	ASLSLFYNNGARPCGCGHEVGATGPTCEPFGGQCPCHAHVIGRDCSRCATGYWGFPPNCRPC	1484
Db	1409	ASLSLFYNNGARPCGCGHEVGATGPTCEPFGGQCPCHAHVIGRDCSRCATGYWGFPPNCRAC	1468
QY	1485	DCGARLDELGTGQICPPTIPDDCLLCQPTFGCHPLVGCCECNCSGPGIQLDPTCD	1544
Db	1469	DCGARLDELGTGQICPPTIPDDCLLCQPTFGCHPLVGCCECNCSGPGIQLDPTCD	1528
QY	1545	TDSGQCKCRPNVTGRRCDTCSPGFHGYPRCPCDCHEAGTAPGVCDPLTGQCYCKENVQ	1604
Db	1529	TDSGQCKCRPNVTGRRCDTCSPGFHGYPRCPCDCHEAGTAPGVCDPLTGQCYCKENVQ	1588
QY	1605	PKDQCSLGTFSLDAANPKGCTRCFCFGATERCRSSSYTRQEFVDMEGWVLLSTDQVVP	1664
Db	1589	PKDQCSLGTFSLDAANPKGCTRCFCFGATERCRSSSYTRQEFVDMEGWVLLSTDQVVP	1648
QY	1665	HERQFGTEMLRADLRHVPEAVPEAFPELYWQAPPSYLGDRVSSYGGTLRYELHSETQ	1724
Db	1649	HERQFGTEMLRADLRHVPEAVPEAFPELYWQAPPSYLGDRVSSYGGTLRYELHSETQ	1708
QY	1725	VFVPMESRPDVLQGNQMSITFLEPAYPTPGHVRGQLQVLEGNFRHTTETRTNVSREELM	1784
Db	1709	VFVPMESRPDVLQGNQMSITFLEPAYPTPGHVRGQLQVLEGNFRHTTETRTNVSREELM	1768
QY	1785	MVLASLEQLQIRALFSQISSAVSLRRVALEVASPAGALASNVELCLCPASVYRGDSCQE	1844
Db	1769	MVLASLEQLQIRALFSQISSAVSLRRVALEVASPAGALASNVELCLCPASVYRGDSCQE	1828

QY 1845 CAPGYRVDVKGLFLGRCVPCQCHGSHDRCLPGSGVCVDCQHNTGEGAHCECQAGFMSSRD 1904
Db 1829 CAPGYRVDVKGLFLGRCVPCQCHGSHDRCLPGSGVCV-CQHNTGEGAHCECQAGFVSSRD 1887
QY 1905 DPSAPCVSCPCPLSVPSNFAEGCVLRGGRTQCLCKPGYAGASCERCAPGFFGNPLVLGS 1964
Db 1888 DPSAPCVSCPCPLSVPSN-----RCAPGFFGNPLVLGS 1920
QY 1965 SCQPCDCSGNDPNLLFSDCDPLTGACRGCLRHTTGPRCEICAPGFYGNALLPGNCTRCD 2024
Db 1921 SCQPCDCSGNDPNLLFSDCDPLTGACRGCLRHTTGPRCEICAPGFYGNALLPGNCTRCD 1980
QY 2025 CTPCGTEACDPHSGHCLCKAGVTGRRCDRCQEGHFGFNGGCGCRPCACGPAEAGESECHPQ 2084
Db 1981 CTPCGTEACDPHSGHCLCKAGVTGRRCDRCQEGHFGFNGGCGCRPCACGPAEAGESECHPQ 2040
QY 2085 SGQCHCRPGTMGPQCRECAPGYWGLPEQGCRRCCQPGGRCDPHTGRCNCPPGLSGERCDT 2144
Db 2041 SGQCHCRPGTMGPQCRECAPGYWGLPEQGCRRCCQPGGRCDPHTGRCNCPPGLSGERCDT 2100
QY 2145 CSQQHQVPVPGGPVGHSHICEVCDHCVVLLDDLERAGALLPAIHEQLRGINASSMAWAR 2204
Db 2101 CSQQHQVPVPGGPVGHSHICEVCDHCVVLLDDLERAGALLPAIHEQLRGINASSMAWAR 2160
QY 2205 LHRLNASIADL-----QSOLRSLPGPRHETAQQOLEVLEQQST 2241
Db 2161 LHRLNASIADLQVLSVLAFFPPQPGPVQAFTFRLPQSOLRSLPGPRHETAQQOLEVLEQQST 2220
QY 2242 SLGQDARRLGQAVGTRDQASQLLAGTEATLGHAKTLLAIRAIVDRTLSELMSQTGHGL 2301
Db 2221 SLPP-----QAVGTRDQASQLLAGTEATLGHAKTLLAIRAIVDRTLSELMSQTGHGL 2273
QY 2302 ANASAPSGEQLRTLAEVERLLWEMRARDLGAPOAAAEALAAQRLARVQEQLSLWE 2361
Db 2274 ANASAPSGEQLRTLAEVERLLWEMRARDLGAPOAAAEALAAQRLARVQEQLSLWE 2333
QY 2362 ENQALATQTRDLRAQHEAGLMDLREALNRAVDATREAQELNSRNOERLEALQRKQELSR 2421
Db 2334 ENQALATQTRDLRAQHEAGLMDLREALNRAVDATREAQELNSRNOERLEALQRKQELSR 2393
QY 2422 DNATLQATLHAARDTLASVFRLLHSLDQAK-EELERLAAASLDGARTPLLQRMQTFSPAGS 2480
Db 2394 DNATLQATLHAARDTLASVFRLLHSLDQAK-EELERLAAASLDGARTPLLQRMQTFSPAGS 2453
QY 2481 KLRLVEAAEAHAQQLGQALNLSSIIIDVNQDRLTQRAIEASNAYSRILOAVQAAEDAAG 2540
Db 2454 KLRLVEAAEAHAQQLGQALNL-SIIIDVNQDRLTQRAIEASNAYSRILOAVQAAEDAAG 2512
QY 2541 QALQQADHTWATVVRQGLVDRAQQLLANSTALEEAMLEQQRLGL-VWA--ALQGART 2595
Db 2513 QALQQADHTWQTVVRQGLVDRAQQLLANSTALEEAMLEQQRLGLGECWAPMGALRPAGT 2572
QY 2596 QLRDVRAKXDQLEAHIAQAQAMLAMDTDETSKKIAHAKAVAAEAQDTATRVQSQLQAMQE 2655
Db 2573 QLRDVRAKXDQLEAHIAQAQAMLAMDTGETSKIAHAKAVAAEAQDTATRVQSQLQAMQE 2632
QY 2656 NVERWQGYEGLRGQDLGQAVLDAGHSVSTLEKTLPLLAKLSILENRGVHNASLAS 2715
Db 2633 NVERWQGYEGLRGQDLGQAVLDAGSAVSTLEKTLPLLAKLSILENRGVHNASLAS 2692
QY 2716 IGRVRELIAQARGAASK-VKVPKFNKGRSGVOLRTPRDLADLAAYTALKFYLOGPEPEPG 2774
Db 2693 IGRVRELIAQARGAASKVKVPKFNKGRSGVOLRTPRDLADLAAYTALKFYLOGPEPEPG 2752
QY 2775 QGTEDRFVVMGSRQATGDMGVSLRDKKXVHVYQLGEAGPAVLSDIDEDIGEQAFAVSLD 2834
Db 2753 QGTEDRFVVMGSRQATGDMGVSLRDKKXVHVYQLGEAGPAVLSDIDEDIGEQAFAVSLD 2812
QY 2835 RTLQFGHMSVTVVERQMIQETKQDTPVAPGAEGLLNLRPDDFVYVGVGYPSTFTPPPLLRFP 2894
Db 2813 RTLQFGHMSVTVVERQMIQETKQDTPVAPGAEGLLNLRPDDFVYVGVGYPSTFTPPPLLRFP 2872
QY 2895 GYRGCIEMDTLNEEVVSLYNFERTFQDLTAVDRCARSKSTGDPWLTGDSYLDGTGFARI 2954

Db 2873 GYRGCIEMDTLNEEVVSLYNFERTFQDLTAVDRCARSKSTGDPWLTGDSYLDGTGFARI 2932
QY 2955 SFDSQISTTKRFEQELRLVSYSGVLFLLKQQSQFCLCLAVQEGSLVLLYDFGAGLKKAVPL 3014
Db 2933 SFDSQISTTKRFEQELRLVSYSGVLFLLKQQSQFCLCLAVQEGSLVLLYDFGAGLKKAVPL 2992
QY 3015 OPPPPLTSASKAIOVFLLGGSRKRVLRVERATVYSVEQNDLELADAYLGGVPPDQLP 3074
Db 2993 OPPPPLTSASKAIOVFLLGGSRKRVLRVERATVYSVEQNDLELADAYLGGVPPDQLP 3051
QY 3075 PSRLWLPPTGGSVRGCVKGIKALGKYVDLKRNTTGVSAAGTADLLVGRAMTFHGHGFLR 3134
Db 3052 PSRLWLPPTGGSVRGCVKGIKALGKYVDLKRNTTGVSAAGTADLLVGRAMTFHGHGFLR 3111
QY 3135 LALSNAVAPLTGNVSYSGFHSQDSALLYRASPDGLCQVSLQQGRVSLQLLRTEVKTOA 3194
Db 3112 LALSNAVAPLTGNVSYSGFHSQDSALLYRASPDGLCQVSLQQGRVSLQLLRTEVKTOA 3171
QY 3195 GFADGAPHYVAFYSNATGVWLYVDDQLQOMKPHRGPPPELOPQEPGPPRLLLGLPESGT 3254
Db 3172 GFADGAPHYVAFYSNATGVWLYVDDQLQOMKPHRGPPPELOPQEPGPPRLLLGLPESGT 3231
QY 3255 IYNFSGCISNVFVQRLGPGQRFVFDLQONLGSVNVSTGCAPALCAQTPGLGPRGLQATARK 3314
Db 3232 IYNFSGCISNVFVQRLGPGQRFVFDLQONLGSVNVSTGCAPALCAQTPGLGPRGLQATARK 3284
QY 3315 ASRRSRQPARHPACMLPPHLRTRTDSYQFGGSLSSHLEFVGLARHNPWPSLSMHVLP 3374
Db 3285 ASRRSRQPARHPACMLPPHLRTRTDSYQFGGSLSSHLEFVGLARHNPWPSLSMHVLP 3332
QY 3375 SRGLLLFTARLRPGSPSLALFLSNHGFVAQMEGLTRLRASQSRQSRPGRWHKVSVRWEK 3434
Db 3333 -----VSVRWEK 3339
QY 3435 NRILLVTDGARAWSOEGPHRQHQGAEBHPQPHTLFVGGLPASSHSSKLPVTVGSGCVKRL 3494
Db 3340 NRILLVTDGARAWSOEGPHRQHQGAEBHPQPHTLFVGGLPASSHSSKLPVTVGSGCVKRL 3399
QY 3495 RLHGRPLGAPTRMAGVTPCILGPLEAGLFFPGSGGVITLDPGATLPDVGLELEVRPLAV 3554
Db 3400 RLHGRPLGAPTRMAGVTPCILGPLEAGLFFPGSGGVITLDPGATLPDVGLELEVRPLAV 3459
QY 3555 TGLIFHLGQARTPPYLOLQVTEKQVLLRADDGAGEFSTSVTRPSVLCGQWHRLAVMKSG 3614
Db 3460 TGLIFHLGQARTPPYLOLQVLPQVLPQVLRADDGAGEFSTSVTRPSVLCGQWHRLAVMKSG 3519
QY 3615 NVLRLEVDAQSNHTVGPPLAAAGAPAPLYLGGLPPEMAVQPPWPAYCGCMRRLAVNRSP 3674
Db 3520 NVLRLEVDAQSNHTVGPPLAAAGAPAPLYLGGLPPEMAVQPPWPAYCGCMRRLAVNRSP 3579
QY 3675 VAMTRSEVHVGAASGCPAA 3695
Db 3580 VAMTRSEVHVGAASGCPAA 3600

RESULT 5
ABB09503
ID ABB09503 standard; protein; 3597 AA.
XX
AC ABB09503;
XX
DT 01-NOV-2007 (first entry)
XX
DE Human laminin alpha-5-like NOV1c protein, SEQ ID NO:6.
XX
KW Human; NOVX; neurological disorder; Alzheimer's disease;
KW Huntington's disease; Parkinson's disease; pain; behavioural disorder;
KW addition; tuberos sclerosis; cancer; immune disorder; allergy;
KW autoimmune disease; myasthenia gravis; asthma; arthritis; diabetes;
KW thyroiditis; cardiovascular disease; hypertension; reproductive disorder;
KW endometriosis; incontinence; psoriasis; scleroderma; alopecia; ulcer;
KW pancreatitis; cirrhosis; glomerular endotheliosis; bacterial infection;

KW polycystic kidney disease; endocrine disorder; obesity; cardiomyopathy;
KW atherosclerosis; cell signal processing-related disorder;
KW metabolic pathway regulation disorder; cytostatic; neuroprotective;
KW antiinflammatory; immunosuppressive; analgesic; antiatherosclerotic;
KW dermatological; antibacterial; antiarthritic; hepatotropic; neurogenesis;
KW differentiation; proliferation; motility; haematopoiesis; wound healing;
KW angiogenesis; forensic biology; transgenic animal; drug screening;
KW gene therapy; NOV1c; laminin alpha-5-like; chromosome 20.

XX Homo sapiens.

OS
XX Key Location/Qualifiers
FH Peptide 1..14
FT /label= Signal_peptide
FT 15..3597
FT Protein
FT /note= "Mature NOV1c protein"

XX WO200253742-A2.

XX 11-JUL-2002.

XX 07-JAN-2002; 2002WO-US000375.

XX 05-JAN-2001; 2001US-0260018P.

XX 08-JAN-2001; 2001US-0260360P.

XX 28-FEB-2001; 2001US-0272411P.

XX 02-MAR-2001; 2001US-0272817P.

XX 05-JUL-2001; 2001US-0303231P.

XX 12-JUL-2001; 2001US-0305060P.

XX 10-SEP-2001; 2001US-0318405P.

XX 12-SEP-2001; 2001US-0318700P.

XX 04-JAN-2002; 2002US-00037417.

XX (CURA-) CURAGEN CORP.

XX Kekuda R, Alsobrook JP, Tehernev VT, Liu X, Spytek KA;

XX Patturajan M, Grosse WM, Lapeley DM, Burgess CE, Vernet CAM, Li L;

XX Gorman L, Edinger S, Sciore P, Ellerman K, Malyankar U;

XX Rotherberg M, Stone D, Boldog F, Guo X, Shenoy S, Anderson D;

XX Padigaru M, Taupier RJ, Miller CE, Eisen A;

XX WPI; 2002-583619/62.

XX N-PSDB; ABQ93881.

XX Novel polypeptides and nucleic acids homologous to transmembrane
PT receptor, thymosin, neuromodulin-like family of proteins for diagnosing,
PT treating cancer, atherosclerosis, neurological, skin and autoimmune
PT disorders.
XX Claim 1c; Page 20-21; 323pp; English.
XX The invention relates to 24 novel human proteins designated NOV1-NOV14
XX (AB09501-AB09524), collectively referred to as NOVX proteins, and
XX nucleic acids encoding them (ABQ93879-ABQ93902). NOVX proteins and
XX nucleotides are useful in the treatment, diagnosis or prevention of NOVX-
XX associated disorders or in the manufacture of a medicament for treating
XX such disorders, with specific applications described for each of the 24
XX NOVX proteins, based on their homology to known proteins. Various
XX disorders are associated with NOVX proteins including neurological
XX disorders (e.g., Alzheimer's, Huntington's and Parkinson's diseases),
XX pain, behavioural disorders, addiction, tuberculous sclerosis, cancers
XX (e.g., colorectal cancer, leukaemia and osteosarcoma), immune disorders
XX (e.g., allergies and autoimmune diseases), myasthenia gravis, asthma,
XX various forms of arthritis, diabetes, thyroiditis, cardiovascular disease
XX (e.g., hypertension), reproductive disorders, endometriosis,
XX incontinence, psoriasis, scleroderma, alopecia, ulcers, pancreatitis,
XX cirrhosis, glomerular endotheliosis, polycystic kidney disease, endocrine
XX disorders, obesity, bacterial infections and particularly cardiomyopathy,
XX atherosclerosis, cell signal processing-related disorders and disorders
XX of metabolic pathway regulation. NOVX nucleic acids and polypeptides may
XX be used to identify cellular receptors or downstream effectors which
XX binds to a NOVX protein, and are also useful as targets for the
XX identification of small molecules that modulate or inhibit processes such

CC as neurogenesis, cell differentiation, cell motility, cellular
CC proliferation, haematopoiesis, wound healing and angiogenesis. NOVX
CC nucleic acid sequences can be used to identify a cell or tissue type and
CC are useful as a source of primers or probes for forensic biology and for
CC identifying and cloning NOVX homologues in other cell types. Cells
CC comprising NOVX nucleic acids are useful for producing non-human
CC transgenic animals which are useful for studying the function and
CC activity of NOVX proteins and for identifying and evaluating modulators
CC of NOVX activity. The present sequence represents the laminin alpha-5-
CC like protein NOV1c. The gene encoding NOV1c is located on chromosome 20
XX
SQ Sequence 3597 AA;

Query Match 90.6%; Score 18231; DB 5; Length 3597;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 3428; Conservative 18; Mismatches 108; Indels 184; Gaps 21;

QY 1 MAKRLCAGSALCVRGPRGPAPLLLVGLALLGAARAREEAGGFSLHPPYFNLAEGARIAA 60
DB 1 MAKRLCAGSALCVRGPRGPAPLL-----LHPPYFNLAEGARIAA 39
QY 61 SATCGEEAPARGSPRTEDLYCKLVGGPVAGGDPNQTIRGQYCDICTAANSNKAHPASNA 120
DB 40 SATCGEEAPARGSPRTEDLYCKLVGGPVAGGDPNQTIRGQYCDICTAANSNKAHPASNA 99
QY 121 IDGTERWWQSPPLSRGLEYNVNTLDLGOVHVAVVLIKFANSRPDLVWLEERSMDFGR 180
DB 100 IDGTERWWQSPPLSRGLEYNVNTLDLGOVHVAVVLIKFANSRPDLVWLEERSMDFGR 159
QY 181 TYQPWQFFASSKRDCLERFGPQTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRPG 240
DB 160 TYQPWQFFAASKRDCLERFGPQTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRPG 219
QY 241 AMNFSYSPLLREFTKATNVRRLRLRLTNTLLHLMGKALRDPVTTRRRYYYSIKDISIGRC 300
DB 220 AMNFSYSPLLREFTKATNVRRLRLRLTNTLLHLMGKALRDPVTTRRRYYYSIKDISIGRC 279
QY 301 VCHGHADACDAKDPDTPRRLQCTCOHNTCGGTCDCRCCPGNFQNPWKPDATANSANECQSCN 360
DB 280 VCHGHADACDAKDPDTPRRLQCTCOHNTCGGTCDCRCCPGNFQNPWKPDATANSANECQ-CE 338
QY 361 CYGHATDCYYDPEVDRRRASQSLDGTYYQGGVVICDQHHTAGVNCERCLPGFYRSPNHPL 420
DB 339 CYGHATDCYYDPEVDRRRASQSLDGTYYQGGVVICDQHHTAGVNCERCLPGFYRSPNHPL 398
QY 421 DSPHVCRRNCESDFTDGTCEDLTGRCYCRPNFSGERCDCVCAEGFTGFPSCYPTFPSSND 480
DB 399 DSPHVCRCNCESDFTDGTCEDLTGRCYCRPNFSGERCDCVCAEGFTGFPSCYRHLPGND 458
QY 481 TREQVLPAGQIVNDCSAAAGTQGNACRKPVRVGRCLCKPNFQGTCELCAFGYGGCQP 540
DB 459 TREQVLPAGQIVNDCSAAAGTQGNACRKPVRVGRCLCKPNFQGTCELCAFGYGGC-P 517
QY 541 CQCSS--PGVADDRCDPDTGQCRVGFEGATCDRCAPGYF-----HFPLCQLCGCSP 591
DB 518 ASVPALEWPMPTAVTLTQASAG--AEWASRGPHVIAVPPATFTSLASHPLRSVAVCGCSP 574
QY 592 AGTLPEGCDEAGRCCLQPEFAGPHCDRCRPGYHGFNCPNCACTCDPRGALDQLCGAGGLCR 651
DB 575 AGTLPEGCDEAGRCCLQPEFAGPHCDRCRPGYHGFNCACTCDPRGALDQLCGAGGLCR 634
QY 652 CRPGYTGTAQCECSPGFHGFPPSCVPCCHCSAEGSLHAAC---DPRSGQCSRPRVTGLRC 707
DB 635 CRPGYTGTAQCECSPGFHGFPPS-----CPATALLKAPCTQPTVTPGVGSAAGP-VRGCGV 688
QY 708 DTCPVGAYNFPFYCEAGSCHPAGLAPVDPALPEAQVPCMCRAHVEGPSDCRCKPFWGLSP 767
DB 689 TRVCPVPTTSPTAKLALATLPVWPPVDPALPEAQVPCMCRAHVEGPSDCRCKPFWGLSP 748
QY 768 SNPEGTRCSCDLRGLGGVAECQPGTGQCFCCKEYHVGQACASCKDGGFFGLDQADYFGCR 827
DB 749 SNPEGTRCSCDLRGLGGVAECQPGTGQCFCCKEYHVGQACASCKDGGFFGLDQADYFGCR 808

QY 828 SCRCDIGALGOSCEPRTGVCRCRPNTQGTCTSEPARDHYLPDLHLRLLEBEAATPEGH 887
Db 809 SCRCDIGALGOSCEPRTGVCRCRPNTQGTCTSEPARDHYLPDLHLRLLEBEAATPEGH 868
QY 888 AVREFGNPLEFENFWRGYAQMAPVQPRIVARLNLTSDDLFWLFRYVNRGAMSVSGRVS 947
Db 869 AVREFGNPLEFENFWRGYAQMAPVQPRIVARLNLTSDDLFWLFRYVNRGAMSVSGRVS 928
QY 948 VREGRSAACANCTAOSQOPVAFPPSTPEAFITVPORGEGEPFVLNPGTWARLVEAEGVLL 1007
Db 929 VREGRSAACANCTAOSQOPVAFPPSTPEAFITVPORGEGEPFVLNPGTWARLVEAEGVLL 988
QY 1008 DYVLLPSAYEALLQLRVTEACTYRPSAQQSGDNCLLYTHPLDGFPSAAGLEALCRQ 1067
Db 989 DYVLLPSAYEALLQLRVTEACTYRPSAQQSPSCCLLYTHPLDGFPSAAGLEALCRQ 1048
QY 1068 DNSLRPPCPTQOLSPSHPLITCTGSDVDVQLQVAVPQGRYALVVEYANEDARQEVGVA 1127
Db 1049 DNSLRPPCPTQOLSPSHPLITCTGSDVDVQLQVAVPQGRYALVVEYANEDARQEVGVA 1108
QY 1128 VHTPQAPQOGLLSLHPCLYSTLCRGRTARDTQDHLAVFHLDSASVRLTAEQARFLLHGV 1187
Db 1109 VHTPQAPQOGLLSLHPCLYSTLCRGRTARDTQDHLAVFHLDSASVRLTAEQARFLLHGV 1168
QY 1188 TLVPIEESPEFVEPRVSCISSHGAFGNPSAACLPSPRFPKPPQPIILRDCQVILPPLGGLP 1247
Db 1169 TLVPIEESPEFVEPRVSCISSHGAFGNPSAACLPSPRFPKPPQPIILRDCQVILPPLGGLP 1228
QY 1248 LTHAQDLTPATSPAGPRPRPPTAVDDAEPTLLREPOATVFTTHVPTLGRYAFLLHGYQ 1307
Db 1229 LTHAQDLTPATSPAGPRPRPPTAVDDAEPTLLREPOATVFTTHVPTLGRYAFLLHGYQ 1288
QY 1308 PAHPTFPVEVLINAGRVWQHANAFCPHGYGCRTLVCEGQALLDVTHSELTVTVRVPE 1367
Db 1289 PAHPTFPVEVLINAGRVWQHANAFCPHGYGCRTLVCEGQALLDVTHSELTVTVRVPE 1348
QY 1368 GRWLWDYVLVVPENVYSFGLREERLDKSYDFISHCAAQGYHISPPSSSLFCRANAASL 1427
Db 1349 GRWLWDYVLVVPENVYSFGLREERLDKSYDFISHCAAQGYHISPPSSSLFCRANAASL 1408
QY 1428 SLFYNNGARPCGCEHVGATGPTCEPFGGQCPCHAHVIGRDCSRCATGYWGFPNCRPCDCG 1487
Db 1409 SLFYNNGARPCGCEHVGATGPTCEPFGGQCPCHAHVIGRDCSRCATGYWGFPNCRPCDCG 1468
QY 1488 ARLCDELGTGICPPRTIPDCLLCQPTQFCHPLVGCRCNCSPGPIQELTDPCTDTS 1547
Db 1469 ARLCDELGTGICPPRTIPDCLLCQPTQFCHPLVGCRCNCSPGPIQELTDPCTDTS 1528
QY 1548 GQCKCRPNVTGRRCDTCSPGFHGYPRCEPCDCHEAGTAPGVCDPLNGQCYCKENVOGPKC 1607
Db 1529 GQCKCRPNVTGRRCDTCSPGFHGYPRCEPCDCHEAGTAPGVCDPLNGQCYCKENVOGPKC 1588
QY 1608 DQCSLGTFLDAANPKGCTRCFCFGATERCRSSSYTRQEFVDMEGWVLLSTDRQVVPHER 1667
Db 1589 DQCSLGTFLDAANPKGCTRCFCFGATERCRSSSYTRQEFVDMEGWVLLSTDRQVVPHER 1648
QY 1668 QPGTEMLRADLRHVPEAVPEAFPELYWQAPPSYLGDRVSSYGGTLRYELHSETQRGDVEV 1727
Db 1649 QPGTEMLRADLRHVPEAVPEAFPELYWQAPPSYLGDRVSSYGGTLRYELHSETQRGDVEV 1708
QY 1728 PMESRPDVVLOQNQMSITFLEPAYPTPGHVHRGQLOLVEGNFRHTETRTNTVSREELNMVL 1787
Db 1709 PMESRPDVVLOQNQMSITFLEPAYPTPGHVHRGQLOLVEGNFRHTETRTNTVSREELNMVL 1768
QY 1788 ASLEQLQIRALFESQISSAVSLRRVALEVASPAGOGALASNVVELCLCPASYRGDSCECAP 1847
Db 1769 ASLEQLQIRALFESQISSAVFLRRVALEVASPAGOGALASNVVELCLCPASYRGDSCECAP 1828
QY 1848 GFYRDVKGLFLGRVCVPCQCHGSHDRCLPGSGVCVDCQHNTEGAHCERCQAGFMSSRDDPS 1907
Db 1829 GFYRDVKGLFLGRVCVPCQCHGSHDRCLPGSGVCV- CQHNTEGAHCERCQAGFVSSRDDPS 1887
QY 1908 APCVSCPCPLSVPSNFAEGCVLRRGRTQCLCKPGYAGASCERCAPGFFGNPLVLGSSCQ 1967

Db 1888 APCVSCPCPLSVPSN-----RCAPGFFGNPLVLGSSCQ 1920
QY 1968 PCDCSGNGDPNLLFSDCDPLTGACRGCLRHTTTPRCETICAPGYGNALLPGNCTRCDCCTP 2027
Db 1921 PCDCSGNGDPNLLFSDCDPLTGACRGCLRHTTTPRCETICAPGYGNALLPGNCTRCDCCTP 1980
QY 2028 CGTEACDPHSGHCLCKAGVTGRRCDRCQEGHFGFGNGCGCRPCACGPAAGSECHPQSGQ 2087
Db 1981 CGTEACDPHSGHCLCKAGVTGRRCDRCQEGHFGFGNGCGCRPCACGPAAGSECHPQSGQ 2040
QY 2088 CHCRPGTMGPQCRECAPGYWGLPEQGCRRCCQPGGRCRCDPHTGRCNCPPGLSGERCDCSTCQ 2147
Db 2041 CHCRPGTMGPQCRECAPGYWGLPEQGCRRCCQPGGRCRCDPHTGRCNCPPGLSGERCDCSTCQ 2100
QY 2148 QHQPVPVGGPVGHSIHCEVCHCVVLLDDLERAGALLPAIHEQLRGINASSMAWARLHR 2207
Db 2101 QHQPVPVGGPVGHSIHCEVCHCVVLLDDLERAGALLPAIHEQLRGINASSMAWARLHR 2160
QY 2208 LNASIADL-----QSQRSPILGPRRHETAQOQLEVLQOQSTSLG 2244
Db 2161 LNASIADLQVLSVLAFFPPQPGPVQAFTRLPQSQRSPILGPRRHETAQOQLEVLQOQSTSLP 2220
QY 2245 QDARRLGGQAVGTRDQASQLLAGTEATLGHAKTLLAAIRAVIDRTLSELMSQTGHLGLANA 2304
Db 2221 P-----QAVGTRDQASQLLAGTEATLGHAKTLLAAIRAVIDRTLSELMSQTGHLGLANA 2273
QY 2305 SAPSGEQLRTLAEVERLLWEMRARDLGAPQAAAAEELAAQRLRLARVQEQLSLWEEHQ 2364
Db 2274 SAPSGEQLRTLAEVERLLWEMRARDLGAPQAAAAEELAAQRLRLARVQEQLSLWEEHQ 2333
QY 2365 ALATQTRDRLAHEAGLMDLREALNRAVDATREAOELNSRNOERLEELQKQELSNDNA 2424
Db 2334 ALATQTRDRLAHEAGLMDLREALNRAVDATREAOELNSRNOERLEELQKQELSNDNA 2393
QY 2425 TLQATLHAARDTLASVFRLLHSLDQAK-BELERLAASLDGARTPLLRMQTFSPAGSKLR 2483
Db 2394 TLQATLHAARDTLASVFRLLHSLDQAK-BELERLAASLDGARTPLLRMQTFSPAGSKLR 2453
QY 2484 LVEAAEAHAQQLGQALNLSIIIDVNQDRLTQRAIEASNAYSRILQAVQAAEDAAQOAL 2543
Db 2454 LVEAAEAHAQQLGQALNLSIIIDVNQDRLTQRAIEASNAYSRILQAVQAAEDAAQOAL 2512
QY 2544 QOADHTWATVVRQGLVDRAQQLLANSTALEAMLOEQRLGL-VWA---ALQGARTQLR 2598
Db 2513 QOADHTWATVVRQGLVDRAQQLLANSTALEAMLOEQRLGLGECWAPMGALRPAGTQLR 2572
QY 2599 DVRAKKDQLEAHIQAAQAMLAMDTDETSSKIAHAKAVAAEQDTATRVQSOLQAMQENVE 2658
Db 2573 DVRAKKDQLEAHIQAAQAMLAMDTDETSSKIAHAKAVAAEQDTATRVQSOLQAMQENVE 2632
QY 2659 RWQOYEGLEGGDLGQAVLDAGHSVSTLEKTLPLQALLAKLSILENRGVHNASLALSASIGR 2718
Db 2633 RWQOYEGLEGGDLGQAVLDAGHSVSTLEKTLPLQALLAKLSILENRGVHNASLALSASIGR 2692
QY 2719 VRELIAQARGAASK-VKVPKMGNGRSGVQLRTPRDLADLAAYTALKFYLQGPPEPGOGT 2777
Db 2693 VRELIAQARGAASKVVKVPKMGNGRSGVQLRTPRDLADLAAYTALKFYLQGPPEPGOGT 2752
QY 2778 EDRFVYMGSRQATGDMGVSLRDKKVHVYVYQGEAGPAVLSDIDIGEQQFAAVSLDRTL 2837
Db 2753 EDRFVYMGSRQATGDMGVSLRDKKVHVYVYQGEAGPAVLSDIDIGEQQFAAVSLDRTL 2812
QY 2838 QFGHMSVTVERQMIQETKGDITVAPGAEGLLNLRPDDFVYVGVGYPSTFTPPPLLRFPGYR 2897
Db 2813 QFGHMSVTVERQMIQETKGDITVAPGAEGLLNLRPDDFVYVGVGYPSTFTPPPLLRFPGYR 2872
QY 2898 GCIEMDTLNEEVVSLYNFERTFQDITAVDRPCARSKSTGDPWLTGSLYDGTGFARISFD 2957
Db 2873 GCIEMDTLNEEVVSLYNFERTFQDITAVDRPCARSKSTGDPWLTGSLYDGTGFARISFD 2932
QY 2958 SQISTTKRFEQELRLVSYSGVLFLLKQSQFLCLAVQEGSLVLLYDFGAGLKKAVPLQPP 3017

Db 2933 SQISTTKRFEQELRLVSYSGVLFELKQSQFLCLAVQEGSLVLLYDFGAGLKKAVPLQPP 2992
Qy 3018 PPLTSASKAIQVFLGGSRKRVLRVERATVYSVEQNDLELADAYLGGVPPDQLPPSL 3077
Db 2993 PPLTSASKAIQVFLGGSRKRVLRVERATVYSVEQNDLELADAYLGGVPPDQL-PSL 3051
Qy 3078 RWFPTGCGSVRGCVKGKIKALGVYDLKRLNTTGVSAAGTADLLVGRAMTFHGHGFLRLAL 3137
Db 3052 RRLFTGCGSVRGCVKGKIKALGVYDLKRLNTTGVSAAGTADLLVGRAMTFHGHGFLRLAL 3111
Qy 3138 SNVAPLTGNVYSGFGFHSQAQDSALLYRASPDGLCOVLSQGRVSLQLLRTEVKTQAGFA 3197
Db 3112 SNVAPLTGNVYSGFGFHSQAQDSALLYRASPDGLCOVLSQGRVSLQLLRTEVKTQAGFA 3171
Qy 3198 DGAPHYVAFYSNATGVWLYVDDQLQMKPHRGPPPELQPDGEGPRLLGLGLESSTIYN 3257
Db 3172 DGAPHYVAFYSNATGVWLYVDDQLQMKPHRGPPPELQPDGEGPRLLGLGLESSTIYN 3231
Qy 3258 FSGCISNVFVQRLGPPQVFDLQNLGSVNVSTGCAPALQATPGLPRGLQATARKASR 3317
Db 3232 FSGCISNVFVQRLGPPQVFDLQNLGSVNVSTGCAPALQATPGLPRGLQATARKASR 3284
Qy 3318 RSRQPARHPACMLPPHLRTTRDSYQFGSLSSHLEFVGILARHNWPSLSMHVLPSSRG 3377
Db 3285 RSRQPARHPACMLPPHLRTTRDSYQFGSLSSHLEFVGILARHNWPSLSMHVLPSSRG 3329
Qy 3378 LLLFTARLRPGSPSLALFLSNHGFVAQMEGLGTRRLRAQSRQRSPRGRWHKVSVRWEKNRI 3437
Db 3330 -----VSVRWEKNRI 3339
Qy 3438 LLVTDGARAWSEGGPHRQHQGAEPHPTLFGGLPASHSSKLPVTVGFGCVKRLRLH 3497
Db 3340 LLVTDGARAWSEGGPHRQHQGAEPHPTLFGGLPASHSSKLPVTVGFGCVKRLRLH 3399
Qy 3498 GRPLGAPTRMAGVTPCILGPLEAGLFFPGSGGVITLDLPGATLPDVGLELEVRPLAVTGL 3557
Db 3400 GRPLGAPTRMAGVTPCILGPLEAGLFFPGSGGVITLDLPGATLPDVGLELEVRPLAVTGL 3459
Qy 3558 IFHLGQARTPPYLQVTEKQVLLRADDDGAGEFSTSVTRPSVLCGOWHRLAVMKSGNVL 3617
Db 3460 IFHLGQARTPPYLQVTEKQVLLRADDDGAGEFSTSVTRPSVLCGOWHRLAVMKSGNVL 3519
Qy 3618 RLEVDAQSNHTVGLLAAAAGAPAPLYLGLPEPMAVQPPPAYCGCMRRLAVNRSVPAM 3677
Db 3520 RLEVDAQSNHTVGLLAAAAGAPAPLYLGLPEPMAVQPPPAYCGCMRRLAVNRSVPAM 3579
Qy 3678 TRSVEVHGAVGASGCPAA 3695
Db 3580 TRSVEVHGAVGASGCPAA 3597

RESULT 6
ABB81589
ID ABB81589 standard; protein; 3635 AA.
XX
AC ABB81589;
XX
DT 19-SEP-2002 (first entry)
XX
DE Mouse laminin alpha 5 amino acid sequence SEQ ID NO:4.
XX
KW Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;
KW tissue repair development; laminin; healing; vascular tissue;
KW re-endothelialisation; vascular injury; cell attachment; cell stasis;
KW proliferation; migration.
XX
OS Mus musculus.
XX
PN WO200250111-A2.
XX
PD 27-JUN-2002.
XX
PF 21-DEC-2001; 2001WO-US051035.

XX 21-DEC-2000; 2000US-0257449P.
PR 28-MAR-2001; 2001US-0279282P.
PR 13-NOV-2001; 2001US-00279282.
XX
PA (BIOS-) BIOSTRATUM INC.
XX
PI Tryggvason K, Doi M, Thyboll J;
XX
DR WPI; 2002-557650/59.
XX N-PSDB; ABQ72907.
PT New human laminin-10 proteins, useful for accelerating the healing of
PT vascular tissue, improving the biocompatibility of grafts, or for
PT promoting re-endothelialization at the site of vascular injuries.
XX
PS Claim 9; Page 94-105; 231pp; English.
XX
CC The present invention describes human laminin alpha 5. Also described is
CC an isolated laminin 10. Laminin 10 has vulnery activity. Laminins are
CC useful in maintaining cell/tissue phenotype as well as promoting cell
CC growth and differentiation in tissue repair development. Specifically,
CC laminin 10 can be used for accelerating the healing injuries of vascular
CC tissue, improving the biocompatibility of grafts useful for treating such
CC injuries, for promoting re-endothelialisation at the site of vascular
CC injuries, and promote cell attachment and subsequent cell stasis,
CC proliferation, differentiation, and/or migration. The present sequence
CC represents mouse laminin alpha 5 which is used in the exemplification of
CC the present invention
XX
SQ Sequence 3635 AA;
Query Match 78.7%; Score 15839; DB 5; Length 3635;
Best Local Similarity 79.4%; Pred. No. 0;
Matches 2874; Conservative 277; Mismatches 452; Indels 18; Gaps 8;
Qy 79 DLYCKLVGGPVAGDPNQTIRGOYCDICTAANSNKAHPASNAIDGTERWQSPPLSRGLE 138
Db 1 DLYCKLVGGPVAGDPNQTIRGOYCDICTAANSNKAHPASNAIDGTERWQSPPLSRGLE 60
Qy 139 YNEVNTLDLGQVHVAVVLIKFANSRPPDLWVLSRMDFGRTYQWPQFASSKRDCLER 198
Db 61 YNEVNTLDLGQVHVAVVLIKFANSRPPDLWVLSRMDFGRTYQWPQFASSKRDCLER 120
Qy 199 FGPOTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRPGAMNFSYSLPREFTKATN 258
Db 121 FGPOTLERITQDDDVICTTEYSRIVPLENGEIVVSLVNGRPGALNFSYSLPREFTKATN 180
Qy 259 VRLRFLRTNTLLHLMGKALRDPVTTRRYYSYKIDISIGRCVCHGHADCAKDPDTPF 318
Db 181 IRLRFLRTNTLLHLMGKALRDPVTTRRYYSYKIDISIGRCVCHGHADCAKDPDTPF 240
Qy 319 RLQCTCQHNTCGGTCDRCPCGFGNQPPKATANSANECQSCNCGHATDCYDPEVDRRR 378
Db 241 RLQACACQHNTCGGSCDRCCPGFNQPPKATANSANECQSCNCGHATDCYDPEVDRRN 300
Qy 379 ASQSLDGTQGGVVICDQHHTAGVNCERCLPGFYRSPNHPDLSPHVCRRNCESDFTDG 438
Db 301 ASQNDNVYQGGVVICDQHHTAGVNCERCLPGFYRSPNHPDLSPHVCRRNCESDFTDG 360
Qy 439 TCEDLTGRCYCRPNFSGRCDVCAEGFTGFPSCYPTPS-SSNDTREQLVPAQIVNCDCS 497
Db 361 TCEDLTGRCYCRPNFTGELCAACAEYTDFFHCYPLPSFPNHTREQLVPAQIVNCDCN 420
Qy 498 AAGTQGNACRKPVRGRCCLKPNFQGTGTHCELCAFGYGPQCPQCSSPGVADRCDDPD 557
Db 421 AAGTQGNACRKPVRGRCCLKPNFQGTGTHCELCAFGYGPQCPQCSSPGVADRCDDPD 480
Qy 558 GQCRVGVFEAGTCDCRCAFGYFHFPLCLQCGSPAGTLPPEGDEAGRCCLQPEFAGPHCD 617
Db 481 GQCMRTGFEGRDCHCALGYFHFPLCLQCGSPAGTLPPEGDEAGRCCLQPEFAGPHCD 540
Qy 618 RCRPGYHGFNQCACCTCDPRGALDQLCGAGGLCRCPGYGTACQECSPGFHGFPCVPC 677

Db 541 RCLPGHYGDCHACADPRGALDQCGVGLCHCRPGNTGATCQECSPGYGFPSCIPC 600
Qy 678 HCSAEGSLHAAACDPRSGQCSRRPVTGLRCDTCVPGAYNFPYCEAGSCHPAGLAPVDPAL 737
Db 601 HCSADGSLHTTCDPTTGQCRCPRTVGLHCDMCPVPGAYNFPYCEAGSCHPAGLAPAL 660
Qy 738 PEAVPCMCRAHVEGPSCDCKPKPGWGLSPSNEGCTRCSCDLRGLTGLGVAECQPGTQC 797
Db 661 PETQAPCMCRAHVEGPSCDCKPKPGWGLSASNEGCTRCSCDPRGLTGLGVTECQ-GNGQC 719
Qy 798 FCKPHVCGQACASCKDGFGLDQADYFGCRSCRCIDIGGALGQSCERTGVCRCPNTQGP 857
Db 720 FCKAHVCGKTCACACKDGFGLDYADYFGCRSCRCIDVGALGQGCERTGACRCRNTQGP 779
Qy 858 TCSEPARDHLYLDDLHLRLLELEAAATPEGHAVRFGFNPLEFENFWSRGYAMAQAPVQPRIV 917
Db 780 TCSEPAKDHLYLDDLHMRLELEAAATPEGHAVRFGFNPLEFENFWSRGYAHMMAIQPRIV 839
Qy 918 ARNLTSPLDLFWLVFRYVNRGAMSVSGRVSVREEGRSAAACANCTAQSQPVAFPPSTEPAF 977
Db 840 ARNLVTSPLDLFRLVFRYVNRGSTSVNGQISVREEGKLSCTNCTEQSQPVAFPPSTEPAF 899
Qy 978 ITVPORGFEPPFVLPNGTVALRVEAEGVLLDYVLLPSAYYEAALLQLRVTEACTYRPSA 1037
Db 900 VTVPORGFEPPFVLPNGIYALLVEAEGVLLDYVLLPSTYYEAALLQHRVTEACTYRPSA 959
Qy 1038 QQSGDNCLLYTHLPDGPSPSAAAGLEALCRQNSLPRPCPTQLSPSHPLITCTGSDVDV 1097
Db 960 LHSTENCLVYAHLPDGPSPSAAAGTEALCRHNSLPRPCPTQLSPSHPLATCFGSDVDI 1019
Qy 1098 QLQVAVPQPGRYALVVEYANEDARQEVGVAVHTPQAPQOGLLSLHPCLYSTLCRGYARD 1157
Db 1020 QLENVAVPQPGQYVLYVEYGEDSHQEMGVAVHTPQAPQOGLVNLHPCPYSSLCRSPARD 1079
Qy 1158 TQDHLAVFHLDEASVRLTAEQARFFLHGVTLPVPIEBFSPFVBEPRVSCISSHGAFGNS 1217
Db 1080 TQHLAIFHLDEASIRLTAEQAHFFLHVSVTLPVVEEFSTFVBEPRVFCVSSHGTENESS 1139
Qy 1218 AACLPSRFPKPPQPIILRDQCQVILPPLPGLPLTHAQDLTPATSPAGRP RPPTAVDPDAEP 1277
Db 1140 AACLASRFPKPPQPIILKDCQVLPPLPDLPLTQSQELSPGAPPEGPQRPPTAVDPNAEP 1199
Qy 1278 TLLREPOATVFTTHVTPLGRYAFLLHGYQPAHPTFPVEVLINAGRVWQHANASFCPHG 1337
Db 1200 TLLRHPQGTVFTTQVFTLGRYAFLLHGYQVHPSPFVEVLINGRIWQHANASFCPHG 1259
Qy 1338 YGCRTLVCEGOALLDVTHSELTVTVRVPGRWLWLDYLVVBPENVISFGLYLRREPLDKS 1397
Db 1260 YGCRTLVCEGOATMLDVTDNELTVTVRVPGRWLWLDYLVVBPENVISFGLYLRREPLDKS 1319
Qy 1398 YDFISHCAAQGYHISPSSSSLFCRNAASLSLFYNNGARPCGCGHEVGATGPTCEPFGQC 1457
Db 1320 YDFISHCATQGYHISPSSSSLFCRNAATSLSLFYNNGALPCGCGHEVGAVSPTCEPFGQC 1379
Qy 1458 PCHAHVIGRDCSRCATGYWGFNCRPCDCGARLDELGTQCICPPRTIPPDCCLCQPTF 1517
Db 1380 PCRGHVIGRDCSRCATGYWGFNCRPCDCGARLDELGTQCICPPRTVPPDCCLVCPQSF 1439
Qy 1518 GCHPLVGCCECNCSPGICQELTDPTCDTSGQCKCRPNVTGRCDTCSPGFHYGPRCRPC 1577
Db 1440 GCHPLVGCCECNCSPGVQELTDPTCDMDSGQCRPNVAGRCDTCAPGFYGYPSRCP 1499
Qy 1578 DCHEAGTAPGVCDPLTGQCYCKENVOGPKDQCSLGTFSLDANPKGCTRCFCGATERC 1637
Db 1500 DCHEAGTMASVCDPLTGQCHCKENVOGSRCDQCRVGTFSLDANPKGCTRCFCGATERC 1559
Qy 1638 RSSSYTRQEFVDMGWLLSTDRQVPHRQPGTEMLRADLRHVPFAVPEAFPELYWQAP 1697
Db 1560 GNSNLARHEFVDMGWLLSSDRQVPHRPEIELLHADLR---SVADTFSELYWQAP 1615
Qy 1698 PSYLGDRVSSYGGTIRYELHSETQRGDVFPMESRPDVVLQGNQMSITFLEPAYTPGHV 1757

Db 1616 PSYLGDRVSSYGGTIRYELHSETQRGDIFIPYESRBDVVLQGNQMSIAFLELAYPPPGQV 1675
Qy 1758 HRGQLQVVEGNFRHTETRTNVSREELMMVLASLEQLQIRALFSQISSAVSLRRVALEVAS 1817
Db 1676 HRGQLQVVEGNFRHLETHNPVSREELMMVLASLEQLQIRALFSQISSAVSLRRVALEVAS 1735
Qy 1818 PAGQALASNVELCLCPASYRSPSCQECAPGFYRDVKGFLGRCVPCQCHGSHDRCLPGS 1877
Db 1736 EAGRPPASNVELCMCPANVRGDSQECAPGYRDTKGLGRCVPCQCHGSHDRCLPGS 1795
Qy 1878 GVCVDCQHNTEGAHCERCQAGMSS-RDDPSAPCVSCPCLSPVPSNMFAGCVLGGRTQ 1936
Db 1796 GICVGCQHNTEGDQECRCRPGFVSSDPSPNAPSPCVSCPCLAVPSNMFADGCVLNGRTQ 1855
Qy 1937 CLCKPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSGNDPNLLFSDCDPLTGACRGCLR 1996
Db 1856 CLCRPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSGNDPNMIFSDCDPLTGACRGCLR 1915
Qy 1997 HTTGPRCEICAPGFYGNALLPGNCTRCDCCTPCGTEACDPHSGHCLCKAGVTGRRCDRCQE 2056
Db 1916 HTTGPHCERCAPGFYGNALLPGNCTRCDCSPCGTETCDPQSGRCLCKAGVTGRRCDRCLE 1975
Qy 2057 GHFGNCGGCRPCACGPAAGSECHPQSGQCHCPGTMGPQCRECAPGYWGLPEQGCRR 2116
Db 1976 GYFGFEOCGCRPCACGPAAGSECHPQSGQCHCPGTMGPQCRECAPGYWGLPEKGCRR 2035
Qy 2117 CQCPGGRCDPHTGRCNCPCPGISGERCDTCSQHQHVVPVPGPVGHSIHCEVCDHCVVLLD 2176
Db 2036 CQCPRGHCDPHTGCHCTCPGISGERCDTCSQHQHVVPVPGKPGHGIHCEVCDHCVVLLD 2095
Qy 2177 DLERAGALLPAIHEQLRGINASSMAWARLHRLNADIADLQSLRSLPGRHETAQOQLEVL 2236
Db 2096 DLERAGALLPAIREQLQGINASSAAWARLHRLNADIADLQSKLRRPPGPRYQAAQLOTL 2155
Qy 2237 EQQSTSLGQDARRLGGQAVGTRDQASQLLAGTEATLGHAKTLLAAIRAVDRTLSELMSQT 2296
Db 2156 EQQSTSLQDTERLGSQATGVQGOAGQLDTESTLGRAQKLESVRAVGRALNELASRM 2215
Qy 2297 GHLGLANASPSGEQLLRLARVERLLWEMRARDIGAPQAAAEAEALAAQRLARVQEQ 2356
Db 2216 GQSGPDALVPSGEQLRWALAEVERLLWDMTRDLDGAQGAVAEAEALAAQRLMARVQEQ 2275
Qy 2357 SSLWEENQALATQTRDLRAQHEAGLMDLREALNPAVDATREAEELNSRNOERLEALQK 2416
Db 2276 TSFWEENQSLATHIRDQLAQYESGLMDLREALNPAVDATREAEELNSRNOERLEALQK 2335
Qy 2417 QELSRDNATLOATLHARDTLASVFRLLHSLDQAKEELERLAASLDGARTPLLMQTF 2476
Db 2336 QELSDQATLKTATLOASLILGHVSELLOQIDQAKEDLEHLAASLDGARTPLLMQTF 2395
Qy 2477 PAGSKRLVEAAEAHAQOLGOLALNLSSIIIDVNDRLTORAIEASNAYSRILOAVQAAE 2536
Db 2396 PASSKVDLVEAAEAHAQOLGOLALNLSSIIIDVNDRLTORAIEASNAYSRILOAVQAAE 2455
Qy 2537 DAAGQALQOQADHTWATVVRQGLVDRAQOQLLANSTALEEAMLEQOQLGLVWALQGARTQ 2596
Db 2456 DAAGQALROASRTWEMVVRQGLAAGAROLLANSALAEETILHGOGLAQRLOAAGIQ 2515
Qy 2597 LRDVRAKQDQLEAHIQAAQAMLMDTDETSKIAHAKAVAAEAQDTATRVQSOLOQAMQEN 2656
Db 2516 LHNWARKNQLAQIQEAQAMLMDTDETSKIAHAKAVAAEAQDTATRVQSOLOQAMQEN 2575
Qy 2657 VERWQOQYEGRLRGQDLGOAVLDAGHSVSTLEKTLPLQLAKLSILENRGVHNASLALSASI 2716
Db 2576 VERWQOQYEGRLRGQDLGOAVLDAGHSVSTLEKTLPLQLAKLSILENRGVHNASLALSANI 2635
Qy 2717 GRVRELIAQARGAASAKVYPMKFNKNGRSGVOLTPRDLADLAAYTALKFYVQ--PEPEPG 2774
Db 2636 GRVRELIAQARGAASAKVYPMKFNKNGRSGVOLTPRDLADLAAYTALKFYVQ--PEPEPG 2695
Qy 2775 QGTEDRFVYMGSRQATGDYMGVSLRDKKVVHVVYQGEAGPAVLSDIDIGEQFAAVSLD 2834
Db 2696 KNTGDHFLVYMGSRQATGDYMGVSLRDKKVVHVVYQGEAGPAVLSDIDIGEQFAAVSID 2755

QY 2835 RTLQFGHMSVTVVEROMIQETKGTDTVAPAGAGLLNLRPDDFVFVGGYPTSTFTPPPLLRFP 2894
Db 2756 RTLQFGHMSVTVVEROMIQETKGTDTVAPAGAGLLNLRPDDFVFVGGYPTSTFTPPPLLRFP 2815
QY 2895 GYRGCIEMDTLNEEVVSLYNFERTFQDITAVDRPCARSKSTGDPWLTGSLYDGTGTFARI 2954
Db 2816 GYLGCIEMETLNEEVVSLYNFERTFQDITAVDRPCARSKATGDPWLTGSLYDGTGTFARI 2875
QY 2955 SFDQSISTTKRFEQELRLVSYSGVLFELKQSQFCLAVQESGLVLLYDFGAGLKKAVPL 3014
Db 2876 SFEKQFSNTRKFDQELRLVSYNGIIFELKQSQFCLAVQESGLVLLYDFGAGLKKADPL 2935
QY 3015 QPPPLTSASAKAIQVFLGGRKRVLRVERATVYSVEQDNDLEADAYLGGVPPDQLP 3074
Db 2936 QPPQALTAASKAIQVFLLAGNRKRVLRVERATVFSVDQDNMLEMADAYLGGVPPDQLP 2995
QY 3075 PSLRWLFPTGSGVRGCVKGIKALGYVDLKRLLNTTGVSAAGCTADLLVGRAMTFHGHGFLR 3134
Db 2996 LSLRQLFPSPGSGVRGCVKGIKALGYVDLKRLLNTTGISFGCTADLLVGRMTTFHGHGFLP 3055
QY 3135 LALSNVAPLTGNVYSGFGFHSQAQDSALLYRASPDGLQVSLQGRVSLQLLRTVEVTKQA 3194
Db 3056 LALPDVAPITEVYVYSGFGFRGTQDNLLYRTSPDGPYQVSLRQGHVTLRFMNQEVETQR 3115
QY 3195 GFADGAPHYVAFYSNATGVWLYVDDQLQOMKPHRGPPPELPQPEGPRLLGLLPESGT 3254
Db 3116 VFADGAPHYVAFYSNATGVWLYVDDQLQOMKPHRGPPPELPQPEGPRLLGLLPVSGT 3175
QY 3255 IYFSGCISNVFQRLGQPVDFDLQNLGSLVNVSTGCPALQATPGLGPRGLQATARK 3314
Db 3176 FHNFGCISNVFQRLGQPVDFDLQNLGSLVNVSTGCPALQATPGLGPRGLQATARK 3228
QY 3315 ASRRSRQPARHPACMLPPHLRTRTDSYQFGSLSHLEFVGLARHNPWPSLSMHVLPK 3373
Db 3229 VSRSRQPSQDLACTPPLGPTIQDAYQFGGFLPSYQFVGISPSHRNRLHLSMLVRPHA 3288
QY 3374 SSRGLLLFTARLPSPSLALFLSNHGFVAQMEGLGTRLRQAQSRORRPPGRWHKVSVRWE 3433
Db 3289 ASQGLLLSTAPMSGRSPSLVFLNHGFVAQTEGPGPRQLQVQSRQHSRAGQWHRVSVRWG 3348
QY 3434 KNRILLVTDGARAWSQEGPHRQHQGAEPHPOHTLTVGGLPASSHSSKLPVTVGFGSCVKR 3493
Db 3349 MQQIQLVVDGSGTQSKALHHRVPRAPRPPQYTLVSVGLPASSYSKLPVSVGFGSGLKK 3408
QY 3494 LRLHGRPLGAPTRMAGVTPCILGPLEAGLFFPGSGGVITLDPGATLPDVGLELEVRPLA 3553
Db 3409 LQLDKQPLRTPTQMGVTPCVSGPLEDGLFFPGSEGVTLPLPKAKMPYVSLELEMRPLA 3468
QY 3554 VTGLIFHLGQARTPPYLOLVTEKQVLLRADDGAGEFSTSVTRPSVLCDGQWHRRLAVMKS 3613
Db 3469 AAGLIFHLGQALATPYMQLKVLTEQVLLQANDGAGEFSTVTPK-LCDGRWHRVAVIMG 3527
QY 3614 GNVLRLEVDQAQSNHTVGPPLAAAGAPAPLYLGLPEPMAVQPPWPAYCGCMRRLAVNRS 3673
Db 3528 RDTLRLEVDQSNHTTGRPLPESLAGSPALLHLGSLPKSSTARPELPAYRGCLRKLKLLINGA 3587
QY 3674 PVAMTRSEVHGAVGASGCPA 3694
Db 3588 PVNVTSVQIQAVGMRGCP 3608

RESULT 7
AAM50357
ID AAM50357 standard; protein; 3635 AA.
XX AC AAM50357;
XX 18-FEB-2002 (first entry)
XX Mouse laminin-15 alpha 5 chain.
XX DE Mouse laminin-15; mouse; retina; eye; therapy; ophthalmological;
KW Laminin-15; mouse; retina; eye; therapy; ophthalmological;

KW antiinflammatory; rod dystrophy; rod-cone dystrophy;
XX retinitis pigmentosa; macular degeneration; retinal detachment.
OS Mus musculus.
XX WO200183516-A1.
XX 08-NOV-2001.
XX 01-MAY-2001; 2001WO-US013943.
XX 01-MAY-2000; 2000US-0200863P.
XX (MASS-) MASSACHUSETTS GEN HOSPITAL.
XX Burgeson RE, Brunken W, Champliand M, Hunter D;
XX WPI; 2002-041478/05.
XX N-PSDB; AAI70816.
XX Novel substantially pure preparation comprising laminin having laminin
PT chain-alpha 5, beta 2, and gamma 3, useful for treating retinal disorders
PT such as retinitis pigmentosa, macular degeneration, retinal detachment.
XX Disclosure; Fig 1A-B; 15pp; English.

The present sequence is that of the alpha 5 chain of mouse laminin-15, a novel member of the laminin family that is produced in the retina. The retina produces 2 novel laminin trimers: laminin-14 (alpha 4, beta 2, gamma 3) and laminin-15 (alpha 5, beta 2, gamma 3). These are expressed within the inter-photorceptor matrix and in the outer plexiform layer, and may serve to stabilise retinal synapses. The invention provides laminin-15 preparations and cells comprising a nucleic acid encoding the laminin alpha 5, beta 2 and gamma 3 chains, and which are capable of producing laminin-15. The laminin-15 preparation is used in claimed methods of: increasing retinal immunophoreceptor matrix stability; increasing the stability of retina photoreceptor compounds, especially an outer segment, inner segment or synapse; increasing retina adhesion; treating a disorder associated with retina degeneration, especially rod dystrophy, rod-cone dystrophy, retinitis pigmentosa, macular degeneration and retinal detachment; increasing the stability of synapses of the central nervous system or peripheral nervous system; stimulating neuroregeneration, axon outgrowth or synapse formation; preparing an implant, e.g. a catheter, artificial joint, retinal implant, timed releasing device, neural cell growth guide or artificial tissue, by coating with the laminin-15 preparation; and increasing photosensitivity by implanting a tip coated with the laminin-15 preparation into an eye. The laminin may be recombinant, and the 3 chains co-expressed in the same cell or expressed in different cells

Query Match 78.7%; Score 15839; DB 5; Length 3635;
Best Local Similarity 79.4%; Pred. No. 0;
Matches 2874; Conservative 277; Mismatches 452; Indels 18; Gaps 8;
QY 79 DLYCKLVGGPVAGGDPNQTIRGOYCDICTAANSNKAHPASNAIDGTERWQSPPLSRGLE 138
Db 1 DLYCKLVGGPVAGGDPNQTIRGOYCDICTAANSNKAHPASNAIDGTERWQSPPLSRGLE 60
QY 139 YNEVNVTLDLGQVHFVAYVLIKFANSRPRDLWVLSRMDPGRTYQPFQFASKRDCLER 198
Db 61 YNEVNVTLDLGQVHFVAYVLIKFANSRPRDLWVLSRMDPGRTYQPFQFASKRDCLER 120
QY 199 FGPOTLERITRDDAAICTEYSRIVPLENGEIVSVLVNRPAGANFYSPLLEFTKATN 258
Db 121 FGPOTLERITQDDDVICTEYSRIVPLENGEIVSVLVNRPAGANFYSPLLEFTKATN 180
QY 259 VRLRFLRNTLLGHLMGKALRDPPTVTRRYYSIKDISIGRCVCHGHADACADKDPDPF 318
Db 181 IRLRFLRNTLLGHLMGKALRDPPTVTRRYYSIKDISIGRCVCHGHADACADKDPDPF 240
QY 319 RLQCTCQHNTCGGTCDRCPCFNFQKPKPATANSANECQSCNCYGHATDCYDPEVDRRR 378

Db 241 RLQACQHNTCGGSCDRCCGFGNQPKPATTDTSANECQSCNCHGHAYDCYYDPEVDRRN 300
QY 379 ASQSLDGTYYQGGVVCIDCOHHTAGVNCERCLPGFYRSNHPPLDSPHVRCNCESDFTDG 438
Db 301 ASQNDNVIYQGGVCLDCOHHHTGINCERCLPGFRAPOPLDSPHVRCDCESDFTDG 360
QY 439 TCEDLTGRCYCRPNFSGERCDVCAEGFTGFPSCYPTPS - SSNDTREQVLPAQIIVNCDCS 497
Db 361 TCEDLTGRCYCRPNFTGELCAACAEGYTDFFHCYELPLPSFPHNDTREQVLPAQIIVNCDCN 420
QY 498 AAGTQGNACRKOPRVGRCLCKPNFQGTCELCAPOFYGPGCCQPCQSSPGVADDDRCDDPT 557
Db 421 AAGTQGNACRKOPRLGRCVKPNFRGAHCELCAPOFGHPSCHPCQCSSPGVANSLCDPES 480
QY 558 GQCRVGFEGATCDRCAPGFHFPPLGQLCGCSPAGTLPEGCD EAGRLCQDFEAGPHCD 617
Db 481 GQCMRTGFEGRCDHICALGYFHFPLCQLCGCSPAGTLPEGCD EAGRCQCRPGFDGPHCD 540
QY 618 RCRPGYHGFNCACTCDPRGALDQLCGAGGLCRCPGYGTACQECSPGFHFPSCVPC 677
Db 541 RCLPGYHGYPDCHACACDPRGALDQCGVGGLCHCRPGNTGATCQECSPGFYFPCIPC 600
QY 678 HCSAEGSLHAACDPRSGQSCRPRVTGLRCDTCVPGAYNFFPYCEAGSCHPAGIAPVDPAL 737
Db 601 HCSADGSLHTTCDPTTGQCRCPRTVTLHCDMCPVSNYFFPYCEAGSCHPAGIAPANPAL 660
QY 738 PEAPVPCMCRAHVEGSPCDRCCKPGFWGLSPSNPEGCTRCSDLRGLTGLGVABEQPGTGQC 797
Db 661 PETQAPCMCRAHVEGSPCDRCCKPGYWLASNPNEGCTRCSDPRGTLGGVTECQ - GNGQC 719
QY 798 FCKPHVCGQACASCKDGFGLDQADYFGCRSCRCIDIGALGQSCPTGVCRCRPNTQGP 857
Db 720 FCKAHVCGKTCACACKDGFGLDYADYFGCRSCRCIDVGGALGQCEPKTGACRCRPNTQGP 779
QY 858 TCSEPARDHVLPDLHLHLRLELEBAATPEGHAVRFGFNPLEFENFSWRGYAQMAYVQPRIV 917
Db 780 TCSEPAKDHVLPDLHLMRLELEBAATPEGHAVRFGFNPLEFENFSWRGYAHMMAIQPRIV 839
QY 918 ARLNLTSPDLFWLVFRVYVNRGAMSVGRVSVREEGRSAAACANTAOQOPVAPRSTEPAF 977
Db 840 ARLNVTSPDLFRLVFRVYVNRGSTSVNGQISVREEGLSSCTNCTEQSQOPVAFPRSTEPAF 899
QY 978 ITVPQRGFGEFVLNPGTWMALRVEABGVLLDYVVLPLPSAYEAAALLQLRVTEACTYRPSA 1037
Db 900 VTVPQRGFGEFVLNPGIWMALRVEABGVLLDYVVLPLPSIYEAALLQHRVTEACTYRPSA 959
QY 1038 QQSGDNCLLYTHPLDGFPSAAGLEALCRQDNLSRPRCPTQELSPSHPLITCTGSDVDV 1097
Db 960 LHSTENCLVYAHPLDGFPSAAGTEALCRHDNSLRPRCPTQELSPSHPLATCFGSDVDI 1019
QY 1098 QLQVAVPQGRYALWVEYANEDARQEVGVAVHTPQAPQOGLLSLHPCLYSTLCRGTDARD 1157
Db 1020 QLEMAVPOPGYVLWVEYVEDSHQBMGVAVHTPQAPQOGLVNLHPCPYSSLCRSPARD 1079
QY 1158 TQDHLAVFHLDSASVRLTAEQARFFLHGVTLPVIEEFSPEFVEPRVSCISSHGAFGPNS 1217
Db 1080 TQHHLAIFHLDSASIRLTAEQAHHFLHSVTLVPVEEFSPEFVEPRVFCVSSHGTENPSS 1139
QY 1218 AACLPFRFPKPPQPIILRDCQVPLPPGLPLTHAQDLTPATSPAGPRPRPPTAVDPAEP 1277
Db 1140 AACLASRFPKPPQPIILKDCQVPLPPDLPLTQOELSPGAPPEGPQPRPPTAVDPAEP 1199
QY 1278 TLLREPQATVFTTHVPTLGRYAFLLHGYQPAHPTFPVEVLINAGRVMQGHANASFCPHG 1337
Db 1200 TLLRHPQGTVFTTQVPTLGRYAFLLHGYQPVHPSFPVEVLINGRIRWQGHANASFCPHG 1259
QY 1338 YGCRTLVVCQOALLDVTHSELTVTVRVBGRWLWLDYVLVVPENYVSFGLYLRPEPLDKS 1397
Db 1260 YGCRTLVLCQGTMLDVTDNELTVTVRVBGRWLWLDYVLVIVEDAYSSTLYLQEEPLDKS 1319
QY 1398 YDFISHCAAQGYHTSPSSSSSLFCRNAASLSLFYNNGARPCGCHVEVGATGPTCEPFGGQC 1457

Db 1320 YDFISHCATQGYHTSPSSSSSPFCRNAATSLSLFYNNGALPCGCHVEGAVSPTCEPFGGQC 1379
QY 1458 PCHAHVIGRDCSRCATGYWGFPPNCRPCDCGARLCDELDTGQCICPPRTIPPDCLLCQPQTF 1517
Db 1380 PCRGHVIGRDCSRCATGYWGFPPNCRPCDCGARLCDELDTGQCICPPRTVPDPCLVCPQPSF 1439
QY 1518 GHPLVGCCEECNCSGPGIQELTDPTCDTDSGQCKRPNVTGRRCDTCSPGFHGYPRCRPC 1577
Db 1440 GHPLVGCCEECNCSGPGVQELTDPTCDMDSGQCKRPNVAGRRCDTCAPGFYGYFPCRCPC 1499
QY 1578 DCHAGTAPGVCDPLTGQCYCKENVQPKCDQCSLGTFSLDAANPKGCTRCFCFEGATERC 1637
Db 1500 DCHAGTMAVCDPLTGQCHCKENVQGSRCDCQCRVGTFSLDAANPKGCTRCFCFEGATERC 1559
QY 1638 RSSSYTRQEFVDMEGWVLLSTDRQVVPHERQPGTEMRLRADLRHVPEAVPEAFPELYWQAP 1697
Db 1560 GNSNLARHEFVDMEGWVLLSSDRQVVPHEHRPEIELHADLR - - - SVADTFSELYWQAP 1615
QY 1698 PSYLGDRVSSYGGTLRYELHSETQRGDVFPVPMESRPDVLQGNQMSITFLEPAYPTPGHV 1757
Db 1616 PSYLGDRVSSYGGTLHYELHSETQRGDIPIFYESRPDVLQGNQMSIAFLELAYPPPGQV 1675
QY 1758 HRGQLQVVEGNFRHTETRTNVSREELMMVLASLEQLQIRALFSQISSAVSLRRVVALEVAS 1817
Db 1676 HRGQLQVVEGNFRHLBTHNPVSREELMMVLAGLEQLQIRALFSQTSSSVSLRRVVALEVAS 1735
QY 1818 PAGQALASNVVELCLCPASVYRGDSQCECAPGYRDYVKGFLGRVCPQCCHGSHDRCLPGS 1877
Db 1736 EAGRPPASNVVELCMCPANXRGDSQCECAPGYRDTKGLGRVCPQCCHGSHDRCLPGS 1795
QY 1878 GVCVDCQHNTGHAHCERCQAGHMS - RDDPSAPCVSCPCPLSVPSNNAFEGCVLRGRTQ 1936
Db 1796 GICVGCQHNTGDCQCRCPGFVSDPSNPASPCVSCPCPLAVPSNNAFADGCVLRGRTQ 1855
QY 1937 CLCKPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSGNDGPNLLFSDCDPLTGACRGCLR 1996
Db 1856 CLCRPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSGNDGPNMIFSDCDPLTGACRGCLR 1915
QY 1997 HTTGPRCEICAPGFYGNALLPGNCTRCDCPCGTEACDPHSGHCLCKAGVTRRRRCRCQE 2056
Db 1916 HTTGPHCERCAPGFYGNALLPGNCTRCDCSPCGTETCDPQSGRCLCKAGVTGQRCRCLE 1975
QY 2057 GHFGFNGCGGCRPCACGPAAGSECHPQSGQCHCRPGTMGQPCRECAPGYWGLPEQGCR 2116
Db 1976 GYFGFEQCGCRPCACGPAAGSECHPQSGQCHCQPGTTGQCLECAPGYWGLPEKGCR 2035
QY 2117 CQCPGGRCDPHTGRCNCPPLSGERCDTCSQOQOVVPVPGPVGHSIHCEVCDHCVVLLLD 2176
Db 2036 CQCPRGHCDPHTGHCTCPPLSGERCDTCSQOQOVVPVPGKFGHGHCEVCDHCVVLLLD 2095
QY 2177 DLERAGALLPAIHEQLRGINASSMAWARLHRLNASADLQSOILRSPGLGPRHETAQQLEVL 2236
Db 2096 DLERAGALLPAIREQLQGINASSAAWARLHRLNASADLQSKLRRPPGPRYQAAQLOTL 2155
QY 2237 EQQSTSLGQDARRLGGQAVGTRDQASQLLAGTEATLGHAKTLIAAIRAVDRTLSELMSQT 2296
Db 2156 EQQSIQLQDTERLGSQATGVQOAGQLLDTTESTLGRAQKLLSVRAVGRALNELASRM 2215
QY 2297 GHLGLANASAPSGEQLLRTLAEVERLLWEMRARDLGAPQAAAEALAAQRLARVQEQL 2356
Db 2216 GQGPSGDALVPSGEQLRWALAEVERLLWDMRTRDLGAQGAFAEALAEQRLMARVQEQL 2275
QY 2357 SSLWEENQALATQTRDLRAQHEAGLMDLREALNRAVDATREAEELNSRNQERLEALQK 2416
Db 2276 TSFWEENQSLATHIRDQLAQYESGLMDLREALNOAVNTTREAELNSRNQERVKEALQWK 2335
QY 2417 QELSRDNATQATLHAARDTTLASVFRLLHSLDQAKEELERLAASLDGARTPLLQRMQTF 2476
Db 2336 QELSQDNATLKATQAASLILGHVSELLQIGIDQAKEDLEHLAASLDGAWTPLLKRMQAF 2395
QY 2477 PAGSKLRLVEAAEAHAQQLGQLALNLSSILDVNQDRLTQRAIBASNAYSRILOAVQAAE 2536
Db 2396 PASSKVDLVEAAEAHAQKLNQLNLAINGILINQDRFIQRAVEASNAYSRILOAVQAAE 2455

2537 DAAGQALQADHTWATVVRQGLVDRAQOLLANSTALEEAMLEQOORLGLVWALQAGARTQ 2596
2456 DAAGQALRQASRTWEMVVRQGLAAGAROLLANSSALEETILGHQRLGLAQGRLLQAAGIQ 2515
2597 LRDVRAKDKOLEAHIAQAQAMLANDTDETSKIAHAKAVAAEAQDTATRVQSOLQAMQEN 2656
2516 LHNWARKNQALAAQIQEAQAQAMLANDTSETSEKIAHAKAVAAEALSTATHVQSOLQGMQKN 2575
2657 VERWQOQYEGRLRGQDLGOAVLDAGHSVSTLEKTLPLLAKLSILENRGVHNASLALSASI 2716
2576 VERWQOLGGLQGDLSQVERDASSSVSTLEKTLPLLAKLSRLENRGVHNASLALSANI 2635
2717 GRVRELIQAARGAASKVKVPMKFNKRSQVQLRTPRDLADLAAYTALKFYLG--PEPEPG 2774
2636 GRVRKLIQAARSAASKVKVSMKFNKRSQVRLRPPRDLADLAAYTALKFHIQSPVPAPEPG 2695
2775 QGTEDRFVYMGSRQATGDYMGVSLRDKKVVHVYQLGEAGPAVLSIDEDIGEQAFAVSID 2834
2696 KNTGDHFVLYMGSRQATGDYMGVSLRNQKVVHVYRLGKAGPTLSIDENIGEQAFAVSID 2755
2835 RTLQFGHMSVTVRQMIQETKGTIVAPGAEGLLNLRPDDFVYVGGYPSTFTPPPLRFP 2894
2756 RTLQFGHMSVTVRQMIQETKGTIVAPGAEGLLNLRPDDFVYVGGYPSTFTPPPLRFP 2815
2895 GYRGCIEMDILNEEWSLYNFERFQDITAVDRPCARSKSTGDPWLTGSLYDGTGFARI 2954
2816 GYLGCIEMETLNEEWSLYNFEQTMLDTAVDKPCARSKATGDPWLTGSLYDGSGFARI 2875
2955 SFDSQISTTKRPEQELRLVSYSYGVFLFKQSQFLCLAVQEGSLVLLYDFGAGLKKAVPL 3014
2876 SFKQFSNTKRFQELRLVSYSYGVFLFKQSQFLCLAVQEGSLVLLYDFGAGLKKADPL 2935
3015 QPPPLTSASKAIQVFLGGSRKRVLRVERATVYSVEQDNDLELADAYYLGVPDPQLP 3074
2936 QPPQALTAASKAIQVFLLAGNRKRVLRVERATVYSVEQDNDLELADAYYLGVPDPQLP 2995
3075 PSLRWLFPTGGVRCVKIKALGKYVDLKRLLNTTGSAGCTADLLVGRAMTFHGHGFLR 3134
2996 LSLRQLFPSSGSGVRCIKIKALGKYVDLKRLLNTTGSAGCTADLLVGRAMTFHGHGFLP 3055
3135 LALSNVAPLTGNTVYSGFGFHSQDSALLYRASPDGLCQVSLQGRVSLQLLRTEVKTOA 3194
3056 LALPDVAPITEVYVYSGFGFRGTQDNNLLYRTSPDGPYQVSLREHVTLRFMNQEVETOR 3115
3195 GFADGAPHYVAFYSNATGVWLYVDDQLQOMKPHRGPPPELQPEGPPRLLLGGLPESGT 3254
3116 VFADGAPHYVAFYSNATGVWLYVDDQLQOMKPHRGPPPELQPEGPPRLLLGGLPESGT 3175
3255 IYNFSGCISNVFQRLGLGPQVDFDLOQLGCVNVSTGCPALQAQTPGLGPRGLQATARK 3314
3176 FHNFGCISNVFQRLGLGPQVDFDLOQLGCVNVSTGCPALQAQTPGLGPRGLQATARK 3228
3315 ASRRSRQPARHPACMLPPLHRLTRTDSYQFGGSLSSHLEFVGLARHNRWPSLSMHLVLRP- 3373
3229 VSRRSRQPSQDLACTPWLPGTIQDAYQFGGLPSYLFQVGISPSHRNRLHLSMLVRPHA 3288
3374 SSRGLLLFTARLRPGSPSLALFLSNHGFVAQMEGLGTRLRQAQRORSRPGRWHKVSVRWE 3433
3289 ASQGLLLSTAPMSGRSPSLVFLNHHGFVAQMEGLGTRLRQAQRORSRPGRWHKVSVRWG 3348
3434 KNRILLVTDGARAWSQEGPHRQHQAEHPQPHTLFVGGPLPASSHSLKLPVTVGFGCVKR 3493
3349 MQQIQLVVDGSGTQSKALHHRVPRAPRQPYTLVGGPLPASSYSSKLPVSVGFGCLKK 3408
3494 LRLHGRPLGAPTRMAGVTPCILGPLEAGLFFPGSGGVITLDPGATLPDVGLELEVRPLA 3553
3409 LQLDKQPLRTPTQMVGTVCVSGPLEDGLFFPGSEGVITLDPGATLPDVGLELEMRPLA 3468
3554 VTGLIFHLGQARTPPYLQVTEKQVLLRADGAGEFSTSVTRPSVLCGQWHRRLAVMKS 3613
3469 AAGLIFHLGQALATPYMQLKVLTEQVLLQANDGAGEFSTVWTPK-LCDGRWHRVAVIMG 3527

3614 GNVLRLEVDACSNTHTVGPLLAAAAGAPAPLYLGLPEPNAVQPPPAYCGCMRRRLAVNRS 3673
3528 RDTLRLEVDTSQNTHTTGRLPESLAGSPALLHLGSLPKSSTARPELPAYRGCLRKLLINGA 3587
3674 PVAMTRSVVEVHGAVGASGCPA 3694
3588 PVNTASVQIQGAVGMRCPS 3608
RESULT 8
ABB81598
ID ABB81598 standard; protein; 2743 AA.
XX
AC ABB81598;
XX
DT 19-SEP-2002 (first entry)
XX
DE Human laminin alpha 5 2743 N-terminal amino acid sequence SEQ ID NO:36.
XX
KW Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;
KW tissue repair development; laminin; healing; vascular tissue;
KW re-endothelialisation; vascular injury; cell attachment; cell stasis;
XX proliferation; migration.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1. .35
FT /label= signal
FT Protein 36. .2743
FT /label= laminin_alpha_5
XX
PN WO200250111-A2.
XX
PD 27-JUN-2002.
XX
PF 21-DEC-2001; 2001WO-US051035.
XX
PR 21-DEC-2000; 2000US-0257449P.
PR 28-MAR-2001; 2001US-0279282P.
PR 13-NOV-2001; 2001US-00279282.
XX
PA (BIOS-) BIOSTRATUM INC.
XX
PI Tryggvason K, Doi M, Thyboll J;
XX
DR WPI; 2002-557650/59.
DR N-PSDB; ABQ72930.
XX
PT New human laminin-10 proteins, useful for accelerating the healing of
PT vascular tissue, improving the biocompatibility of grafts, or for
PT promoting re-endothelialization at the site of vascular injuries.
XX
PS Disclosure; Page 223-231; 231pp; English.
XX
CC The present invention describes human laminin alpha 5. Also described is
CC an isolated laminin 10. Laminin 10 has vulnery activity. Laminins are
CC useful in maintaining cell/tissue phenotype as well as promoting cell
CC growth and differentiation in tissue repair development. Specifically,
CC laminin 10 can be used for accelerating the healing injuries of vascular
CC tissue, improving the biocompatibility of grafts useful for treating such
CC injuries, for promoting re-endothelialisation at the site of vascular
CC injuries, and promote cell attachment and subsequent cell stasis,
CC proliferation, differentiation, and/or migration. The present sequence
CC represents the 2743 N-terminal amino acid sequence of human laminin alpha
CC 5, which is used in the exemplification of the present invention
XX
SQ Sequence 2743 AA;
Query Match 75.2%; Score 15120; DB 5; Length 2743;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2743; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKRLCAGSALCVRGPRGPAPLLLVGLALLGAARAREEAGGFSLHPPYFNLAEGARIAA 60
Db 1 MAKRLCAGSALCVRGPRGPAPLLLVGLALLGAARAREEAGGFSLHPPYFNLAEGARIAA 60
QY 61 SATCCEAPARGSPRPTEDLYCKLVGGPVAGGDPNQITIRGOYCDICTAANSNKAHPASNA 120
Db 61 SATCCEAPARGSPRPTEDLYCKLVGGPVAGGDPNQITIRGOYCDICTAANSNKAHPASNA 120
QY 121 IDGTERWQSPPLSRGLEYNVNVTLDLGQVHFVAYVLKIFANSRPDLWYLSRMDFR 180
Db 121 IDGTERWQSPPLSRGLEYNVNVTLDLGQVHFVAYVLKIFANSRPDLWYLSRMDFR 180
QY 181 TYQPWQFFASSKRDCLERFPQOTLERITRDAAICTTEYSRIVPLENGEIVVSLVNGRPG 240
Db 181 TYQPWQFFASSKRDCLERFPQOTLERITRDAAICTTEYSRIVPLENGEIVVSLVNGRPG 240
QY 241 AMNFSYSPLLREFTKATNVRLRFLRNTLLGHLMGKALRDPVTTRYYYSIKDISIGRC 300
Db 241 AMNFSYSPLLREFTKATNVRLRFLRNTLLGHLMGKALRDPVTTRYYYSIKDISIGRC 300
QY 301 VCHGHADACDAKOPTDFRLQCTCOHNTCGFTCDRCPCPGFNQOPWKPATANSANECQSCN 360
Db 301 VCHGHADACDAKOPTDFRLQCTCOHNTCGFTCDRCPCPGFNQOPWKPATANSANECQSCN 360
QY 361 CYGHATDCYYDPEVDRRAASQSLDGTYYQGGVVICDQHHTAGVNCERCLPGFYRSNHP 420
Db 361 CYGHATDCYYDPEVDRRAASQSLDGTYYQGGVVICDQHHTAGVNCERCLPGFYRSNHP 420
QY 421 DSPHVCRRNCESDFTDGTCEDLTGRCYCRPNFSGERCDVCAEGFTGFPSCYPTPSSND 480
Db 421 DSPHVCRRNCESDFTDGTCEDLTGRCYCRPNFSGERCDVCAEGFTGFPSCYPTPSSND 480
QY 481 TREQVLPAGQIVNCDGSAAGTQGNACRDKPRVGRCLCKPNFQGHCELCAAPGYGRCQP 540
Db 481 TREQVLPAGQIVNCDGSAAGTQGNACRDKPRVGRCLCKPNFQGHCELCAAPGYGRCQP 540
QY 541 CQCSSPGVADDRCDPDTGQCRVGFEGATCDRCAPGYFHFPLCQCGSPAGTLPBGCD 600
Db 541 CQCSSPGVADDRCDPDTGQCRVGFEGATCDRCAPGYFHFPLCQCGSPAGTLPBGCD 600
QY 601 EAGRCLCQEFAGHCDRCRPGYHGFNCOACTCDPRGALDQCGAGGLCRCPGYTGTA 660
Db 601 EAGRCLCQEFAGHCDRCRPGYHGFNCOACTCDPRGALDQCGAGGLCRCPGYTGTA 660
QY 661 CQECSPGFHGFPCVPCCHSAEGLHAACDPRSGQSCSRPRVTGLRCDTVPAGYNYFYC 720
Db 661 CQECSPGFHGFPCVPCCHSAEGLHAACDPRSGQSCSRPRVTGLRCDTVPAGYNYFYC 720
QY 721 EAGSCHPAGLAPVDPALPEAQVPCMCRAHVEGSPCDRCCKPGFWGLSPSNPEGCTRCSCDL 780
Db 721 EAGSCHPAGLAPVDPALPEAQVPCMCRAHVEGSPCDRCCKPGFWGLSPSNPEGCTRCSCDL 780
QY 781 RGTGGVAECQPGTGQCFCCKPHVCGQACASCKDGFGLDQADYFGCRSCRCIDGGALQS 840
Db 781 RGTGGVAECQPGTGQCFCCKPHVCGQACASCKDGFGLDQADYFGCRSCRCIDGGALQS 840
QY 841 CEPRTGVCRCRNPNTQGTCTSEPARDHYLPDLHLRLELEEAATPEGHAVRFGFNPLEFEN 900
Db 841 CEPRTGVCRCRNPNTQGTCTSEPARDHYLPDLHLRLELEEAATPEGHAVRFGFNPLEFEN 900
QY 901 FSWRGYAQMAYQPRIVARLNLTSPLFWLVFRYVNRGAMSVSGRVSREEGRSAAACANC 960
Db 901 FSWRGYAQMAYQPRIVARLNLTSPLFWLVFRYVNRGAMSVSGRVSREEGRSAAACANC 960
QY 961 TAQSQPVAFPSTEPAFITVPQRFGEFVLPNPGTALRVEAEGVLLDYVVLPSAYYEA 1020
Db 961 TAQSQPVAFPSTEPAFITVPQRFGEFVLPNPGTALRVEAEGVLLDYVVLPSAYYEA 1020
QY 1021 ALLQLRVTEACTYRPSAQSGDNCLLYTHPLPDGFPSSAGLEALCRQDNLSPRCPTQL 1080
Db 1021 ALLQLRVTEACTYRPSAQSGDNCLLYTHPLPDGFPSSAGLEALCRQDNLSPRCPTQL 1080
QY 1081 SPSHPPLITCTGSDVDVQLQVAVPQGRYALVVEYANEDARQEVGVAVHTPQAPQOGLL 1140

Db 1081 SPSHPPLITCTGSDVDVQLQVAVPQGRYALVVEYANEDARQEVGVAVHTPQAPQOGLL 1140
QY 1141 SLHPCLYSTLCRGRTARDTQDHLAVFHLDSASVRLTAEQARFLLHGVTLVPIEESPEFV 1200
Db 1141 SLHPCLYSTLCRGRTARDTQDHLAVFHLDSASVRLTAEQARFLLHGVTLVPIEESPEFV 1200
QY 1201 EPRVSCISSHGAFAFGPNSAACLPSPFPKPPQPIILRDCQVPIPLPGLPLTHAQDLTPATSP 1260
Db 1201 EPRVSCISSHGAFAFGPNSAACLPSPFPKPPQPIILRDCQVPIPLPGLPLTHAQDLTPATSP 1260
QY 1261 AGPRPRPTAVDPDAEPTLLREPPQATVFTTHVPTLGRYAFLLHGYPAPHTFPFVEVLIN 1320
Db 1261 AGPRPRPTAVDPDAEPTLLREPPQATVFTTHVPTLGRYAFLLHGYPAPHTFPFVEVLIN 1320
QY 1321 AGRVWQGHANASFCPHGYGRTLVVCEGQALLDVTHSELTVTVRVPGRWLWLDYVLVVP 1380
Db 1321 AGRVWQGHANASFCPHGYGRTLVVCEGQALLDVTHSELTVTVRVPGRWLWLDYVLVVP 1380
QY 1381 ENVYSFGYLREEPLDKSYDFISHCAAQGYHISPSSSSLFCRNAAASLSLFYNNGARPCGC 1440
Db 1381 ENVYSFGYLREEPLDKSYDFISHCAAQGYHISPSSSSLFCRNAAASLSLFYNNGARPCGC 1440
QY 1441 HEVGATGPTCEPFGGQCPCHAHVIGRDCSRCATGYWGFNCRPCDCGARLDELDTGQCIC 1500
Db 1441 HEVGATGPTCEPFGGQCPCHAHVIGRDCSRCATGYWGFNCRPCDCGARLDELDTGQCIC 1500
QY 1501 PPRTIPDDCLLCQPQTFGCHPLVGCCECNCSPGIGIQLTDPTCDTDSGQCKCRPNVTGRR 1560
Db 1501 PPRTIPDDCLLCQPQTFGCHPLVGCCECNCSPGIGIQLTDPTCDTDSGQCKCRPNVTGRR 1560
QY 1561 CDTCSPGFHGYPRCPCDCHEAGTAPGVCDPLTGQCYCKENVQPKDCQCSLGTFSLDAA 1620
Db 1561 CDTCSPGFHGYPRCPCDCHEAGTAPGVCDPLTGQCYCKENVQPKDCQCSLGTFSLDAA 1620
QY 1621 NPKGTRCFCFGATERCRSSSYTRQEFVDMEGWVLLSTDTRQVVPHERQPGTEMLRADLRH 1680
Db 1621 NPKGTRCFCFGATERCRSSSYTRQEFVDMEGWVLLSTDTRQVVPHERQPGTEMLRADLRH 1680
QY 1681 VPEAVPEAFPELYWQAPPSYLGDRVSSYGGTLRYELHSETQRGDVVPVPMESRPDVVLQGN 1740
Db 1681 VPEAVPEAFPELYWQAPPSYLGDRVSSYGGTLRYELHSETQRGDVVPVPMESRPDVVLQGN 1740
QY 1741 QMSITFLEPAYPTPGHVHRGQLQLVEGNFRHTTTRNTVSRREELMMVLASLEQLQIRALFS 1800
Db 1741 QMSITFLEPAYPTPGHVHRGQLQLVEGNFRHTTTRNTVSRREELMMVLASLEQLQIRALFS 1800
QY 1801 QISSAVSLRRVALEVASPAGQALASNVELCLCPASVYRGDSQCECAPGFYRDVKGLFLGR 1860
Db 1801 QISSAVSLRRVALEVASPAGQALASNVELCLCPASVYRGDSQCECAPGFYRDVKGLFLGR 1860
QY 1861 CVPCQCHGSHDRCLPQSGVVCVDCQHNTEGAHCERCAQAGFMSSRDDPSAPCVSCPCPLSVP 1920
Db 1861 CVPCQCHGSHDRCLPQSGVVCVDCQHNTEGAHCERCAQAGFMSSRDDPSAPCVSCPCPLSVP 1920
QY 1921 SNNFAEGCVLRGGRTQCLCKPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSNGDPLNLL 1980
Db 1921 SNNFAEGCVLRGGRTQCLCKPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSNGDPLNLL 1980
QY 1981 FSDCDPLTGACRGLRHTTGPRCEICAPGFYGNALLPGNCTRCDCCTPCGTEACDPHSGHC 2040
Db 1981 FSDCDPLTGACRGLRHTTGPRCEICAPGFYGNALLPGNCTRCDCCTPCGTEACDPHSGHC 2040
QY 2041 LCKAGVTGRRRCRQCEGHFGFNGCGGCRPCACGPAAGSECHQFQSGQCHCRPGTMGPQCR 2100
Db 2041 LCKAGVTGRRRCRQCEGHFGFNGCGGCRPCACGPAAGSECHQFQSGQCHCRPGTMGPQCR 2100
QY 2101 ECAPGYWGLPEQGCRCRCQPGGRCDDHTGRCNCPPLSGERCDCSCQHQVVPVPGGPVGH 2160
Db 2101 ECAPGYWGLPEQGCRCRCQPGGRCDDHTGRCNCPPLSGERCDCSCQHQVVPVPGGPVGH 2160
QY 2161 SIHCEVCDHCVVLLDDLERAGALLPAIHEQLRGINASSMAWARLHRLNASIADLQSQLR 2220

Db 2161 SIHCEVCDHCVVLLDDLERAGALLPATHEQLRGINASSMAWRLHRLNASIADLQSLR 2220

QY 2221 SPLGPRHETAQOLEVLEQQSTSLGQDARRLGGQAVGTRDQASQLLAGTEATLGHAKTLA 2280

Db 2221 SPLGPRHETAQOLEVLEQQSTSLGQDARRLGGQAVGTRDQASQLLAGTEATLGHAKTLA 2280

QY 2281 AIRAVDRITLSELMSTQTHLGLANASAPSGEQLLRTLAEVERLLWEMRARDLGAPQAAAEA 2340

Db 2281 AIRAVDRITLSELMSTQTHLGLANASAPSGEQLLRTLAEVERLLWEMRARDLGAPQAAAEA 2340

QY 2341 ELAAAQRLARVQEQSLSSWEENQALATQTRDLAQHEAGLMDLREALNRAVDATREAOE 2400

Db 2341 ELAAAQRLARVQEQSLSSWEENQALATQTRDLAQHEAGLMDLREALNRAVDATREAOE 2400

QY 2401 LNSRNQERLEALQKQELSRDNATLQATLHAARDTLASVFRLLHSLDQAKEELERLAAS 2460

Db 2401 LNSRNQERLEALQKQELSRDNATLQATLHAARDTLASVFRLLHSLDQAKEELERLAAS 2460

QY 2461 LDGARTPLLRMQTFSPAGSKLRLVEAAEAHAQQLGOLALNLSSIIIDVNDRLTORAIE 2520

Db 2461 LDGARTPLLRMQTFSPAGSKLRLVEAAEAHAQQLGOLALNLSSIIIDVNDRLTORAIE 2520

QY 2521 ASNAYSRILOVQAEDAAGQALQQAADHTWATVVRQGLVDRAQQLLANSTALEEAMLOEQ 2580

Db 2521 ASNAYSRILOVQAEDAAGQALQQAADHTWATVVRQGLVDRAQQLLANSTALEEAMLOEQ 2580

QY 2581 QRLGLVWAALQAGARTQLRDVRAKQDLQEAHQAQAAMLAMDTDETSKXIAHAKAVAAEAQ 2640

Db 2581 QRLGLVWAALQAGARTQLRDVRAKQDLQEAHQAQAAMLAMDTDETSKXIAHAKAVAAEAQ 2640

QY 2641 DTATRVQSLOAMQENVERWQGYEGLRGQDLGQAVLDAGHSVSTLEKTLPLQLLAKLSIL 2700

Db 2641 DTATRVQSLOAMQENVERWQGYEGLRGQDLGQAVLDAGHSVSTLEKTLPLQLLAKLSIL 2700

QY 2701 ENRGVHNASLALSASIGRVRELIAQARGAASKVKVPMKFNRS 2743

Db 2701 ENRGVHNASLALSASIGRVRELIAQARGAASKVKVPMKFNRS 2743

RESULT 9

ABB09504
ID ABB09504 standard; protein; 1640 AA.

AC ABB09504;

DT 01-NOV-2002 (first entry)

XX Human laminin alpha-5-like NOV1d protein, SEQ ID NO:8.

XX Human; NOVX; neurological disorder; Alzheimer's disease;
KW Huntington's disease; Parkinson's disease; pain; behavioural disorder;
KW addition; tuberculous sclerosis; cancer; immune disorder; allergy;
KW autoimmune disease; myasthenia gravis; asthma; arthritis; diabetes;
KW thyroiditis; cardiovascular disease; hypertension; reproductive disorder;
KW endometriosis; incontinence; psoriasis; scleroderma; alopecia; ulcer;
KW pancreatitis; cirrhosis; glomerular endotheiosis; bacterial infection;
KW polycystic kidney disease; endocrine disorder; obesity; cardiomyopathy;
KW atherosclerosis; cell signal processing-related disorder;
KW metabolic pathway regulation disorder; cytostatic; neuroprotective;
KW antiinflammatory; immunosuppressive; analgesic; antiatherosclerotic;
KW dermatological; antibacterial; antiallergic; hepatotropic; neurogenesis;
KW differentiation; proliferation; motility; haematopoiesis; wound healing;
KW angiogenesis; forensic biology; transgenic animal; drug screening;
KW gene therapy; NOV1d; laminin alpha-5-like; chromosome 20.

XX Homo sapiens.

OS WO200253742-A2.

PN 11-JUL-2002.

PD 07-JAN-2002; 2002WO-US0000375.

PF XX

PR 05-JAN-2001; 2001US-0260018P.
PR 08-JAN-2001; 2001US-0260360P.
PR 28-FEB-2001; 2001US-0272411P.
PR 02-MAR-2001; 2001US-0272817P.
PR 05-JUL-2001; 2001US-0303231P.
PR 12-JUL-2001; 2001US-0305060P.
PR 10-SEP-2001; 2001US-0318405P.
PR 12-SEP-2001; 2001US-0318700P.
PR 04-JAN-2002; 2002US-00037417.
XX

(CURA-) CURAGEN CORP.

XX Kekuda R, Alsobrook JP, Tchernev VT, Liu X, Spytek KA;
XX Patturajan M, Grosse WM, Lepley DM, Burgess CE, Vernet CAM, Li L;
PI Gorman L, Edinger S, Sciore P, Ellerman K, Malyankar U;
PI Rothenberg M, Stone D, Boldog F, Guo X, Shenoy S, Anderson D;
PI Padigaru M, Taupier RJ, Miller CE, Eisen A;

XX WPI; 2002-583619/62.
DR N-PSDB; ABQ93882.

XX Novel polypeptides and nucleic acids homologous to transmembrane
PT receptor, thymosin, neuromodulin-like family of proteins for diagnosing,
PT treating cancer, atherosclerosis, neurological, skin and autoimmune
PT disorders.

XX Claim 1c; Page 23; 323pp; English.

PS The invention relates to 24 novel human proteins designated NOV1-NOV14
XX (ABB09501-ABB09524), collectively referred to as NOVX proteins, and
CC nucleic acids encoding them (ABQ93879-ABQ93902). NOVX proteins, and
CC nucleotides are useful in the treatment, diagnosis or prevention of NOVX-
CC associated disorders or in the manufacture of a medicament for treating
CC such disorders, with specific applications described for each of the 24
CC NOVX proteins, based on their homology to known proteins. Various
CC disorders are associated with NOVX proteins including neurological
CC disorders (e.g., Alzheimer's, Huntington's and Parkinson's diseases),
CC pain, behavioural disorders, addiction, tuberculous sclerosis, cancers
CC (e.g., colorectal cancer, leukaemia and osteosarcoma), immune disorders
CC (e.g., allergies and autoimmune diseases), myasthenia gravis, asthma,
CC various forms of arthritis, diabetes, thyroiditis, cardiovascular disease
CC (e.g., hypertension), reproductive disorders, endometriosis,
CC incontinence, psoriasis, scleroderma, alopecia, ulcers, pancreatitis,
CC cirrhosis, glomerular endotheiosis, polycystic kidney disease, endocrine
CC disorders, obesity, bacterial infections and particularly cardiomyopathy,
CC atherosclerosis, cell signal processing-related disorders and polypeptides
CC of metabolic pathway regulation. NOVX nucleic acids and polypeptides may
CC be used to identify cellular receptors or downstream effectors which
CC binds to a NOVX protein, and are also useful as targets for the
CC identification of small molecules that modulate or inhibit processes such
CC as neurogenesis, cell differentiation, cell motility, cellular
CC proliferation, haematopoiesis, wound healing and angiogenesis. NOVX
CC nucleic acid sequences can be used to identify a cell or tissue type and
CC are useful as a source of primers or probes for forensic biology and for
CC identifying and cloning NOVX homologues in other cell types. Cells
CC comprising NOVX nucleic acids are useful for producing non-human
CC transgenic animals which are useful for studying the function and of NOVX
CC activity. The present sequence represents the laminin alpha-5-like
CC protein NOV1d. The gene encoding NOV1d is located on chromosome 20

XX Sequence 1640 AA;

Query Match 42.2%; Score 8499.5; DB 5; Length 1640;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1640; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 2051 CDRCEGHFGNGCGGCRPCACGPAAGSECHPQSGCHCRPGTMGPQCRECAPGYWGLP 2110
Db 1 CDRCEGHFGNGCGGCRPCACGPAAGSECHPQSGCHCRPGTMGPQCRECAPGYWGLP 60
QY 2111 EQGCRRCQCPGGRCDPHTGRCNCPPLSLGERCDTCSQHQVVPVPGPVGHSIHCEVCDHC 2170
Db 61 EQGCRRCQCPGGRCDPHTGRCNCPPLSLGERCDTCSQHQVVPVPGPVGHSIHCEVCDHC 120

QY 2171 VVLLDDLERAGALLPAIHEQLRGINASSMAWAEHLRLNASIADLQSLRSPGLPRHETA 2230
Db 121 VVLLDDLERAGALLPAIHEQLRGINASSMAWAEHLRLNASIADLQSLRSPGLPRHETA 180
QY 2231 QQLEVLQEQSTSLGQDARRLGGQAVGTRDQASQALLAGTEATLGHAKTLLAAIRAVDRTLS 2290
Db 181 QQLEVLQEQSTSLGQDARRLGGQAVGTRDQASQALLAGTEATLGHAKTLLAAIRAVDRTLS 240
QY 2291 ELMSQTGHLGLANASAPSGEQQLLRTLAEVERLLWEMRARDLGAPOAAAEAEALAAQRLLA 2350
Db 241 ELMSQTGHLGLANASAPSGEQQLLRTLAEVERLLWEMRARDLGAPOAAAEAEALAAQRLLA 300
QY 2351 RVQEQSLSSWERNQALATQTRDRLLAQHEAGLMDLREALNRAVDATREAEQELNSRQERLE 2410
Db 301 RVQEQSLSSWERNQALATQTRDRLLAQHEAGLMDLREALNRAVDATREAEQELNSRQERLE 360
QY 2411 EALQKQKQELSRDNATLQATLHAARDTLASVFRLLHSLDQAKEELERLAASLDGARTPLIQ 2470
Db 361 EALQKQKQELSRDNATLQATLHAARDTLASVFRLLHSLDQAKEELERLAASLDGARTPLIQ 420
QY 2471 RMOQTFSPAGSKRLRLVERAEAAHQALQALNLSSIIIDVNQDRLTQRAIEASNAYSRILO 2530
Db 421 RMOQTFSPAGSKRLRLVERAEAAHQALQALNLSSIIIDVNQDRLTQRAIEASNAYSRILO 480
QY 2531 AVQAAEDAAGQALQADHTWATVVRQGLVDRAQQLLANSTALEEAMLEQEQRLGLVWAAL 2590
Db 481 AVQAAEDAAGQALQADHTWATVVRQGLVDRAQQLLANSTALEEAMLEQEQRLGLVWAAL 540
QY 2591 QGARTQLRDVRAKQDQLEAHQAQAQAMAMTDTSKIAHAKAVAAEAQDTATRVQSOL 2650
Db 541 QGARTQLRDVRAKQDQLEAHQAQAQAMAMTDTSKIAHAKAVAAEAQDTATRVQSOL 600
QY 2651 QAMQENVERWQGYEGLRGQDLQAVLDAGHSVSTLEKTLPLQLLAKLSILENRGVHNASL 2710
Db 601 QAMQENVERWQGYEGLRGQDLQAVLDAGHSVSTLEKTLPLQLLAKLSILENRGVHNASL 660
QY 2711 ALSASIGRVRELIQAARGAASKVKVPMKFNRSRGVQLRTPRDLADLAAYTALKFYLGPE 2770
Db 661 ALSASIGRVRELIQAARGAASKVKVPMKFNRSRGVQLRTPRDLADLAAYTALKFYLGPE 720
QY 2771 PEPGQGTEDRFVYMGRSQATGYMGVSLRDKKXVHVYQGEAGPAVLSIDEDIGEQAFAA 2830
Db 721 PEPGQGTEDRFVYMGRSQATGYMGVSLRDKKXVHVYQGEAGPAVLSIDEDIGEQAFAA 780
QY 2831 VSLDRTLQFGHMSVTVRQMIQETKGDVAPGAEGLLNLRPDDEFFVYGVGYPSTFTPPPL 2890
Db 781 VSLDRTLQFGHMSVTVRQMIQETKGDVAPGAEGLLNLRPDDEFFVYGVGYPSTFTPPPL 840
QY 2891 LRFPGYRGCIEMDTLNEEVVSLYNFERTFQDFTAADRPCARSKSTGDPWLTGSLYLDGTG 2950
Db 841 LRFPGYRGCIEMDTLNEEVVSLYNFERTFQDFTAADRPCARSKSTGDPWLTGSLYLDGTG 900
QY 2951 FARISFDSQISTTKRFEQELRLVSYSGVLFLLKQOSQALCLAVQEGSLVLLYDFGAGLKK 3010
Db 901 FARISFDSQISTTKRFEQELRLVSYSGVLFLLKQOSQALCLAVQEGSLVLLYDFGAGLKK 960
QY 3011 AVPLQPPPLTSASKAIQVFLLGSRKRVLRVERATVYSVQDNDLELADAYYLGVP 3070
Db 961 AVPLQPPPLTSASKAIQVFLLGSRKRVLRVERATVYSVQDNDLELADAYYLGVP 1020
QY 3071 DQLPPSLRWLPPTGGSVRGCVKGIKALGKYVDLKLRLNTTGVSACTADLLVGRAMTFHGH 3130
Db 1021 DQLPPSLRWLPPTGGSVRGCVKGIKALGKYVDLKLRLNTTGVSACTADLLVGRAMTFHGH 1080
QY 3131 GFLRLALSNVAPLTGNVYSGFGFHSQAQSALLYRASPDGLCVLSQCGNVSQLLRTEV 3190
Db 1081 GFLRLALSNVAPLTGNVYSGFGFHSQAQSALLYRASPDGLCVLSQCGNVSQLLRTEV 1140
QY 3191 KTQAGFADGAPHYVAFYSNATGVWLYVDQLQOMKPHRGPPPELQPEGPRLNLLGGLP 3250
Db 1141 KTQAGFADGAPHYVAFYSNATGVWLYVDQLQOMKPHRGPPPELQPEGPRLNLLGGLP 1200

QY 3251 ESGTIYNFSGCISNVFQRLGQPVDFDLQNLGSLVNVSTGCAPALQAQTPGLGPRGLQA 3310
Db 1201 ESGTIYNFSGCISNVFQRLGQPVDFDLQNLGSLVNVSTGCAPALQAQTPGLGPRGLQA 1260
QY 3311 TARKASRRSRQPARHPACMLPPHLRTTRDSYQFGGSLSSHLEFVGILARHNRWPSLSMHV 3370
Db 1261 TARKASRRSRQPARHPACMLPPHLRTTRDSYQFGGSLSSHLEFVGILARHNRWPSLSMHV 1320
QY 3371 LPRSSRGLLLFTARLRPGSPSLALFLSNHGFVAQMEGLGTRLRQAQRQRSRPGRWHKVS 3430
Db 1321 LPRSSRGLLLFTARLRPGSPSLALFLSNHGFVAQMEGLGTRLRQAQRQRSRPGRWHKVS 1380
QY 3431 RWEKNRILLVTDGARAWSQEGPHRQHQAEHPQPHLTFVGGLPASSHSSKLPVTVGFSGC 3490
Db 1381 RWEKNRILLVTDGARAWSQEGPHRQHQAEHPQPHLTFVGGLPASSHSSKLPVTVGFSGC 1440
QY 3491 VKRLRLHGRPLGAPTRMAGVTTCILGPLEAGLFFPGSGGVITLDPGATLPDVGLELEVR 3550
Db 1441 VKRLRLHGRPLGAPTRMAGVTTCILGPLEAGLFFPGSGGVITLDPGATLPDVGLELEVR 1500
QY 3551 PLAVTGLIFHLGQARTPPYLQQLQVTEKQVLLRADDDGAGEFSTSVTRPSVLCDGQWHLAV 3610
Db 1501 PLAVTGLIFHLGQARTPPYLQQLQVTEKQVLLRADDDGAGEFSTSVTRPSVLCDGQWHLAV 1555
QY 3611 MKSGNVLRLEVDAQSNHTVGPGLLAAAGAPAPLYLGGLPPEPMAVQPPPAYCGCMRRLAV 3670
Db 1556 MKSGNVLRLEVDAQSNHTVGPGLLAAAGAPAPLYLGGLPPEPMAVQPPPAYCGCMRRLAV 1615
QY 3671 NRSPVAMTRSVVEHGVAGSGCPAA 3695
Db 1616 NRSPVAMTRSVVEHGVAGSGCPAA 1640

RESULT 10
AAM39009
ID AAM39009 standard; protein; 1601 AA.

XX AAM39009;

XX 22-OCT-2001 (first entry)

XX Human polypeptide SEQ ID NO 2154.

DE Human; neotropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.

XX Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US034263.

XX 23-DEC-1999; 99US-00471275.

XX 21-JAN-2000; 2000US-00488725.

XX 25-APR-2000; 2000US-00552317.

XX 20-JUN-2000; 2000US-00598042.

XX 19-JUL-2000; 2000US-00620312.

XX 03-AUG-2000; 2000US-00653450.

XX 14-SEP-2000; 2000US-00662191.

XX 19-OCT-2000; 2000US-00693036.

XX 29-NOV-2000; 2000US-00727344.

(HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;

DT	29-JAN-2004	(first entry)
XX	Novel protein (useful for identifying genetic disorders) #249.	
DE	novel gene; novel protein; tissue marker; molecular weight marker;	
XX	chromosome marker; genetic disorder.	
KW	Unidentified.	
OS	WO2003054152-A2.	
XX	03-JUL-2003.	
PN	10-DEC-2002; 2002WO-US039555.	
XX	10-DEC-2001; 2001US-0339739P.	
PR	11-DEC-2001; 2001US-0339453P.	
PR	14-MAR-2002; 2002US-0365091P.	
PR	14-MAR-2002; 2002US-0365384P.	
PR	12-APR-2002; 2002US-0372381P.	
PR	12-APR-2002; 2002US-0372615P.	
PR	22-APR-2002; 2002US-00128558.	
PR	24-APR-2002; 2002US-0376045P.	
XX	(HYSE-) HYSEQ INC.	
PA	Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;	
XX	Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;	
PI	Ma Y, Wang D, Chen R, Xu C, Boyle BJ;	
PI	WPI; 2003-569235/53.	
XX	N-PSDB; ADE07183.	
DR	New polynucleotides, useful for expressing recombinant proteins for	
XX	analysis, characterization or therapeutic use, or as markers for tissues	
PT	in which the corresponding protein is preferentially expressed.	
PT	Claim 20; SEQ ID NO 1160; 1177pp; English.	
XX	The invention comprises the amino acid and coding sequences of novel	
PS	proteins. The DNA and protein sequences of the invention are useful as:	
XX	markers for tissues in which the corresponding protein is preferentially	
CC	expressed; as molecular weight markers on gels; as chromosome markers or	
CC	tags; to identify chromosomes or to map related gene positions; and to	
CC	compare with endogenous DNA sequences in patients to identify potential	
CC	genetic disorders. The present amino acid sequence represents a protein	
CC	of the invention.	
XX	Sequence 3332 AA;	
SQ	Query Match 34.4%; Score 6916; DB 7; Length 3332;	
	Best Local Similarity 39.3%; Pred. No. 0;	
	Matches 1478; Conservative 541; Mismatches 1225; Indels 514; Gaps 68	
QY	16 PRG-----PAPLLLVGLALGA--ARAREE-AGGGFSLRPPVFNLAEGARIAASATC 64	
Db	7 PRGRALGPVLPTPTLLLVLRVLPACGATARDPGAAGLSLHPTTNNLAEARIWATATC 66	
QY	65 GEEAPARGSPRPTELDYCKLVGGPVAGGDPNQTIRGOYCDICTAANSKRAHPASNAIDGT 124	
Db	67 GERGPGEGRPOP--ELYCKLVGGPTAPGS-GHTIQGQFCDYCNSEDRKAHPVTNAIDGS 123	
QY	125 ERWQSPPLSRGLYNEVNVTLDLGQVHFHAYVLKIFANSRPDLWVLSRSMDFGRTPQ 184	
Db	124 ERWQSPPLSSGTQYRNVNLTLDLGLQVHFHAYVILKIFANSRPDLWVLSRSMDFGRTPQ 183	
QY	185 WQFASSKRDCLERFGPQTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRPGAMNF 244	
Db	184 WQYFAHSKVDCLKEFGREANMAVTRDDVLCVTEYSRIVPLENGEVVSVLINGRPGAKNF 243	
QY	245 SYSPLLEFTKATNVRLRFLRTNTLLGHLMGKALRDPPTVTRRYYSIKDISIGGRVCVHG 304	
Db	244 TSHTIREFTKATNIRLRLRFLRTNTLLGHLSKAQRDPPTVTRRYYSIKDISIGGCVCNG 303	

QY 1379 VPENVYSGYLREPLDKSYDFISHCAAQGYHISPSSSSLFCRNAAASLSLFYNNGARPC 1438
Db 1206 VPAENYDYQILHKSKMDKLEFITNCGKNSFYLDPTASRFCKNSARSLVAFYHKGALPC 1265
QY 1439 GCHVEGATGPTCEPFGGQCPCHAHVIGRDCSRCATGYWGFPPNCRPCDCGARGLDELGTQC 1498
Db 1266 ECHPTGATGPHCSPEGGQCPQPNVIGRQCTRCATGHYGFPRCKPCSCGRRICEWMTGQC 1325
QY 1499 ICPRTIPDDCLLQOPQTGCHPLVGCCECNCSGGPGTQELTDPTCDTSDGGQCKRPNVTG 1558
Db 1326 RCPRTVRPQCEVCETHSPSPHFMAGCEGNCNRRRTIEAAMPECDRDSGQCRCKPRITG 1385
QY 1559 RRCDTCSPGFHGYPRCPCDCHEAGTAPGVCDPLTGQCYCKENVQPKDCQCSLGTFSLD 1618
Db 1386 RQDRCASGFYRFEPCVPCNCRDGTGTEPGVCDPTGACGLCKENVGTECNVREGSPHLD 1445
QY 1619 AANPKGCTRCFCFGATERCRRSSSYTROEPVDMEGVLLSTDRQVPHERQPGTEMLRADL 1678
Db 1446 PANLKGCTSCFCFVNNQCHSHKRRTKFVDMGLGWLHLETAADRVDIPVSFNPFGNSMVADL 1505
QY 1679 RHVPEAVPEAFPELYWQAPPSYGLDRVSSYGGTLRYELHSETQRGDVFVPMESRPDDVVLQ 1738
Db 1506 QELPATIHS- ---SWAPTSYLGDVSSYGGYLTQYQAKSFGPLPGDM - VLEKXKPDVQLT 1560
QY 1739 GNQMSITFLEPAYPTPGHVHRGQLQVVEGNFRHTETRTNVRSREELMVLASLQQLRAL 1798
Db 1561 GQHMSIYEETNTPRPDLRHGRVHVVEGNFRHASSRAPVSREELMTVLSRLADVRIQGL 1620
QY 1799 FSQISSAVSLRRVALEVASPAGQALASNVLCPCASVYRGDSQCECAPGFYRDVKGLFL 1858
Db 1621 YFTETQRLTSEVGLSEASDTGSGRIALAVEICACPPAYAGDSQCGSPGYRDKGLYT 1680
QY 1859 GRCVPCOCHGHSRCLPGSGVYVDCQHNTEGAHCERCQAGFMSSRDDPSAPCVSCPPLS 1918
Db 1681 GRCVPCNCGHNSQCQDGSIGICVNCQHTAGEHCERCQEGYGNVHGS --CRACPCP-- 1736
QY 1919 VPSNNFAGCVLRGGRTQCLCKPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSNGDPN 1978
Db 1737 -HTNSFATGCVVNGDVRCSCKAGYTGTCERCAPGYFNPQKFGGSCQPCSCNSNGQ-- 1793
QY 1979 LLFSDCDPLTGACRGCLRHTTGPRCEICAPGFYGNALLPGNCTRCDCTPCGTEACDPHSG 2038
Db 1794 --LGSCPLTGDCIN----- 1806
QY 2039 HCLCKAGVTGRRCDRCQEGHFGNGCGCRPCACGPAAGSECHPQSGQCHCRPGTMGPQ 2098
Db 1807 -----QE-----PKDSSPAEE----- 1817
QY 2099 CRECAPGYWGLPEQGCRRRCQCPGGRCDPHTGRCNCPPLGSGERCDCSCQHQVVPQGPV 2158
Db 1818 ----- 1817
QY 2159 GHSIHCEVCDHCVLLDDDLERAGALLPAIHEQLRGINASSMAWARLHRLNASIADLQSQ 2218
Db 1818 -----CDDCDSVCVMTLLNDLATMGEQLRLVKSQLOGLSASAGILLEQMRHMETQAKDLRNQ 1872
QY 2219 LRSPLGPRHETAQOLEVLEQQSTSLGQDARRLGGQAVGTRDQASQLLAGTEATLGHAKTL 2278
Db 1873 LLNYSRAISNHGSKIEGLERELTDLNQEFETLQEKAVQVNSRKAQTLNNNNVRATQSAKEL 1932
QY 2279 LAAIRAVDRTLSELMSQ-TGHLGLANASAPSGEQLLRTLAEVERLLWEMRARDLGAQAA 2337
Db 1933 DVKIKNVIRNVHILLKQISGTDGEGN-NVPSGD-FSREWAEARQWRELNRNFGKHLRE 1990
QY 2338 AEAEALAAQRLARVQEQLSLWEEENQALATQTRDRLAQHEAGLMDLREALNRAVDATRE 2397
Db 1991 AEADKRESQLLNRIRTWQTHQGENNGLANSIRDSLNEYEAKLSDLRARLQEAQAAQKQ 2050
QY 2398 AQELNSRNQERLEALQRK-QELSIRDNATLQATLHAARDTLASVFRLLHSLDQAKEELER 2456
Db 2051 ANGLNQEN-ERALGAIQROVKEINSLQSDFTKYLTADSSLLQTNIALQLMERSQKEYEK 2109
QY 2457 LAASLDGARTPLLQRMQTFSPAGSKRLVBAEAAHAQQLGQLALNLSIILDVNQDRLTQ 2516

Db 2110 LAASLINEARQELSDKVRRELSRSGAKTSLVEEAERHARSLOELAKQLEEKRNASGDELVR 2169
QY 2517 RAIEASNAYSRILOAVQAAEDAAGQALQADHTWTAVVRQGLVDRAQOLLANS-TALEEA 2575
Db 2170 CAVDAATAYENILNAIKAEDAANRAASASESALQTVIKEDLPRKAKTSSNSDKLLNEA 2229
QY 2576 MLQEQRLGLVWAALQGARTQIRDVRAKDKQLEAHIAQAQ-AMLAMDTDETSKKTIAHAKA 2634
Db 2230 KMTQKLLKQEVSPALNNLQTLNIVTVQKEVIDTNTLTDGLHGIQRGDIDAMISSAKS 2289
QY 2635 VAABEQDTATRVQSOLQAMQENVERWQOYEGRLGQDLGQAVLDAGHSVSTLEKTLPOL 2694
Db 2290 MVRKANDITDEVLDGLNPIQTDVERIKDTYGRQTQNEDEFKKALTADNSVNKLTKLPLDLW 2349
QY 2695 AKLSILENRGVHNASLA---LSASIGRVRRELIAQARGAASKVKVPMKFNRSRGVQLRTP 2750
Db 2350 RKIESI-----NQQLPLGNISDNMDRIRELIQQARDAASKVAVPMRFNGKSGVEVRLP 2403
QY 2751 RDLADLAAYTALKFYLOGPEPEPGQGTEDRFVVMYMGSRQATGDMGVSLRDKKVVHVVQL 2810
Db 2404 NDLEDLKGYTSLSLFLQRPNSRENGGTENFMVYLGNDASRDYIGMAVVDGQLTCVNL 2463
QY 2811 GEAGPAVLSDIDEDIGE-----FAAVSLDRTLQFQGHMSVTVVERQMIQ-ETKG--DTVAP 2861
Db 2464 GDR-EAELQVDQILTKSETKEAVMDRVKFORIYQFARLNTKGATSSKPETPGVYDMDGR 2522
QY 2862 GAEGLLNLRPDDFVYVGGYSPSTFTPPPLLRFPYRGCIEMDTLNEEVVSLYNFERTFOL 2921
Db 2523 NSNTLLNLDPENWVYVGGYPPDFKLPRLSPFPYKGCIELDDLNENVLNLYNEKKTFLN 2582
QY 2922 DTAVDRPCARSKSTGDPWLTDGSLYEGTGTFARISFDSQISTTKRFEQELRLVSYSGVLPF 2981
Db 2583 NTTEVEPCRRRKEE-----SDKNYFEGTGYARVPTQPH-APIPTFGQTIQTTVDRGLLFF 2636
QY 2982 LKQSQQLCLAVQEGSLVLYDFGAGLKK-----AVPLQPPPLTSASKAIQVFLGGS 3035
Db 2637 AENGDRFISLNIEDGKLMVRYKLSNHELPERGVGDAIN-----NGRDHSIQI-KIGKL 2688
QY 3036 RKRVLVRVERATVSVVEQDNDLELADAYVYLGVPDQPPSLRWLFP-TGGSVRGCVKGI 3094
Db 2689 QKRMWINVD--VQNTIIDGEVDFSTYVYLGGI-----PIAIRERFNISTPAFRGCMKNL 2740
QY 3095 KALGKYVDLKRNL-TTGVSAGCTADLLVGRAMTFHGHGFLRLALSNAVA-PLTGNVYSGFG 3152
Db 2741 K--KTSGVVRNLNDTVGVTKKCEDWKLVRSAFSRGG--QLSFTDLGLPPTDHLQASFG 2795
QY 3153 FHSAQDSALLYRASPDGLCOVSLQOGRVSLQLLRT--VKIQAGFADGAPHYVAFYSN 3209
Db 2796 FQTFQPSGILLDHQWTWRNLQVLTEDGVIELSTSDSGGPIFKSPQYMDGLLHYVSVISD 2855
QY 3210 ATGVWLYVDDQLQOMKPHRPPPELQPEGPRLLLGLLPESGTYNFSGCISNVFVQR 3269
Db 2856 NSGLRLLIDQLLRNS-----KRLKHISSRSQSLRGG-----SNFEGCISNVFVQR 2902
QY 3270 LLGPQRVFDLQONLGSVNVST-GCA-----PALQAOPTPGLG 3304
Db 2903 LSLSPVELDLTSNSLKRDSVSLGGCSLNKPPFLMLLKGSTRFNKTKTFRINQLLODTPVAS 2962
QY 3305 PRGLQATARKASRRSRQPARHPACMLPPHLRTRDSYQFGGSLSSHLEF--VGILARHRN 3362
Db 2963 PRSVKVV-----QDACSPLEKTOANHGALQFGDIPITSHLLFKLPQELLKPRS 3009
QY 3363 WPSLSMHVLPSSRGLLLTARLRPGSPSLALFLSNHGFVAQMEGLGTRLRQAQRQSRP 3422
Db 3010 QFAVDMQT--TSSRGLVFHTG---TKNSFMALYLSKGRLVFALGTDGKKLRIKSKECND 3064
QY 3423 GRWHKVSVRWEKNRILLVTDGARAMWSQEGPHRQHQGAHPQPHTLFVG-----GLPASSH 3477
Db 3065 GKWHTVVFHGDGKGRLVWDGLRA--REG-----SLPGNSTISIRAPVYLGSPPSGK 3114
QY 3478 SSKLPVTVFGSGCVKRLRLHGRPLGAPTRMAGVTPCILGLEAGLFFPGSGGVITLDLP 3537

Db 3115 PKSLP-TNSFVGLKQNFQDLSKPLYPSSSFGVSSCLGPLEKGYFSEEGHVLAHSV 3173
QY 3538 ATLPDVGLEVRPLAVTGLIFHLGQARTPPYLQVTEKQVLLRADDDGAGEFSTSTVRP 3597
Db 3174 LLGPEFKLVFSIRPSRLTGILHIG-SQPKHLCVYLEAGKVTASMDSGAGGTSTSTPK 3232
QY 3598 SVLCDGQWHLAVMKSGNVLRLEVDQAQSNHTVGPPLAAAGAPAPLYLGLPEPMAVQPW 3657
Db 3233 QSLCDGQWHSVAVTIKQIHLELDTSSVTAGQIPFPAPASTQEPHLGAPANLTTLRI 3292
QY 3658 P--PAYCGCMRRLAVNRSPVAMTRSVEHGAVGASGCP 3693
Db 3293 FVWKSFFGCLRNHVNHPVPVTEALEVGPVSLNGCP 3330

RESULT 12

ABB64954

ID ABB64954 standard; protein; 3712 AA.

XX

AC ABB64954;

XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 21654.

XX Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.

OS Drosophila melanogaster.

XX WO200171042-A2.

PD 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US009231.

PR 23-MAR-2000; 2000US-0191637P.

PR 11-JUL-2000; 2000US-00614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li FWD, Myers EW;

PI WPI; 2001-656860/75.

DR N-PSDB; ABL09057.

XX New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.

PT Disclosure; SEQ ID NO 21654; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 3712 AA;

Query Match 25.3%; Score 5093; DB 4; Length 3712;
Best Local Similarity 31.6%; Pred. No. 1.6e-280;
Matches 1245; Conservative 611; Mismatches 1542; Indels 540; Gaps 121;

QY 45 LHPYPFNLAEAGARIAASATCGEEAPARGSPRPTEDLYCKLVGGPVAGGDPN-OTIRGOYC 103

Db 24 LTPYPFNLATGRKIYATATCGQDTDG-----PELYCKLVGANTTEHDHIDYSVIQGVQC 76

QY 104 DICTAANSNKAHPASNAIDGTERWQSPPLSRGLEYNVNTLTLQVPHVAVYLKIFAN 163
Db 77 DYCDTPVPERNHPPENAIDGTEAWQSPPLSRGMKNEVNLITINFEQEFHVAYLFI RMGN 136
QY 164 SPRDLWVLESMDFRTYQPWQFFASSKRDCLERFGPQTLERITRDDAAICTEYSRIV 223
Db 137 SPRGLWTLKSTDYKWTWPHQFSDTPADCEYFGKDYKPIITRDDVICTEYSKIV 196
QY 224 PLENGEIVVSLVNGRPGAMNFSYSPLLREFTKATNVRRLRNTLLGHLMGKALRDPV 283
Db 197 PLENGEIPVMLLNERPSTNYFNSTVLOEWTRATNVRIRLLRTKNLGLHMSVARQDPTV 256
QY 284 TRRYYSIKDISIGGRVCVCHGHADACDAKDPDTPPR-LOCTCOHNTCCGTCDCRCCPGFNQ 342
Db 257 TRRYYSIKDISIGGRCMCNHGHADTCVDKPKSPVIRILACRQCHHTCGIQNECCPGFEQ 316
QY 343 QPWKPATANSANECQSCNICYGHATDCYYDPEVDVRRRASQSLDGTGYQGGVVCIDCOHHTAG 402
Db 317 KKWRQNTNARPFNCEPCNCHGHSNECKYDEEVNRKGLSLDIHGHYDGGVVCQNCQHNVTG 376
QY 403 VNCERCLPGFYRSPNHLDSPHVCRRCNCESDFTDGTCEDLTGRCYCRPNFSGERCDCVCA 462
Db 377 INCNKCKPKYRPKGKHNEDTVCSPCQDVFSTGHCEEBETGNCCEAAFPQPPSCDSCA 436
QY 463 EGTGFPSCYPTPSSSNDTREQVLPAGQIVNDCSAAAGTQGNACRKPVRGRCCLCKPNFQ 522
Db 437 VGYGYPCN-----RE-----CECNLNGTNGYHCEASG-QQCPCKINFA 475
QY 523 GTHCELCAFGYF-PGQPCQCSSPGVADRDCTDTCQCRVGFEGATCDRCAPGYFHF 581
Db 476 GAYCKQCAEGYGFPECKACECNKIGSITNDCNVTGECCKLTNFGDNCERCKHGYFNY 535
QY 582 PLCQLCGCSPAGTLPEGCD-EAGRCCLQPFAGPHCDRCRPGYHGPNCQACTCDPRGAL 640
Db 536 PTCSYCDNDQGTSEICNKGQICREGFGPRCDQCLPGFVNYPDCKPCNCSSTGSS 595
QY 641 DQLCGAGGLCRCPGYGTACQECSPGFHGFPPSCVPCCHCSAEGSLHAAACDPRSGQCSCR 700
Db 596 AITCDNTGKCNCLNPNFAGKQCTLTAGYVYVYDCLPCHCDSHSGQVSCN-SDGQCLCQP 654
QY 701 RVTGLRCDTCVPGAYNFPYCEAGSCHPAGLAPVDPALPEAQP-----CMCRAHVEGPS 756
Db 655 NFDGRQCDSCKEGFYFPSCDCDNCDPAGV-IDKFAGCGSVFVGLCKCKERVITGRICN 712
QY 757 RCKPGFWGLSPNPEGCTRCSCDLRGLTGLGVAECQPGTGQCFXKPHVCQACASCKDGF 816
Db 713 ECKPLYWNLNISNTEGEICDCWTDTISALDCTSKSGQCPCKPHTQGRRCQECRDGTF 772
QY 817 GLDQADYFGCRSCRDIGGALGQSCBPRTVGCRCPNTQGTQSCBPARDHYPDLHLRL 876
Db 773 DLDSASLFGCKDCSDVGGSWQVCDXISGCKCHPRITGLACTQPLTTHFFFTLHQFOY 832
QY 877 ELBEAATPEGHAVRPGFNPLEFENFWSRGYQAQMAPVQPRIVARINLTSPDLFWLVRYVN 936
Db 833 EYEDGSLPSGTQVRYDYDEAAFPFGSSKGVVFNAIQNDVRNEVNVFKSSLYRIVRYVN 892
QY 937 RGAMSVGRVSVREGRSAACANCTAQSPVAFPPSTEPAFITV--PQGFGEFPFVLPNG 994
Db 893 PNAENVTATISVTDNPLE-----VDQHVKVLQPTSEFPQFVTVAGPLGVKPSAIVLDPG 947
QY 995 TWALRVEA-EGVLLDYVLLPSAYVEAALLQLRVTEACTYRPSAQSGDNCCLLYTHLPD 1053
Db 948 RYVFTTKANKNVMLDYFVLLPAAVYEAGILTRHISNPCEL-----GNMELCRHYKYASVE 1002
QY 1054 GFPSAAGLEALCRQDNLPRPCPTQLSPSHPLIT-----CTGSDVDVQLQVAVPQP 1106
Db 1003 VFPSPA--TPFVIGENSKPTNPVETVTDPEHLQIVSHVGDIPVLSGSQNELHYIVDVP 1060
QY 1107 GRYALVVEY-ANEDARQEVGAVHTPQAPQQLLSLHPCLYSTLCRGTARDTQDHLAVF 1165
Db 1061 GRYIFVIDYISDNFPDYSYINLKLKNDPDSVTSVLLYPCLYSTICR-TSVNEDGMEKSF 1119
QY 1166 HLDSE--ASVRLTA---EQARFFLHGVTLVPIEEFSPFVPRVSVCISSHGAFGPNSAAC 1220

1120	YINKEDLPV	IISADIEDGSRFPIISVTAIPVDQWSIDYINBSPCVI	-----HDQOC	1172			
1221	LPSRFPKPP	QPIILRDCQVIPLEPGLPLTHAQDLTPATSPAGRP	RPPTAVDPDAEPTLL	1280			
1173	ATPKFRSVP	-----DSKKIEFE-----TDHEDRIATNKP	-----PYASLDERVKLVHL	1215			
1281	-REPQATVV	FTTHV-----PTLGRYAFLLHGYP	PAHPTFPVEVLINAGR-VWQGHANASFC	1334			
1216	DSQNEATIV	IESKVDATKPNL--FVILVKYIQSPHKYQVYYTL	TAGKNQYDGFIDIOHC	1273			
1335	PHGYGCR	TLVWCEGOALLDVTHSELTVTVRVPEGRWLWLDY	VLVVPENVVSYFGYLREEPL	1394			
1274	PSSSGCR	GVIRPAGEGSFEI-DDEFKFTITDRSQSVL	DYLVVPLKQYNDLLVEETF	1332			
1395	DKSYDPISH	CAAQYHISPSSSSLFCRNAAAASLSLFYNNGAR	PCGCHVEVGATGPTCEPFG	1454			
1333	DQTKXFI	QNCGHDFHITHNASD-FCKKSVFSLTADYNSG	ALPCNDYAGSTSFECHPFG	1391			
1455	GQCPCHAV	IGRDCSRCATGYWGFPNCRPCDC-GARL	CDELIGQICPPRTIPPDCLLCQ	1513			
1392	GQCOCKPN	VIERTCGACRSRYGFPDCKPCKPCNSAMCEPT	TGECMCPNVIGDLCEKCA	1451			
1514	PQTFGCH	PLVGCEECNCSGPGIQELTDPDCTDSGQCKR	PNVTRRCDDTCSPGFHGYPR	1573			
1452	PNTYGFH	QHVIGCEECACNPMGIAN-GNSQCDL	FNGTCECRQNI	EGRACDVCSNGYFNFPH	1510		
1574	CRPCDCH	EAGTAGVCDPLTGQCYCKENVOGPKCDQCS	LGTFSLDAANPKGCTRCFCFGA	1633			
1511	CEQCSCH	KPGTELEVCDKIDGACFKKNVVRGDCDQ	CVDTYNLQESNPDGCTTCFCFGK	1570			
1634	TERCRSS	YTRQEFVDMEGWLLSTDRQVVPHERQ	-----PGTEM-----LRAD--	1677			
1571	TSRC-DS	AYLRVYNVLSLLKHVSITTPF	---HEESIKFDMWPVPADEILLNETTLKADFT	1626			
1678	LRHVEAV	PEAFPELYWQAPPSYL--GDRVSSYGGTL	RYELHSETQRGDVFPMESRPD	1734			
1627	LREVNDR	PAYFGVL-----DYLNQNNHISAYG	DDLAYTLHFTSGFDGKYI---VAPD	1677			
1735	VVLQGN	OMSITFLEPAYTPGHVHRGQLQ	VEGNFRHTETRNTVSREELMMVLASLEQLQ	1794			
1678	VILFSEH	NALVHTSYEQPSRNEPFTNRVNI	VESNFQ-TISGKPVSRADFMVLRDLKVIF	1736			
1795	IRALFSQ	ISSAVSLRRVALEVASPAGQGA-----	LASNVELCLCPASVRGDSCQECAPGF	1849			
1737	IRANYEQ	TLVTHLSDVYLTDADEADGTGEYQFLA--	VERCSCPPGYSGHSCDDCAPGY	1794			
1850	YRDVKGL	FLGRCPVQCQCHGSDRCLPGSGVCV	CDQHNTGAHCERCQAGFM--SSRDDPSA	1908			
1795	YRDPSP	PGYGYCIPCECNHSETCDCATGIC	SKQHGTEGDHCERCVCVSYGNATNGTPG	1854			
1909	PCVSCPC	PLSVPSNNFAEGCVL--RGGRTQCL	CKPGYAGASCERCAPGFFGNPLVLGSSC	1966			
1855	DCMICAC	PLPDSNNFATSCEISESGDQIHCECK	PGYTGPCECSCANGFYGEFESIGQVC	1914			
1967	QPCDCS	GNDDNLLFSDCDPLTGACRGCL	RHTTGPCEICAPGYGNALLPGNCTRCDCT	2026			
1915	KPCECS	GNINPEDQGS-CDTRTGECL	RCLNNTFGAACNLCPAGFYGDAIKLKN	CQSCDDC	1973		
2027	PCGTEA	CDPHSGHCLCKAGVTGRRCDRCQ	EGHFGFNGCGGCRPCACGPA	AESECHPQSG	2086		
1974	DLGTQ	TCDPFVGVTCHENVIGDRCDR	CKPDPHYGFESVGCACDCGAA	SNSTQCDPHTG	2033		
2087	QCHCRP	GTMGPPQCR	EACAPGYWGLPEQGCRRRCQCPGG	-----RCDPHTGR	CNCPPLSGER	2141	
2034	HCACKS	GVTRQCDRCAVDHWKYEKDGCT	PCN	CNQYSRGFCGNPNTGKCQCLPGVIGDR	2093		
2142	CDTCSQ	QHQPVP	PGFVGHSIHCEVCDHCVVLL	DDLERAGALLPAIHEQL	RGINASSMA	2201	
2094	CDACPN	RWVL	IKDEG-----CQECN	NCHALLDVTDRMYQIDSV---LED	FN	SVTLA	2143
2202	WARLHRLN	-----ASIADLQ	SQLRSP	GLPRHET-AQQL	2233		

Db	2144	FFTSQKLNYYDQLADELEPKVKLLDPSVDSLSPSKKANSELESDAKSYAKQVNOQTLANAF	2203
Qy	2234	EVLEQQSTSLGQDARRLGGQAVGTRDQASQLLAGTEATLGHAKTL-LAAIRAVDRTLSEL	2292
Db	2204	DIRERSSTTLG-NITVAYDEAVKSADQAKEAIASVEAL---SKNLEAAAATKIDAALAEQA	2259
Qy	2293	MSQTHGLGLANASAPSGEQLLRLTAEVERLLWEMRRARDLGAPQAAAEEALAAQORLLARV	2352
Db	2260	QHILGOINGTSELTTPNEQVL---EKARKLYE-EVNTLVLPKAKQNKSLNALKNIDIGEF	2314
Qy	2353	QEQLSSLEENQALATQTRDLRLAQHEAGLMDLREALN-RAVDATREAQELNSRNQERLEE	2411
Db	2315	SDHLEDLFWNSEASQAKSAD-----VERRNVANQKAFD-----NSKFDTVSEQ	2357
Qy	2412	ALQRKQEL-SRDNATLQATLHAARDTTLASVFRLLHSLDQAKEELERLAASLDGARTPLLQ	2470
Db	2358	KLQAEKNIKDAGNFLINGDL-----TLNQINQKLDNLRDALNELNSFNKNVD-EELPVRE	2411
Qy	2471	RMQTFSPAGSKLRLVEAAEHAQQLGQLALNLSSIILDVNQDRLTQRAIEASNAYSRILO	2530
Db	2412	DQHKEADA-----LTDQAEQKAAELAIAQDLAAQYTDMTAS--AEPAIKAAATAYS	2464
Qy	2531	AVQAAEDAAGQALQQAADHTWTVVRQGLVDRAQQOLLANSTALEEAMLQEQQ-----	2581
Db	2465	AVEAAQKLSQDAISAGN--ATDKTDGIEERAHLADTGSTDLLQRAQSLQKVQDDLEPR	2522
Qy	2582	-----RLGLVWAALQGARTQLRDVRAKDKQLEAHIOA-----AQAMLAMDTDETSKK	2628
Db	2523	LNASAGKVQKISAVNNATEHQDKDINKLIDQLPAESQORDMWKNSNANASDALEILKNVLE	2582
Qy	2629	IAHAKAVAAEAQ-DTATRVQSOLQAMQENVERWQGYEGLRGQDLGQAVLDAGHSVSTLE	2687
Db	2583	ILEPVSQTPKLEKAHGINRDLTLTNKDVSQANKQLDDVEG-----SVSKLS	2630
Qy	2688	KTLPQLLAKLSILENRGVHNASALSASIGRVRELIAQARGAAKVKVPMKFNGRSGVOL	2747
Db	2631	E-----LAEDIEEQHRVGSQSRQLGQBIENLKAQVEAARQLANSIKVGVNFKPSTILEL	2685
Qy	2748	RTPRDLADLAAYTALKFYLGQPEPEPGQGTEDRFVMYMG----SRQATCDYMGVSLRDKK	2803
Db	2686	KTPEKTKLLATRTNLSTYFRTTEP-----SGFLLYLGNDNKTAQKNDFVAIVEINGY	2738
Qy	2804	VHVYQVQGEAGPAVLSIDEDI--GEQFAAVSLDRTLQFGHMSVTVERQWIKETKGDTV--	2859
Db	2739	PILITIDLGN-OPERITSDKYVADGRWYQAV-VDR--MGPNAKLTIREEL--PNGDVVEH	2791
Qy	2860	-----APGAEGILNLRPDDFVFYVGGYP--STFTPPPLLRFPYRGCIEMDTLNEEWSL	2912
Db	2792	SKSGYLEGSQNLHVQDKNSRLF-VGGYPGISDFNAPPDITTNPSFGDIEDLKIGDES	2850
Qy	2913	YNF-----ERTFQDLDTAVDRPCARSKSTGDPWLTDGSLYLDGTGPARISFDSQIS	2961
Db	2851	WNFVYGGDDNQACARDVLLEKKKPVTLGLRFGKNGYVQNLATSNLKSRSSTQPSFKADKD	2910
Qy	2962	TTKRFEQELRLVSYSGVLFFFLKQQSQFLCLAVQEGSLVLLYDFGAGLKKAVPLQPPPLT	3021
Db	2911	TS-----NGLFFYGRDKHYMSIEMIDGAIFFNISLGE-----2944	
Qy	3022	SASKAIQVFLGGSRKRV-----LVRVER-----ATVYSVEQDNDELEA	3060
Db	2945	---GGVQ---SGSQDRYNDNQWHKVQAEERNGLLKVDDIVISRTNAPLEADLELPKL	2997
Qy	3061	DAYYLGVPDPQLPPSLRWLFPPTGGSVRGCVKGIKALGYVDLKLRLNT-TGVSAGCTADL	3119
Db	2998	RRLYEGG-HPRLNTSIS-LQP---NFDGCDNVVINQGVVDLTYEYVTGGVVEGCSAKF	3052
Qy	3120	LVGRAMTFHGHGFLRLALSNVAPLTGNVYSGFGFHSQAQDSALLYRASPD--GLCQVSLQ	3177
Db	3053	STVVSYPHEYGFRLR--MNNVSS-DNNLHVVLVHFKTTQPNGVLFYAANHQSSTIGLSLQ	3109
Qy	3178	QGRVSLQLLRT-EVKTQAGFADGAPHYVAFYSNATGVWLIVDDQLQOMKPHRGPPPELOP	3236
Db	3110	DGLLKLNSMGSQLVIDDRILNDGEDHVVTVQHTQGEHLRLTVDVDDNKRGLG-----SP	3161

QY 3237 QP---EGPPRLILGLPES-----GTIYNFSGCISNVFVQRLGPGQVFDL---QQ 3281
Db 3162 QPLILEGCD-IFAGLPDNYRTPNALASLAYFVGCISDVTN-----EELINFANSAEK 3215
QY 3282 NLGSVNVSTGCAPALCAQTPGLCP----- 3305
Db 3216 KNGNIN---GCPPHVLAYPESLVPSYPSGDNVESPSWNSADTLPLPKPDIESTLPPTTP 3272
QY 3306 -----RGLQATARKASRRSRQPAR-----HPA 3327
Db 3273 TTTTTTTTTTTTTTTTTTTTTTSPDIVDEEKEIEAKTPQKILTRPPAKLNLPSPDER 3332
QY 3328 CMLPPH-----LRTTRDSYQFGGSLSSHLEFVGILARHNWPSLSMHVLPSSRGLLLFTA 3383
Db 3333 CKLPEQPNFVDFTAGYRFYGLREBQRLQINSLPVKVRHHDIGISFRTERPNGLLIY-A 3391
QY 3384 RLRPGSPSLALFLSNHGFVAQMEGLGTRLRQA--SRQSRPGRWHKVSVRWEKNRILLVT 3441
Db 3392 GSKQRDDFAVYLLDGRVTEYR-VGAQLQAKITTEAELNDGTWHTVEVVRTQKVSLLI 3450
QY 3442 DGARAWSQEGPHRQHQAHPQP-----HTLFVGG-----PASSHSSKLPVTVG 3487
Db 3451 D-----KLEQPGSVDLNAERSAPVLAVELPIYLGKVNKFLESEVKNLTDFKTEVPY--F 3502
QY 3488 SGCVKRLRLHGRPLGAPTRMAGVTPCILGLEAGLPPGSGGVITLDLPGLATLPDVGLEL 3547
Db 3503 NGCLKNIKFDAMDLETPEEFGVVPVPC-SEQVERGLFNNQKAFVKI-----FDHFDVGTGEM 3557
QY 3548 EV---RPLAVTGLIFHLGQARTPPYLQVTEKQVLLRADDDGAGEFSTSVTRPS--VLC 3601
Db 3558 KISFDFRPRDPNGLLFVHGKNSYAILL-VDNTLYFTVKTDLKNIVSTNYKLPNNESFC 3616
QY 3602 DGQWHLRAVMKSGNVLRLVD-AQSNHTVGPGLLAAAAGAPAPLYLGLPEPMAVQWPW-- 3658
Db 3617 DGKTRNVQAISKVFVNIADVFISSNPGVGNESVITRTNRPLFLGG---HVAFORAPGI 3673
QY 3659 ---PAYCGMRRRLAVNRSPVAMTRSEVHVGAVGASGCP 3693
Db 3674 KTKSKFGKISKVEVNRQMINITPNMVV-GDIWQGYCP 3710

RESULT 13
ID AAM50358
XX AAM50358 standard; protein; 953 AA.
AC AAM50358;
XX
DT 18-FEB-2002 (first entry)
XX
DE Human laminin-15 alpha 5 chain.
XX
KW Laminin-15; human; retina; eye; therapy; ophthalmological;
KW antiinflammatory; rod dystrophy; rod-cone dystrophy;
KW retinitis pigmentosa; macular degeneration; retinal detachment.
XX
OS Homo sapiens.
XX WO200183516-A1.
XX
PD 08-NOV-2001.
XX
PF 01-MAY-2001; 2001WO-US013943.
XX
PR 01-MAY-2000; 2000US-0200863P.
XX
PA (MASS-) MASSACHUSETTS GEN HOSPITAL.
XX
PI Burgeson RE, Brunken W, Champlaud M, Hunter D;
XX WPI; 2002-041478/05.
DR N-PSDB; AAI70817.
XX

PT Novel substantially pure preparation comprising laminin having laminin
chain alpha 5, beta 2, and gamma 3, useful for treating retinal disorders
such as retinitis pigmentosa, macular degeneration, retinal detachment.
XX
PS Disclosure; Fig 2A; 58pp; English.
XX
CC The present sequence is that of the alpha 5 chain of human laminin-15, a
novel member of the laminin family that is produced in the retina. The
retina produces 2 novel laminin trimers: laminin-14 (alpha 4, beta 2,
gamma 3) and laminin-15 (alpha 5, beta 2, gamma 3). These are expressed
within the inter-photoreceptor matrix and in the outer plexiform layer,
and may serve to stabilise retinal synapses. The invention provides the
laminin-15 preparations and cells comprising a nucleic acid encoding the
laminin alpha 5, beta 2 and gamma 3 chains, and which are capable of
producing laminin-15. The laminin-15 preparation is used in claimed
methods of: increasing retina immunophotoreceptor matrix stability;
increasing the stability of retina photoreceptor compounds, especially an
outer segment, inner segment or synapse; increasing retina adhesion;
treating a disorder associated with retina degeneration, especially rod
dystrophy, rod-cone dystrophy, retinitis pigmentosa, macular degeneration
and retinal detachment; increasing the stability of synapses of the
central nervous system or peripheral nervous system; stimulating an
neuroregeneration, axon outgrowth or synapse formation; preparing an
implant, e.g. a catheter, artificial joint, retinal implant, timed
releasing device, neural cell growth guide or artificial tissue, by
coating with the laminin-15 preparation; and increasing photosensitivity
by implanting a tip coated with the laminin-15 preparation into an eye.
CC The laminin may be recombinant, and the 3 chains co-expressed in the same
cell or expressed in different cells
XX
SQ Sequence 953 AA;

Query Match 24.9%; Score 5002; DB 5; Length 953;
Best Local Similarity 100.0%; Pred. No. 3.5e-276;
Matches 953; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2743 SGVQLRTPRDLADLAAYTALKFYLGQPEPEPGQGTEDRFVYMGSRQATGDYMGVSLRDK 2802
Db 1 SGVQLRTPRDLADLAAYTALKFYLGQPEPEPGQGTEDRFVYMGSRQATGDYMGVSLRDK 60
QY 2803 KVHWVYQLGEAGPAVLSIDEDIGEOPAAVSLDRTLQFGHMSVTVERQMIQETKGDVAPG 2862
Db 61 KVHWVYQLGEAGPAVLSIDEDIGEOPAAVSLDRTLQFGHMSVTVERQMIQETKGDVAPG 120
QY 2863 AEGLLNLRPDDFVYVGGYPTFTPPPLLRPPGYRGCIEMDTLNEEVSLYNFERTFQLD 2922
Db 121 AEGLLNLRPDDFVYVGGYPTFTPPPLLRPPGYRGCIEMDTLNEEVSLYNFERTFQLD 180
QY 2923 TAVDRPCARSKSTGDPWLTDGSLDGTGTFARISFDSQISTTKRFEQELRLVSYGVLF 2982
Db 181 TAVDRPCARSKSTGDPWLTDGSLDGTGTFARISFDSQISTTKRFEQELRLVSYGVLF 240
QY 2983 KQSQFLCLAVQEGSLVLLYDFGAGLKKAVPLQPPPLPITSASKAIQVFLGGSRRKVLVR 3042
Db 241 KQSQFLCLAVQEGSLVLLYDFGAGLKKAVPLQPPPLPITSASKAIQVFLGGSRRKVLVR 300
QY 3043 VERATVYSVEQDNDLELADAYILGGVPPDQLPPLSLRWLFPPTGGSVRGCVKGIKALGKYVD 3102
Db 301 VERATVYSVEQDNDLELADAYILGGVPPDQLPPLSLRWLFPPTGGSVRGCVKGIKALGKYVD 360
QY 3103 LKRLNTTGVSAAGTADLLVGRANTFHGHFLRLALSNAVAPLTGNVYSGFGFHSQDSALL 3162
Db 361 LKRLNTTGVSAAGTADLLVGRANTFHGHFLRLALSNAVAPLTGNVYSGFGFHSQDSALL 420
QY 3163 YYRASPDGLCOVSLQOQGRVSLQLLRTEVKTQAGFADGAPHYVAFYSNATGVWLYVDDQLQ 3222
Db 421 YYRASPDGLCOVSLQOQGRVSLQLLRTEVKTQAGFADGAPHYVAFYSNATGVWLYVDDQLQ 480
QY 3223 QMKPHRGPPPELOPQPEGPPRLILGGLPESGTIYNFSGCISNVFVQRLGPGQVFDLQON 3282
Db 481 QMKPHRGPPPELOPQPEGPPRLILGGLPESGTIYNFSGCISNVFVQRLGPGQVFDLQON 540
QY 3283 LGSVNVSTGCAPALCAQTPGLGPRGLQATARKASRRSRQPARHPACMLPPLHRTTRDSYQ 3342

Db 541 LGSVNVSTGCAPALQATPGTGLGPRGLQATARKASRRSQPARHPACMLPPHRLTRDSYQ 600
QY 3343 FGGSLSSHLEFVGGILARHNWPSLSMHVLPSSRGLLLFTARLPSPSLALFLSNHGFV 3402
Db 601 FGGSLSSHLEFVGGILARHNWPSLSMHVLPSSRGLLLFTARLPSPSLALFLSNHGFV 660
QY 3403 AQMEGLGTRLRRAQSRQSRPGRWHKVSVRWEKNRILLVTDGARAWSEQGPHRQHQAHP 3462
Db 661 AQMEGLGTRLRRAQSRQSRPGRWHKVSVRWEKNRILLVTDGARAWSEQGPHRQHQAHP 720
QY 3463 QPHTLFVGGLPASSHSSKLPVTVGFGSCVVKRLRLHGRPLGAPTRMAGVTPCIIPLPGL 3522
Db 721 QPHTLFVGGLPASSHSSKLPVTVGFGSCVVKRLRLHGRPLGAPTRMAGVTPCIIPLPGL 780
QY 3523 FFPGGSGVITLDPGATLPDVGLGLEVRPLAVTGLIFHLGQARTPPYLQVTEKQVLLR 3582
Db 781 FFPGGSGVITLDPGATLPDVGLGLEVRPLAVTGLIFHLGQARTPPYLQVTEKQVLLR 840
QY 3583 ADDGAGEFSTSVTRPSVLCDSQWHRRLAVMKSGNVLRLEVDQAQSNHTVGPPLAAAGAPAP 3642
Db 841 ADDGAGEFSTSVTRPSVLCDSQWHRRLAVMKSGNVLRLEVDQAQSNHTVGPPLAAAGAPAP 900
QY 3643 LYLGLPEPMAVQPPPAYCGCMRRRLAVNRSPVAMTRSVVHGVAGSGCPAA 3695
Db 901 LYLGLPEPMAVQPPPAYCGCMRRRLAVNRSPVAMTRSVVHGVAGSGCPAA 953

RESULT 14
ABB09502
ID ABB09502 standard; protein; 908 AA.
AC ABB09502;
XX
DT 01-NOV-2002 (first entry)
XX
DE Human laminin alpha-5-like NOV1b protein, SEQ ID NO:4.
XX
KW Human; NOVX; neurological disorder; Alzheimer's disease;
KW Huntington's disease; Parkinson's disease; pain; behavioural disorder;
KW addiction; tuberous sclerosis; cancer; immune disorder; allergy;
KW autoimmune disease; myasthenia gravis; asthma; arthritis; diabetes;
KW thyroiditis; cardiovascular disease; hypertension; reproductive disorder;
KW endometriosis; incontinence; psoriasis; scleroderma; alopecia; ulcer;
KW pancreatitis; cirrhosis; glomerular endometriosis; bacterial infection;
KW polycystic kidney disease; endocrine disorder; obesity; cardiomyopathy;
KW atherosclerosis; cell signal processing-related disorder;
KW metabolic pathway regulation disorder; cytostatic; neuroprotective;
KW antiinflammatory; immunosuppressive; analgesic; antiatherosclerotic;
KW dermatological; antibacterial; antiarthritic; hepatotropic; neurogenesis;
KW differentiation; proliferation; motility; haematopoiesis; wound healing;
KW angiogenesis; forensic biology; transgenic animal; drug screening;
KW gene therapy; NOV1b; laminin alpha-5-like; chromosome 20.
XX
OS Homo sapiens.
XX
PN WO200253742-A2.
XX
PD 11-JUL-2002.
XX
PF 07-JAN-2002; 2002WO-US0000375.
XX
PR 05-JAN-2001; 2001US-0260018P.
PR 08-JAN-2001; 2001US-0260360P.
PR 28-FEB-2001; 2001US-0272411P.
PR 02-MAR-2001; 2001US-0272817P.
PR 05-JUL-2001; 2001US-0303231P.
PR 12-JUL-2001; 2001US-0305060P.
PR 10-SEP-2001; 2001US-0318405P.
PR 12-SEP-2001; 2001US-0318700P.
PR 04-JAN-2002; 2002US-00037417.
XX
PA (CURA-) CURAGEN CORP.

XX Kekuda R, Alsobrook JP, Tchernev VT, Liu X, Spytek KA;
PI Patturajan M, Grosse WM, Lepley DM, Burgess CE, Vernet CAM, Li L;
PI Gorman L, Edinger S, Sciore P, Ellerman K, Malyankar U;
PI Rothenberg M, Stone D, Boldog F, Guo X, Shenoy S, Anderson D;
PI Padigaru M, Taupier RJ, Miller CE, Eisen A;
XX
DR WPI; 2002-583619/62.
DR N-PSDB; ABQ93880.
XX
PT Novel polypeptides and nucleic acids homologous to transmembrane
PT receptor, thymosin, neuromodulin-like family of proteins for diagnosing,
PT treating cancer, atherosclerosis, neurological, skin and autoimmune
PT disorders.
XX
PS Claim 1c; Page 17; 323pp; English.
XX
CC The invention relates to 24 novel human proteins designated NOV1-NOV14
CC (ABB09501-ABB09524), collectively referred to as NOVX proteins, and
CC nucleic acids encoding them (ABQ93879-ABQ93902). NOVX proteins, and
CC nucleotides are useful in the treatment, diagnosis or prevention of NOVX-
CC associated disorders or in the manufacture of a medicament for treating
CC such disorders, with specific applications described for each of the 24
CC NOVX proteins, based on their homology to known proteins. Various
CC disorders are associated with NOVX proteins including neurological
CC disorders (e.g., Alzheimer's, Huntington's and Parkinson's diseases),
CC pain, behavioural disorders, addiction, tuberous sclerosis, cancers
CC (e.g., colorectal cancer, leukaemia and osteosarcoma), immune disorders
CC (e.g., allergies and autoimmune diseases), myasthenia gravis, asthma,
CC various forms of arthritis, diabetes, thyroiditis, cardiovascular disease
CC (e.g., hypertension), reproductive disorders, endometriosis,
CC incontinence, psoriasis, scleroderma, alopecia, ulcers, pancreatitis,
CC cirrhosis, glomerular endometriosis, polycystic kidney disease, endocrine
CC disorders, obesity, bacterial infections and particularly cardiomyopathy,
CC atherosclerosis, cell signal processing-related disorders and disorders
CC of metabolic pathway regulation. NOVX nucleic acids and polypeptides may
CC be used to identify cellular receptors or downstream effectors which
CC binds to a NOVX protein, and are also useful as targets for the
CC identification of small molecules that modulate or inhibit processes such
CC as neurogenesis, cell differentiation, cell motility, cellular
CC proliferation, haematopoiesis, wound healing and angiogenesis. NOVX
CC nucleic acid sequences can be used to identify a cell or tissue type and
CC are useful as a source of primers or probes for forensic biology and for
CC identifying and cloning NOVX homologues in other cell types. Cells
CC comprising NOVX nucleic acids are useful for producing non-human
CC transgenic animals which are useful for studying the function and
CC activity of NOVX proteins and for identifying and evaluating modulators
CC of NOVX activity. The present sequence represents the laminin alpha-5-
CC like protein NOV1b. The gene encoding NOV1b is located on chromosome 20
XX
SQ Sequence 908 AA;

Query Match 23.6%; Score 4756.5; DB 5; Length 908;
Best Local Similarity 99.5%; Pred. No. 3.3e-262;
Matches 908; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 2783 MYNGSRQATGDMGVSLRDKKVVHVVYQLGAGPAVLSIDEDIGEQFAAVSLDRTLQFGHM 2842
Db 1 MYNGSRQATGDMGVSLRDKKVVHVVYQLGAGPAVLSIDEDIGEQFAAVSLDRTLQFGHM 60
QY 2843 SVTVRQMIQETKGTVPAGAEGLLNLRPDDFVYVGGYPSFTFPPLLRFPYRGCIEM 2902
Db 61 SVTVRQMIQETKGTVPAGAEGLLNLRPDDFVYVGGYPSFTFPPLLRFPYRGCIEM 120
QY 2903 DTLNEEVVSLYNFERTFQDLDVADRPCARSKSTGDPWLTDGSLDGTGFARISFDSQIST 2962
Db 121 DTLNEEVVSLYNFERTFQDLDVADRPCARSKSTGDPWLTDGSLDGTGFARISFDSQIST 180
QY 2963 TKRFEQELRLVSYSGVLPFLKQSQFLCLAVQEGSLVLLYDFGAGLKAVPLQPPPLTSS 3022
Db 181 TKRFEQELRLVSYSGVLPFLKQSQFLCLAVQEGSLVLLYDFGAGLKAVPLQPPPLTSS 240
QY 3023 ASKAIQVFLGSGSRKRVLRVERATVYSVEQNDLELADAYLGGVPPDQLPPSLRWLFP 3082

Db 241 ASKAIQVFLGSRKRVLRVERATVYSVEQNDLEADAYLGGVPPDQLPSLRWLFP 300
QY 3083 TGGSVRGCVKGIKALGKYVDLKRNTTGVSAAGTADLLVGRAMTFHGHGFLRLALSNVAP 3142
Db 301 TGGSVRGCVKGIKALGKYVDLKRNTTGVSAAGTADLLVGRAMTFHGHGFLRLALSNVAP 360
QY 3143 LTGNVYSGFGFHSADQSALLYRASPDGLCQVSLQOGRVSLQLLRTTEVKTQAGFADGAPH 3202
Db 361 LTGNVYSGFGFHSADQSALLYRASPDGLCQVSLQOGRVSLQLLRTTEVKTQAGFADGAPH 420
QY 3203 YVAFYSNATGVWLYVDDQLQOMKPHRGPPPELQPOEGEPRLLLGGLPESGTYNFSGCI 3262
Db 421 YVAFYSNATGVWLYVDDQLQOMKPHRGPPPELQPOEGEPRLLLGGLPESGTYNFSGCI 480
QY 3263 SNVFORLLGQRFVFDLQONLGSVNVSTGCAPALQATPGLGPRGLQATARKASRRSRQP 3322
Db 481 SNVFORLLGQRFVFDLQONLGSVNVSTGCAPALQATPGLGPRGLQATARKASRRSRQP 540
QY 3323 ARHPACMLPPLHRTTRDSYQFGGSLSSHLEFVVGILARHNWPSLSMHVLPSSRGLLLFT 3382
Db 541 ARHPACMLPPLHRTTRDSYQFGGSLSSHLEFVVGILARHNWPSLSMHVLPSSRGLLLFT 600
QY 3383 ARLRPGSPSLALFLSNHGFVAQMEGLGTRLRQAQRSPRGRWHKVSVRWEKRIILLVTD 3442
Db 601 ARLRPGSPSLALFLSNHGFVAQMEGLGTRLRQAQRSPRGRWHKVSVRWEKRIILLVTD 660
QY 3443 GARAWSQEGPHRQHQGAHPQPHTLFVGGPLPASSHSSKLPVTVGFGCVKRLRLHGRPLG 3502
Db 661 GARAWSQEGPHRQHQGAHPQPHTLFVGGPLPASSHSSKLPVTVGFGCVKRLRLHGRPLG 720
QY 3503 APTRMAGVTPCITLGPLEAGLFFPGSGVITLDPGATLPDVGLLEVRPLAVTGLIFHLG 3562
Db 721 APTRMAGVTPCITLGPLEAGLFFPGSGVITLDPGATLPDVGLLEVRPLAVTGLIFHLG 780
QY 3563 QARTPPYLQVTEKQVLLRADDGAGEFSTVTRPSVLCDGQWHRLAVMKSNNVLRLEVD 3622
Db 781 QARTPPYLQVTEKQVLLRADDGAGEFSTVTRPSVLCDGQWHRLAVMKSNNVLRLEVD 835
QY 3623 AQSNHTVGPLLAAAAGAPAPLYLGLPEPMAVQPPPPAYCGCMRRRLAVNRSVPAMTRSVE 3682
Db 836 AQSNHTVGPLLAAAAGAPAPLYLGLPEPMAVQPPPPAYCGCMRRRLAVNRSVPAMTRSVE 895
QY 3683 VHGA VGASGCPAA 3695
Db 896 VHGA VGASGCPAA 908

RESULT 15

AD09114
ID ADE09114 standard; protein; 1486 AA.
XX
AC ADE09114;
XX
DT 29-JAN-2004 (first entry)
XX
DE Novel protein-related contig polypeptide sequence #180.
XX
KW novel gene; novel protein; tissue marker; molecular weight marker;
KW chromosome marker; genetic disorder; contig.
XX
OS Unidentified.
XX
PN WO2003054152-A2.
XX
PD 03-JUL-2003.
XX
PF 10-DEC-2002; 2002WO-US039555.
XX
PR 10-DEC-2001; 2001US-0339739P.
PR 11-DEC-2001; 2001US-0339453P.
PR 14-MAR-2002; 2002US-0365091P.
PR 14-MAR-2002; 2002US-0365384P.

PR 12-APR-2002; 2002US-0372381P.
PR 12-APR-2002; 2002US-0372615P.
PR 22-APR-2002; 2002US-00128558.
PR 24-APR-2002; 2002US-0376045P.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;
PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
XX
DR WPI; 2003-569235/53.
XX
PT New polynucleotides, useful for expressing recombinant proteins for
PT analysis, characterization or therapeutic use, or as markers for tissues
PT in which the corresponding protein is preferentially expressed.
XX
PS Disclosure; SEQ ID NO 2658; 1177pp; English.
XX
CC The invention comprises the amino acid and coding sequences of novel
CC proteins. The DNA and protein sequences of the invention are useful as:
CC markers for tissues in which the corresponding protein is preferentially
CC expressed; as molecular weight markers on gels; as chromosome markers or
CC tags; to identify chromosomes or to map related gene positions; and to
CC compare with endogenous DNA sequences in patients to identify potential
CC genetic disorders. The present amino acid sequence was used in the
CC exemplification of the invention.
XX
SQ Sequence 1486 AA;

Query Match 20.2%; Score 4058; DB 7; Length 1486;
Best Local Similarity 45.5%; Pred. No. 4.4e-222;
Matches 759; Conservative 219; Mismatches 483; Indels 206; Gaps 22;

Qy 45 LHPPYFNLAEGARIAAASATCGEAPARGSPRPTELYCKLVGGPVAGDPNQIRGQYCD 104
Db 12 LHPTYFNLAE-AEDLATATCGERGEGRPQP--ELYCKLVGGPTAPGS-GHTIQGQFCD 67
Qy 105 ICTAANSNKAPASNAIDGTERWWSQPLSLRGLEYNNVNTLDLQVHFVAYVLIKFPANS 164
Db 68 YCNSEDPRKAHPTNAIDGSEWWSQPLSLSGTQYNNVNTLDLQVHFVAYVLIKFPANS 127
Qy 165 PRPDLWVLSRMDFGRTYQPWQFFASSKRDCLERFGPQTLERITRDDAAICTTEYSRIVP 224
Db 128 PRPDLWVLSRMDFGRTYQPWQFFASSKRDCLERFGPQTLERITRDDAAICTTEYSRIVP 187
Qy 225 LENGEIVVSLVNGRPGAMNFSYPLLRFTKATNVRLEFRTNTLLHLMGKALRDPVT 284
Db 188 LENGEIVVSLVNGRPGAMNFSYPLLRFTKATNVRLEFRTNTLLHLMGKALRDPVT 247
Qy 285 RRYYSIKDISIGRCVCHGHADACDAKDPDTPFRLLQCTCOHNTCGTCDRCPCGFNQPP 344
Db 248 RRYYSIKDISIGRCVCHGHADACDAKDPDTPFRLLQCTCOHNTCGTCDRCPCGFNQPP 305
Qy 345 WKPATANSANECQSCNCGHATDCYDPEVDRRRRASQSLDGTQYGGGVVICDQHHTAGVN 404
Db 306 WRPAWEQSHCEACNCHGHASNCYDPEVDRRRRASQSLDGTQYGGGVVICDQHHTAGVN 365
Qy 405 CERCLPGFYRSPNHPDLSPHVCRRNCESDFTDGTCELTGRCYCRNFSGERCDVCAEG 464
Db 366 CEQCAKGYRYPYGVVDPADPGCIPSCDPEHADG-CEQSGRCHCKPNFHDNCEKCAIG 424
Qy 465 FTGFPSC-----YP--TPSSNDTREQVLPAGQIVNCDSCSAAGTQGNACRKDPVRGRLC 517
Db 425 Y-NFPFCLRIPIFPVSTPSSDPV-----AGDIKGCDCNL----- 458
Qy 518 KPNFQGTCHCELCAFGFYGPGCQPCQSSPGVADDRCDPDTGQCRCRVFEGATCDRCAPG 577
Db 459 ----- 458
Qy 578 YHFHPLCQLCCSPAGTLPEGCEAGRCCLCQPFAGHCDRCRPGYHGFNCACTCDPR 637
Db 459 -----EGVLPICDAHGRCLCRPGVEGPRCDTCRSGFYSFPICOA----- 498

Search completed: May 18, 2004, 14:41:09
Job time : 140.335 secs

QY 638 GALDQLCAGGLCRPRPGYTGTACQECSPGFHGFPCVPHCHCSAEGSLHAACDPRSGQCS 697
Db 499 -----CWCSALGSSYQMPCCSSVTGQCE 519
QY 698 CRPRVTGLRCDTVCVPGAYNFPYCEAGS--CHPAGLAPVDPALPEAQVPCMCRAHVEGPSC 755
Db 520 CRPGVTGQRCRCLSGAYDFPHCQSSSACDPAGTINWNLGY-----CQCKLHVEGPTC 573
QY 756 DRCKPGFWGLSPSNPEGTRCSCDLRGTGLGVABECQPGTQCFCCKPHVCGQACASCKDGF 815
Db 574 SRCKLLYNWLDKENPSCGSECKCHKGGTVSGTGECRQGDGDCHCKSHVGGSDCDEG 633
QY 816 FGLDQADYFGCRSCRCDDIGGALGQSCPEPTGVCRCRPNTQGPTCSEPARDHYLPDLHLR 875
Db 634 FALEKSNYFGCQCQCQCDIGGALSSCMCSGPGVCQCREHVVGKVCQRPENNYFFPDLHMK 693
QY 876 LELIEAATPEGHAVRFGFNPLEFENFSWRGYAQMAVPQ--PRIVARLNLTSDDLFWLVR 933
Db 694 YEIEDGSTPNGRDLRFGFDPLAFPEFSWRGYAQMASVQNDVRITLNVKSSGSLFRVILR 753
QY 934 YVNRGAMSVGRVSVREGRSAACANCTAQSQPVAFPPSTEPAFITVPQRGEGEPFVLNP 993
Db 754 YVNPCTEAVSGHITIYPSWGA-----AQSKIEIIFLPSKEPAFVTLPGNGPADPFSITP 806
QY 994 GTWALRVEAEGVLLDYVVLPSAYYEAALLQLRVTEACTYRPSAQSGDNCCLLYTHLPLD 1053
Db 807 GMWVACIKAEGLLDYLVLLPRDYEASDLQLPVTEPCAYAGPPQ---ENCLLYQHLPT 863
QY 1054 GFPSAAGLEALCRQDNLPRPCPTEQLSPSHPLITCTGSDVDVQLQVAVPOPGRYALV 1113
Db 864 RFPCTRSCEARHFLLDGEPRPVAVRQPTPAHPVMVDLSGREVELHLRVRIPQVGPYVWV 923
QY 1114 EYANEDARQEVGVAVHTPQAPQOGLLSLHPCLYSTLCRGTDARTDQDLHAFVHLDSEASV 1173
Db 924 EYSTEAAQLFVVDANVKSSGSLVLAGQVNIYSCNYSVLCRSAVIDHMSRIAMYELLTDADI 983
QY 1174 RLTAEQARFFLHGVTLVPIEEFSEFVEPRVSCISSHGAFGPSAAACLPSPFPKPPQPII 1233
Db 984 QLKGHMARELLHQVCIIPIEEYSAEYVRPQVHCIASYGRFVNQSATCVSLAHEPTPTALI 1043
QY 1234 LRDCQVIFLPPGLPLTHAQDLTATSPAGPRPRPPTAVDPDAEP-TLLREPOATVVFTTH 1292
Db 1044 L-----DVLSGRPFPH---JPQSSPS-----VDVLPGVTLKAPQNVTLRGR 1083
QY 1293 VPTLGRYAFLLHGYPQAHPTFFVEVLINAGRVWQGHANASFCPHGYGCRTLVCCEGQALL 1352
Db 1084 VPHLGRYVFEVTHFYQAAHPTFPQAVSVDGGWPRAGSFHASFCPHVLGCRDQVIVXGQIEF 1143
QY 1353 DVTHSELTVTVRVEGRWLWLDVVLVVPENVYSFGYLREBELDKSYDFISHCAAQGYHIS 1412
Db 1144 DISEPEVAATVKVPEGKSLVLRVLVVAENYDYQILHKXSMDKSLEFITNCGKNSFYLD 1203
QY 1413 PSSSLFCRNAAAASLSLFYNNGARPCGCHEVGATGPTCEPFGGQCPCHAHVIGRDCSRCA 1472
Db 1204 POTASRFCNKSARSLSVAFYHKGALPCECHPTGATGPHCSPEGGSAAHASPSSSGSAPAVQ 1263
QY 1473 TGYWGFPMC--RPCDCGARLCCDELTCQCICPPRTIPDCLLCQPOTFGCHPLVGCHECNC 1530
Db 1264 QATYGFPRCKPKPCSCGRRLCCEMTGQCRCPRTVRPQCEVCETHSFSLHPMAGCEGCNC 1323
QY 1531 SGPGIQELTDPTCDTDSGQCKRCRPNVTGRRCDTCSPGFHGYPRCRPCDCHEAGTAPGVC 1590
Db 1324 SRRGTIEAAMPRCDRDSGQCGCKPRITGRQCDRCASGFYGFPECVPCNCNRDGTGEGVCD 1383
QY 1591 PLTGQCYCKENVQGPCKDCQCSLGTFSILDAANPKGCTRCFCGATERCRSSSYTROEFVDM 1650
Db 1384 PGTGACLCCKENVEGTECNVCREGSFHLDPANLKGCTSCFCFVNNQCHSHKRRTKFVDM 1443
QY 1651 EGWVLLSTDRQVVPHERQPGTEMLRADLRHVPEAVPEAFPELYWQAP 1697
Db 1444 LGWHLETADRVDPVPSFNPGSNSMVADLQELPATIHSA----SWVAP 1486

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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:30:58 ; Search time 27.952 Seconds
(without alignments)
6824.493 Million cell updates/sec

Title: US-10-037-182-2
Perfect score: 20118
Sequence: 1 MAKRLCAGSALCVGRGPA.....AMTRSVEVHGAVGASGCPAA 3695

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15839	78.7	3635	4	US-09-845-583A-2
2	5002	24.9	953	4	US-09-845-583A-4
3	3141.5	15.6	3106	4	US-09-562-702A-10
4	3133.5	15.6	3084	4	US-09-562-702A-12
5	3104	15.4	3111	2	US-08-460-309-4
6	3104	15.4	3111	2	US-08-125-077-4
7	3103.5	15.4	3110	4	US-09-562-702A-6
8	3103.5	15.4	3110	4	US-09-561-709B-7
9	3101.5	15.4	3110	4	US-09-562-702A-2
10	3099.5	15.4	3088	4	US-09-562-702A-8
11	3097.5	15.4	3089	4	US-09-562-702A-4
12	2854	14.2	3075	2	US-08-460-309-5
13	2854	14.2	3075	2	US-08-125-077-5
14	2260.5	11.2	1713	3	US-08-600-982-24
15	2260.5	11.2	1713	5	PCT-US94-10261A-24
16	2136.5	10.6	1792	4	US-09-561-818A-4
17	2136.5	10.6	1800	4	US-09-561-818A-8
18	2136.5	10.6	1816	4	US-09-561-818A-2
19	2136.5	10.6	1824	4	US-09-561-818A-6
20	2111.5	10.5	1792	4	US-09-561-818A-12
21	2111.5	10.5	1816	4	US-09-561-818A-10
22	1604	8.0	1799	4	US-09-845-583A-6
23	1573.5	7.8	1786	4	US-09-562-702A-14
24	1573.5	7.8	1786	4	US-09-561-818A-14
25	1573.5	7.8	1786	4	US-09-561-709B-9
26	1572.5	7.8	1786	4	US-09-562-702A-18
27	1572.5	7.8	1786	4	US-09-561-818A-18

28	1564.5	7.8	1765	4	US-09-562-702A-16
29	1564.5	7.8	1765	4	US-09-561-818A-16
30	1558	7.7	1725	4	US-09-562-702A-20
31	1558	7.7	1725	4	US-09-561-818A-20
32	1556.5	7.7	1761	4	US-09-561-709B-1
33	1535	7.6	1798	4	US-09-561-709B-11
34	1524	7.6	1798	4	US-09-845-583A-8
35	1460	7.3	1587	4	US-09-561-709B-3
36	1460	7.3	1587	4	US-09-562-702A-30
37	1355.5	6.7	1605	4	US-09-561-818A-26
38	1355.5	6.7	1605	4	US-09-562-702A-32
39	1329.5	6.6	1572	4	US-09-561-818A-28
40	1329.5	6.6	1572	4	US-09-562-702A-22
41	1317	6.5	1609	4	US-09-561-818A-22
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43	1317	6.5	1617	4	US-09-562-702A-24
44	1295.5	6.4	1576	4	US-09-561-818A-24
45	1295.5	6.4	1576	4	US-09-561-818A-24

ALIGNMENTS

RESULT 1
US-09-845-583A-2
; Sequence 2, Application US/09845583A
; Patent No. 6635616
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Brunken, William Joseph
; APPLICANT: Champliand, Marie-France
; APPLICANT: Hunter, Dale
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
; FILE REFERENCE: 10287-056001
; CURRENT APPLICATION NUMBER: US/09/845,583A
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/200,863
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3635
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-845-583A-2

Query Match	78.7%	Score 15839;	DB 4;	Length 3635;
Best Local Similarity	79.4%	Pred. No. 0;		
Matches 2874;	Conservative 277;	Mismatches 452;	Indels 18;	Gaps 8;
QY	79	DLYCKLVGGPVAGDPNQITIRGOYCDICTAANSNKAHPASNAIDGTERWWQSPPLSRGLE	138	
Db	1	DLYCKLVGGPVAGDPNQITIRGOYCDICTAANSNKAHPASNAIDGTERWWQSPPLSRGLE	60	
QY	139	YNEVNTLDLGQVHFVAYVLIKFANSRPPDLWVLSRMDFGRTYQPWFQFFASSKRDCLER	198	
Db	61	YNEVNTLDLGQVHFVAYVLIKFANSRPPDLWVLSRMDFGRTYQPWFQFFASSKRDCLER	120	
QY	199	FGPQTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRPGAMNFSYSPLLREFTKATN	258	
Db	121	FGPQTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRPGAMNFSYSPLLREFTKATN	180	
QY	259	VRLRFLRTNLLGHLMGKALRDPVTTRRYYSIKDISIGRCVCHGHADACDAKDPDPF	318	
Db	181	IRLRLRFLRTNLLGHLMGKALRDPVTTRRYYSIKDISIGRCVCHGHADACDAKDPDPF	240	
QY	319	RLQCTCQHTNCGGTCDCRCCPGFNQCPWKPATANSANECQSCNCGYGHATDCYYDPEVDRR	378	
Db	241	RLQACQHTNCGGTCDCRCCPGFNQCPWKPATATDSANECQSCNCGYGHAYDCYYDPEVDRN	300	
QY	379	ASQSLDGTYYQGGGVICIDQHTTAGVNCERCLPGFYRSPNHLPSHVCRRCNCESDFTDG	438	
Db	301	ASQNQDNVYQGGGVICIDQHTTAGVNCERCLPGFFRAPDQPLDSPHVCRCPCDCESDFTDG	360	

QY 439 TCEDLTGRVCYCRPNFSGERCDCVCAEGFTGFPSCYPTPS-SSNDTREQVLPAGQIWNCDQS 497
Db 361 TCEDLTGRVCYCRPNFTGELCAACAEYTDFFHCYPLPSFFENDTREQVLPAGQIWNCDN 420
QY 498 AAGTQGNACRKDPVGRCLCKPNFQTHCELCAFGYGPQCFCQCSSPGVADRDCTPDT 557
Db 421 AAGTQGNACRKDPVGRCLCKPNFQTHCELCAFGYGPQCFCQCSSPGVANSLCDPES 480
QY 558 GQCRVRVFEAGTCDRCAPGYFHFPLCQCGCSPAGTLPBEGDEAGRCLCQPFAGPHCD 617
Db 481 GQCMRTGFEGRCDCHCALGYFHFPLCQCGCSPAGTLPBEGDEAGRCLCQPFAGPHCD 540
QY 618 RCREGYHGFNCACTCDPRGALDQCGAGGLCRCPGVTGTATCQECSPGFHGFPPSCVPC 677
Db 541 RCLPGYHGYEDCHACACDPRGALDQCGGVGGLCHCRPGNTGATCQECSPGFYGFPPSCIPC 600
QY 678 HCSAEGSLHAACDPRSGQCSRCRPRVTGLRCDTCTVPGAYNFPYCEAGSCHPAGLAPVDPAL 737
Db 601 HCSADGSLHTTCDPTTGQCRRCRPRVTGLHCDMCMVPGAYNFPYCEAGSCHPAGLAPANPAL 660
QY 738 PEAQVPCMAHVEGSPCDRCCKPFGWGLSPSNPEGCTRCSCDLRGLTGGVAECQPGTGQC 797
Db 661 PETQAPCMCAHVEGSPCDRCCKPGYWGGLSASNPEGCTRCSCDPRGLTGGVTECQ-GNGQC 719
QY 798 FCKPHVCGQACASCKDGFGLDQADYFGCRSCRCIDIGALGQSCBPRTGVCRCRPNTOGP 857
Db 720 FCKAHVCGKTCACCKDGFGLDQADYFGCRSCRCIDIGALGQSCBPRTGVCRCRPNTOGP 779
QY 858 TCSEPARDHYLPDLHLRLLELEEAATPEGHAVRFGFNPLEFENFWSRGYQAQMAPVQPRIV 917
Db 780 TCSEPARDHYLPDLHLRLLELEEAATPEGHAVRFGFNPLEFENFWSRGYAHMAIQPRIV 839
QY 918 ARNLNLTSPDLFWLVFRVYNRGAMSVGRVSVREEGRSAAACANCTAQSQVAFPPSTPEAF 977
Db 840 ARNLNLTSPDLFWLVFRVYNRGAMSVGRVSVREEGRSAAACANCTAQSQVAFPPSTPEAF 899
QY 978 ITVPQGRGEPFVLPNGTVALRVEAGVLLDYVLLPSAYEALQLRVTEACTYRPSA 1037
Db 900 ITVPQGRGEPFVLPNGTVALRVEAGVLLDYVLLPSAYEALQLRVTEACTYRPSA 959
QY 1038 QQSGDNCLLYTHPLDGFPPSAGLEALCRQDNLSPRCPTEQLSPSHPLITCTGSDVDV 1097
Db 960 LHSTENCLLYTHPLDGFPPSAGLEALCRQDNLSPRCPTEQLSPSHPLITCTGSDVDV 1019
QY 1098 QLQVAVPQGRYALVVEYANEDARQEVGAVHTPQAPQQLSLHPLCLYSTLCRGTD 1157
Db 1020 QLEMAVFPQGRYALVVEYANEDARQEVGAVHTPQAPQQLSLHPLCLYSTLCRGTD 1079
QY 1158 TQHLAVFHLDSASVRLTAEQARFFLHGVTLPTEFSPFVEPRVSCISSHGAFGPNS 1217
Db 1080 TQHLAVFHLDSASVRLTAEQARFFLHGVTLPTEFSPFVEPRVSCISSHGAFGPNS 1139
QY 1218 AACLSRFPKPPQPIILRDCQVPLPPGLPLTHAQDLTPATSPAGPRPRPPTAVDPDAEP 1277
Db 1140 AACLSRFPKPPQPIILRDCQVPLPPGLPLTHAQDLTPATSPAGPRPRPPTAVDPDAEP 1199
QY 1278 TLLREBQATVFTTHVPTLGRYAFLLHGYQPAHPTFPVEVLINAGRVWQGHANASFCPHG 1337
Db 1200 TLLRHFGQTVFTTQVPTLGRYAFLLHGYQPAHPTFPVEVLINAGRVWQGHANASFCPHG 1259
QY 1338 YGCRTLVCEGOALLDVTHSELTVTVRVPGRWMLWDYVLVVPENYVSFGYLREEPDKS 1397
Db 1260 YGCRTLVCEGOALLDVTHSELTVTVRVPGRWMLWDYVLVVPENYVSFGYLREEPDKS 1319
QY 1398 YDFISHCAAQGYHISPPSSSLFCRNAAASLSLFYNGARPCGCHVEGATGPTCEPFGQC 1457
Db 1320 YDFISHCATQGYHISPPSSSLFCRNAAASLSLFYNGARPCGCHVEGATGPTCEPFGQC 1379
QY 1458 PCHAHVIGRDCSRCATGYWGFNCRPCDCGARLDELGTGQICPPRTIPPDCCLCQPOTF 1517
Db 1380 PCRGHVIGRDCSRCATGYWGFNCRPCDCGARLDELGTGQICPPRTIPPDCCLCQPOTF 1439

QY 1518 GCHPLVGCBEBCNCSGPGIQELTDPTCDTDSGQCKCRPNVTGRRCDTCSPGFHGYPRCRPC 1577
Db 1440 GCHPLVGCBEBCNCSGPGVQELTDPTCDTDSGQCKCRPNVAGRRCDTCAAPFYGYPSCRPC 1499
QY 1578 DCHEAGTAPGVCDPLTGQCYCKENVOGPKDQCSLGTFSLDANPKGCTRCFCFGATERC 1637
Db 1500 DCHEAGTMASVCDPLTGQCHCKENVOGSRCDQCRVGTFSLDANPKGCTRCFCFGATERC 1559
QY 1638 RSSSYTROEFVDMEGWVLLSTDROVVPHERQPGTEMLRADLRHVEAPVEAFPELYWQAP 1697
Db 1560 GNSNLARHFEFVDMEGWVLLSSDRQVVPHEHRPEIELLHADLR---SVADTFSELYWQAP 1615
QY 1698 PSYLGDRVSSYGGTILRYELHSETQRGDVFPVPMESRPDVVLQGNQMSITFLEPAYPTPGHV 1757
Db 1616 PSYLGDRVSSYGGTILHYELHSETQRGDIPIPIYESRPDVVLQGNQMSIAFLELAYPPPGQV 1675
QY 1758 HRGQLOLVEGNFRHTETRTNTVSREELMMVLASLEQLQIRALFSQISSAVSLRRVALEVAS 1817
Db 1676 HRGQLOLVEGNFRHTETRTNTVSREELMMVLASLEQLQIRALFSQISSAVSLRRVALEVAS 1735
QY 1818 PAGQALASNVLELCLCPASVYRGDSQCECAPGYRDKGLFLGRCPVPCQCHGSHDRCLDPS 1877
Db 1736 BAGRGPPASNVLELCLCPANVYRGDSQCECAPGYRDKGLFLGRCPVPCQCHGSHDRCLDPS 1795
QY 1878 GVCVDCQHNTEGAHCERCQAGFMSS-RDDPSAPCVSCPCPLSVPSNPFAGCVCVLRGRTQ 1936
Db 1796 GICVGCQHNTEGDCERCRCRPGFVSSDPSNPASPCVSCPCPLAVPSNPFADGCVLRNGRTQ 1855
QY 1937 CLCKPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSNGNBDNLLFSDCDPLTGACRGCLR 1996
Db 1856 CLCKPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSNGNBDNLLFSDCDPLTGACRGCLR 1915
QY 1997 HTTGPRCEICAPGFYGNALLPGNCTRCDCCTPCGTEACDPSHGHCLCKAGVTGRRCDRCQE 2056
Db 1916 HTTGPHCERCAPGFYGNALLPGNCTRCDCCTPCGTEACDPSHGHCLCKAGVTGRRCDRCQE 1975
QY 2057 GHFGFNGCGGCRPCACGPAAGSECHPSQSGQCHCRPGTMGPOCRECAPGYWGLPEQGCR 2116
Db 1976 GHFGFNGCGGCRPCACGPAAGSECHPSQSGQCHCRPGTMGPOCRECAPGYWGLPEQGCR 2035
QY 2117 CQCPGRCDDHTGRCNCPPLSGERCDTCSQHQHVPPGVPVGHSHICEVCDHCVVLLLD 2176
Db 2036 CQCPGRCDDHTGRCNCPPLSGERCDTCSQHQHVPPGVPVGHSHICEVCDHCVVLLLD 2095
QY 2177 DLERAGALLPAIHEQLRGINASSMAWARLHRLNASIADLQSLRSPGLPRHETAQQLQVL 2236
Db 2096 DLERAGALLPAIHEQLRGINASSMAWARLHRLNASIADLQSLRSPGLPRHETAQQLQVL 2155
QY 2237 EQQSTSLGQDARLLGGQAVGTRDQASQLLAGTEATLGHAKTLAAIRAVIDRILSELMSQT 2296
Db 2156 EQQSTSLGQDARLLGGQAVGTRDQASQLLAGTEATLGHAKTLAAIRAVIDRILSELMSQT 2215
QY 2297 GHGLANASAPSGEQLLRTLAVERLLWEMRARDLGAPOAAAEEAELAAQRLMARVQEOL 2356
Db 2216 GHGLANASAPSGEQLLRTLAVERLLWEMRARDLGAPOAAAEEAELAAQRLMARVQEOL 2275
QY 2357 SSLWEENQALATQTRDRLAQHEAGLMDLREALNRAVDATREAOELNSRQERLEALQK 2416
Db 2276 TSFWEENQALATQTRDRLAQHEAGLMDLREALNRAVDATREAOELNSRQERLEALQK 2335
QY 2417 QELSRDNATLQATLHAARDTLASVFRLLHSLDQAKEELERLAASLDGARTPLQRMQTF 2476
Db 2336 QELSRDNATLQATLHAARDTLASVFRLLHSLDQAKEELERLAASLDGARTPLQRMQTF 2395
QY 2477 PAGSKLRLVEAAEAHAQQLGQALNLSIIIDVNDRLTORAIEASNAYSRILOAVQAAE 2536
Db 2396 PASSKVLVEAAEAHAQQLGQALNLSIIIDVNDRLTORAIEASNAYSRILOAVQAAE 2455
QY 2537 DAAGQALQOQADHTWATVVRQGLVDRAQQLLANSTALEAMLEQOQLGLVWALQAGARTQ 2596
Db 2456 DAAGQALQOQADHTWATVVRQGLVDRAQQLLANSTALEAMLEQOQLGLVWALQAGARTQ 2515
QY 2597 LRDVRAKQDQLEAHIQAAQAMLAWDTDETSKKIAHAKAVAAEAQDTATRVQSQLOAMQEN 2656

QY 3403 AQMEGLGTRLRAQSRQRSPGRWHKVSVRWEKNRILLVTDGARAWSOEGPHRQHQAHP 3462
Db 661 AQMEGLGTRLRAQSRQRSPGRWHKVSVRWEKNRILLVTDGARAWSOEGPHRQHQAHP 720
QY 3463 QPHTLVGGLPASSHSSKLPVTVGSGCVKRLRLHGRPLGAPTRMAGVTPCILGLEAGL 3522
Db 721 QPHTLVGGLPASSHSSKLPVTVGSGCVKRLRLHGRPLGAPTRMAGVTPCILGLEAGL 780
QY 3523 FFPSSGGVITLDLPGLATPDVGLLEVRPLAVTGLIFHLGQARTPPYLQVTEKQVLLR 3582
Db 781 FFPSSGGVITLDLPGLATPDVGLLEVRPLAVTGLIFHLGQARTPPYLQVTEKQVLLR 840
QY 3583 ADDGAGEFSTSVTRPSVLCDGQWHRRLAVMKSGNVLRLEVDQAQSNHTVGPPLAAAAGAPAP 3642
Db 841 ADDGAGEFSTSVTRPSVLCDGQWHRRLAVMKSGNVLRLEVDQAQSNHTVGPPLAAAAGAPAP 900
QY 3643 LYLGLPEPMAVQPPWPAYCGCMRRLAVNRSPVAMTRSVEVHGAVGASGCPAA 3695
Db 901 LYLGLPEPMAVQPPWPAYCGCMRRLAVNRSPVAMTRSVEVHGAVGASGCPAA 953

RESULT 3

US-09-562-702A-10
; Sequence 10, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 3106
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-562-702A-10

Query Match 15.6%; Score 3141.5; DB 4; Length 3106;
Best Local Similarity 23.8%; Pred. No. 1.3e-185;
Matches 975; Conservative 471; Mismatches 1161; Indels 1485; Gaps 131;
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QY 70 ARGSPRPTEDLYCKLVGPPVAGGDPNQITRQYCDICTAANSN--KAHPASNAIDGTERW 127
Db 60 -----EMYCKLVEHV-----PGQPVENPQCRICNQNSSNPYQORHPITNAIDGKNTW 105
QY 128 WQSPPLSRGLEYNVNTLDLQOVFHVAVVLIKFANSPPRDLWVLSRMDFGRTYQWQF 187
Db 106 WQSPSIKNGVEYHYVITLDLQOVFOIAVIVKAANSPPRGNWILERSLD-DVEYKPMQY 164
QY 188 FASSKRDCL-----ERFGPQTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRPGA 241
Db 165 HAVTDTECLTLYNIYPTGPPS---YAKDDEVICTSFYSKIHPLENGEIHISLINGRPSA 221
QY 242 MNFSYSPLLREFTKATNVLRLFLRTNLLHLMGKALR-----DPTVTRRYYSIKDISI 296
Db 222 DD--PSPELLEFTSAYIRLRFQIRITNADLMFAHKDPEIDPIVTRRYYSVKDISV 279
QY 297 GGRCVCHGHADACDAKDPTDPF--RLQCTCQHTCGGTCDCCCPGFPKWKATANSAN 354

Db 280 GGMCIYGHARAC---PLDPATNKSRCCEHNTGSCDRCCPGFHQKPRAGTFLTKS 335
QY 355 EQSCNCYGHATDCYYDPEVDRRRASQSLDGTQGGVVICDQHHTAGVNCERCLPGFYR 414
Db 336 ECEACNCHGKAECCYYDETIVASRNLSLNHKGYYGGVVCINCHTNTAGINCETCVDGFFR 395
QY 415 ----SPNHPLDSPHVCRRNCNCRSDFTDGTCEDL-----TGRCYCRPNFSGER 457
Db 396 PKGVSENY----PRPCQPCCHD---PTGSLSEVCVKDEKAYAQRLKPGSCHCKTGFGGVN 448
QY 458 CDVCAEGFTGFPSCYPTPSSSNDTREQVLPAGQIVNDCSAAAGTQGNACRKPDPVGRCLC 517
Db 449 CDRCVRGYHGYPCQP-----CNCISGLG-----STNEDPCVGPCCSC 484
QY 518 KPNFQGTHTCELCAPGFYG-----PGCQPCQCSSPGVADRDCTPDGTQCRCRVGFEGATC 571
Db 485 KENVEGEDCSRCKSGFFNLQEDNQKGCCECFCS--GVS----- 520
QY 572 DRCAPGYFHFPLCQLCGCSPAGTLPAG-----CDEAGRCLCQPEFAGPHCDRCRPGYHGF 626
Db 521 NRCQSSWYTY-----GNIQDMRGWYLTDLGRIRMAPQLONPD----SPQQISI 565
QY 627 PNCQA-----CTCDPRGALDQLCGAGG----- 648
Db 566 SNSEARKSLLDGYWWSAPPPYLGNRLLPAVGGQLSFTISYDLEEBEDDTEKLLQLMIIFEG 625
QY 649 ----- 648
Db 626 NDLRISTAYKEYLEPSEHVEVSLKEEAFTHTGNLPTVRKDFMIVLNTLGEILQIT 685
QY 649 -----LCRCRPGYGTACQECSPG----- 667
Db 686 YNLGMDAIFRLSSVNLESVPYPTDRIATDVEVCQPPGYSGSCSETCWPERRVNGTI 745
QY 668 FHGFPSCVPCHCSAEGSLHA-ACDPRSGQC-SORPRVTGLRCDTCVPGAYNFYCEAGSC 725
Db 746 FGGI--CEPCQCF-----HAEACDDITGECLNCKDHTGGPYCNECLPGFYGDP--TRGS- 796
QY 726 HPAGLAPVDPALPEAQVPCMCRAHV-----EGPSCDRCK 759
Db 797 -----PEDCQPCACPLNIPSNFSPCHLDRSLGLICDECIPTGTGPRCERCA 844
QY 760 PGFWGLSPSNPEG-CTRCSDLRGTGLGVAEQPGTGQC-FCKPHVCGQACASCKGFFG 817
Db 845 EGYFG-QPSVPGGSCQPCQNDNLDYSIPGSCDSLGSCLICKPGTGTGRYCELADGYFG 903
QY 818 LDQADYFGCRSCRCIDIGGALGQSCPEPTGVCRCRPNTOGPTCEPAEDHYLPDLHLRL 877
Db 904 -DAVNTKNQPCRCRDINGSFSEDCHTRTGQCBRCRPNVQGRHCD----- 946
QY 878 LEEAATPEGHAVRFGFNPLEFENFWSRGYAQWAPVQPRIVARLNLTPDLFWLVFRYVNR 937
Db 947 ----- 946
QY 938 GAMSVSGRVSVREGRSAAACANCTAQSQPVAFPPSTEPAFITVPQRGFGEPVLPNGTWA 997
Db 947 ----- 946
QY 998 LRVEAEGVLLDYVVLPSAYYEAALLQLRVTEACTYRPSAQQSGDNCLLYTHPLDGFPS 1057
Db 947 ----- 946
QY 1058 AAGLEALCRQDNLPRPCPTEQLSPSPHPPLITCTGSDVDVQLQVAVPQPGRYALVVEYAN 1117
Db 947 ----- 946
QY 1118 EDARQEVGAVHTPQAPQQLLSLHPLCLYSTLCRGRTARDTDHFLAVFHLDSASVRLTA 1177
Db 947 ----- 946
QY 1178 EQARFFLHGVTLLVPIEEFSPFVEPRVSCISSHGAFGPNAAACLPSPFPKPPQPIILRDC 1237

947 Db -----CKPETF----- 952
1238 QYIPLPPGLPLTHAQDLTPATSPAGPRPPPTAVDPDAEPTLLREPOATVFTTHVFTLG 1297
953 Db -----GLQL----- 956
1298 QYAFALLHGYQPAHPTFPVEVLINAGRVWQHANASFCPHGYGCTLVVCEGQALLDVTHS 1357
957 Db -----GRGC----- 960
1358 QYELTVTVRVPEGRWLWDYVLVVPENVYSFGYLREEPLDKSYDFISHCAAQGYHISPSSSS 1417
961 Db ----- 960
1418 QYLFCRNAAASLSLFYNNGARPCGCGCHEVGATGPTCEPFGGQCPCHAHVIGRDCSRCATGYWG 1477
961 Db -----LPCNCSFGSKSFDCEA-SGQCWCQPGVAGKKCDRCACHGYFN 1001
1478 QYFP--NCRPCDCG--ABLCDELGTQCICPPTIPPDCLLCPQPTFCGCHPLVGCCECNCSSGP 1533
1002 DbFQEGGCIACDCSHLGNCDPKTGQCICPNTTGEKCECLPNTWGHSHVITGCKVCNCSTV 1061
1534 QYGIQELTDPTCDTSDGCKCRPNVTGRRCDTSCPGFHGYPRCPCDCHEAGTAPGVCD--- 1590
1062 DbG---SLASQCNVNTGQCSCHPKFSGMKCECSRGHWNYPCLTCLDCFLPGTDAITTCULET 1118
1591 QYPLTGQCYCKENVQGPCKDCQCSLGTFSLSDAANPKGCTRCFCFGATERCRSSSYTR 1644
1119 DbRKSCSDQTGQCSCKVNVGVHCDRCRPGFGLDAKNPLGCSscyCGVTSCQSEAKGL- 1177
1645 QYQBFVDMEGVLLSTDBQVVPHERQPGTGMRLADLRHV-----PEAV---PEAFPEL 1692
1178 DbIRTVTLTSDQTLIP-----LVDEALQHTTTKGIAFQKPEIVAKMDEVRCQL 1224
1693 QY---YQAPPSSYLGRVSSYGGTLRYELHSETQDGVFVPMESRPDVVLQ---NQMSI 1744
1225 DbHLEPPYKWLPOQPEGKKLMAYGGKLYAIFYEARDETGFATY--KQVVIIRGGTPTTHARI 1282
1745 QYTFLEPAYPTPGHVHRCQLQOLVEGNFRH---TETRTVTSREELMMVLASLEQLQIRALPS 1800
1283 DbITRMAAPLIGQLTRHEIEMTEKEWKYIGDDPRISRTVTREDFLDILYDIHYILIKATYG 1342
1801 QYQISSAVSLRRVALEVASP---AQGALASNVLCCLCPASVYRGSQCCECAPGFYR----- 1851
1343 DbNVVRQSRISEISMEVAEPGHVLAGSPP-AHLIERCDCPPGYSGLSCECTCAPGFYRLRSEP 1401
1852 QY--DVKGLFLGRVCPQCHGSHDRCLPGSGVGVDCQHNTEGAHCERCQAGFMSSRDDPSAP 1909
1402 DbGGRTPGPTLTGTCVPCQNGHSSQCDPETSVCQNCQHTTAGDFCERCALGYGIYVIRGLPND 1461
1910 QYCVSCPCPLSVPSNNFAEGCVLRGGRT-QC-LCKPGYAGASCERCAPGFFGNPLVLGSSCQ 1967
1462 DbQCFACPLISPSNNFSPSCVLEGLDYRCTACPRGYEGQYECERCAPGYTGSPSPGSCQ 1521
1968 QYPCDCSGNDPNLLFSDCDPLTGACRGCLRHTTGPRCEICAPGFVGNALLPGNCTRCDCTP 2027
1522 DbEC-----ECDP-----YGSLLPVP----- 1534
2028 QYCGTEACDPHSGHCLCKAGVTGRRCDRCQEGHFGNGCGCRPCACGPAEGSECHPQSGQ 2087
1535 Db-----CDRVTGLCTCRPGATGRKCDGCEHWH-----AREGAEC----- 1567
2088 QYCHCRPGTMGPQCRECAPGYWGLPEQCGCRRCQCPGGRCDPHTGRCNCPPLSGERCDCSCQ 2147
1568 Db----- 1567
2148 QYQHQPVPVPGPVGHSIHCEVCDHCVLLDDLERAGAL-----LPATHEQLRGINAS 2198
1568 Db-----VFCG--DECTGLLLGLDLARLEQMTMNTNINLTGFLPAPYKILYGLENT 1611
2199 QYSMAWARLHRLNASTADLOSQSLRSPGPRHETAQQLEVLQOQSTSL----- 2243
1612 DbT-----QELKHLSPQAPERLIQLAEGNVNLTVMETNELLTRATKYT 1654

2244 QY-----GQDARRLGGQAVGRDQASQLLAGTEA-----TLGHAKTLLAAIRAIVDR 2287
1655 DbADGEQTQDAERTNSRAESLEEFIKGLVQDAEAINEKAVKJNETLGNQD-----KTAER 1708
2288 QYTLSELMSTQTHLGLANASAPSGEQLLRTLAEVERLLWEMRRARDLGAPOAAAEAEALAAQOR 2347
1709 DbNLEELQK-----EIDRMLKELRSKDLQTOKEVAEDELVAAG 1745
2348 QYLLARVQEQSLSSWEENQALATQTRDRLAQHEAGLMDLREALNRAVDATREAOELNSRNOE 2407
1746 DbLLKRVNKLFGEPRAQNEDEKMDLQKLAELAEYKKNLDDAWDLREATDKTRDANRLSAANQK 1805
2408 QYRLEELQKQELSRDNATLQATLHAARDTTLASVFRLLHSLDQAKEELERLAASLDGARTP 2467
1806 DbNMTILETKKEAIEGSKRQIENTLKEGNDILDEANQQLGEINSVIDYVDDIKTKLPMPMSEE 1865
2468 QYLLQRMOTFPAGSKRLVE---AAEAHAQQLGQLALNLSSIIILDVNQD---RLTQRAIEA 2521
1866 DbLSDKIDDLAQEIKDRRLAEKVFQAESHAQ-----LNDSSAVLDGILDEAKNISFNATAA 1920
2522 QYSNAYSRIILQAAEAEDAAGQA--LQQAHTWTATVVRQGLVDRAQQLLANSTALEEAMLOE 2579
1921 DbFRAYSNIKDYIDEAEKVAREAKELAQGATKLATSPQGLLKEDAKGSLQKSFRI---LNE 1976
2580 QYQORLGLVWAALQGARTQLRDVRAKKDQLEAH-----IQAAQAMLAMDTDETSKKIAHA 2632
1977 DbAKKLA---NDVKGNHNDLNDLKTRELTADLRNSGLLGAINDTMDKLSAITNDTAAKLOAV 2033
2633 QYKAVAAEAQDTATRVQSOLQAMQENVERWQOYEGE-----RGQDLGQAVLDAGH 2681
2034 DbKEKAREANDTAKAVLAQVKDLHQNLQDLGKQNYNKLADSVAKTNAVNVKDPKKNKIADAGT 2093
2682 QYSVSTLEKTLPLLAKLSILENRGVHNASLASASIGRVRELIAQARGAASKVKVPMKFNG 2741
2094 DbSVRNLEQEAADRLIDKL-----KPIKELEDNLKKNISEIKELINQARKQANSIKVSVSSGG 2148
2742 QYRSGVQLRTPRDLADLAAYTALKFYLOQPEPEPGQSTEDRFVVMGSRQATGDYMGVSLRD 2801
2149 DbDC---VRTYRPEIKKGSYNNIVVHVK-----TAVADNLLFYLGSAKFI-DFLAIEMRK 2197
2802 QYKKVHWVY---QLGEAGPAVLISIDEDIGEQAFAVSLDRTLQFGHMSVTV---ERQMIQE 2853
2198 DbGKVSFLWIVSGVGRVGFDPDLTIDD---SYWYRIEASRTGRNGSISVRALDGPKASMVPS 2254
2854 QYTKGDTVAPGAEGLLNLRPDFFVYVGGYPSFTFPPLLRFPFGYRGCIEMDTLNEEWSLY 2913
2255 DbTY-HSVSPPGYTILDVDANAMLF-VGGLTGKIKKADAVRVTFTGCMGETYFDNKKPIGLW 2312
2914 QYNFERTFQDITAVDRPCARSKSTGDPWLTDGS-YLDGTGFARIS---FDSQISTTKRFEQ 2968
2313 DbNF-REKEGDC--KGCTVSPQVED--SEGTIQPDGEGYALVSRPIRWYPNISTVM---F 2362
2969 QYELRLVSYSGVLFFL--KQSQFCLAVQEGSLVLLYDFGAGLKKAVPLQPPPLTSASKA 3026
2363 DbKFTTFSSALLMYLATRDLKDFMSVELSDGHVKVSYDLGSGMTSVVSNQ-----NHNDGK 2417
3027 QYIQVFLLGSSRKRVLVRVERATVYSVEQDN-----DLELADAYILGGVPPDQLP 3074
2418 DbWKAFTLSRIQKQANISI--VDIDSNQEEENVATSSGNNFGLDLKADDDKIYFGGL----- 2469
3075 QYPSLRWLFPTGGSVR-----GCVKGIK-ALGKYVDLKRNLNTTGVSACTADLLVG 3122
2470 DbPTLRNL-----SMKARPEVNVKYSGLCKDIEISRTPPYNILSSPDYVGVTKGCSLENV-- 2522
3123 QYRAMTFHGFGFLRLALSINVAPLTGNVYSGFGFHSQAQDSALLY--RASP 3169
2523 DbNTVSFPKPGFVELAAVSDVGT--EINLSFSFTRNESGIILGSGGTLTPPRKRRTQTQ 2579
3170 QYGLCQVSLQQGRVSLQL-----LRTEVKTAG-FADGAPHYVAFYSNATGWM-LYVDD- 3219
2580 DbAYYAIPLNKGRLVHLSSGTRTMRKIVIKPEPNLFDHGREHSV-HVERTRGIFTVQIDED 2638

QY 1021 ALLQLRVTEACTYRPSAQSGDNCLLYTHLPUDGFPSPAAGLEALCRQDNLSPRCPTEQL 1080
Db 925 ----- 924
QY 1081 SPSHPPLITCTGSDVDVQLQVAVPQGRYALVVEYANEDARQEVGVAVHTTPQRAPOQGLL 1140
Db 925 ----- 924
QY 1141 SLHPCLYSTLCRGRTARDTQDHLAVFHLDSASVRLTAEQARFFLHGVTLPVPIEFSPEFV 1200
Db 925 ----- 924
QY 1201 EPRVSCISSHGAFGPSAACLPSRFPKPPQPIILRDCQVILPPLPGGLPLTHAQDLTPATSP 1260
Db 925 ----- 934
QY 1261 AGPRPRPPTAVDPDAEPTLLREPQATVFTTHVPTLGRYAFLLHGVQPAHPTFPVEVLIN 1320
Db 935 ----- 934
QY 1321 AGRVWQGHANASFCPHGYGCRTLVVCEGOALLDVTHSELTVTVRVPGRWLWLDYVLVVP 1380
Db 935 ----- 938
QY 1381 ENVYSFGLREELDKSYDFISHCAAQGYHISPSSSSLFCRNAASLSLFYNNGARPCGC 1440
Db 939 ----- 943
QY 1441 HEVGATGPTCEPFGGQCPCHAHVIGRDCRCATGYWGFPP--NCRPCDCG--ARLCCDELTG 1496
Db 944 NSFSGSKSFCEA-SGQCWCQPGVAGKKCDRCAGHYFNFQEGGCIACDCSHLGNNDPKFTG 1002
QY 1497 QCICPPRTIPDCLLCPQPTFGCHPLVGCBECCNSGPGIQELTPTCDTDSGQCKCRPNV 1556
Db 1003 QCICPPNTTGEKCECLPNTWGHISIVTGCKVCNCSTVG---SLASQCNVNTGQCSCHKPF 1059
QY 1557 TGRRCDTCSPGFHGYPRCRPCDCHEAGTAPGVCD-----PLTGQCYCKENVOGPKC 1607
Db 1060 SGMKCECSRGHWNYPCLTLCDCFLPGTDAATCDLETRKCSGSDQTGQCSCKVNVEGVHC 1119
QY 1608 DQCSLGTFSLDAAANPKGCTRCFCFGATERCRSSSYTRQEFVDMEGWVLLSTDQVVPHER 1667
Db 1120 DRCRPGKFGLDKAPLGCSSCYCFGVTSQCSSEAKGL-----IRTVTLSDQETILP--- 1170
QY 1668 QPGTEMLRADLRHV-----PEAV-----PEAPPEL-----YMQAPPSYLGDRVSSYGG 1710
Db 1171 -----LVDEALQHTTKGIAFOKPEIIVAKMDEVROELHLEFPYWKLPQQFEGKLMAYGG 1225
QY 1711 TLRYELHSETQRGDVFPVPMESRPDVVLOG---NQMSITFLEPAYTPPGHVHRGQLQVVG 1767
Db 1226 KLYAIYFEARDETGFATY--KPQVIRGGTPTTHARIITRMAAPLIGQLTRHEIEMTEK 1283
QY 1768 NFRH---TETRNTVSREELMMVLASLEQLQIRALFSQISSAVSLRRVALEVASP-----A 1819
Db 1284 EWKYGDPPRISRTVTREDFLDILYDIHYLIKATYGNVVRQSRISSEISMEVAEPGHVLA 1343
QY 1820 GQALASNVLCPCASYRGDSCQECAPGFYR-----DVKGLEFLGRVCVPCQCHGSDR 1872
Db 1344 GSPP-AHLIERCDCPPGYSGLSCETCAPGFYRLRSEPGGRTPGPTLGTCTVPCQCNHSSQ 1402
QY 1873 CLPGSGVCVDCQHNTEGAHCERCQAGFMSRRDDPSAPCVSCPCPLSVPSNNFAEGCVLRG 1932
Db 1403 CDPETSVQCNCQHTAGDFCERCALGYGIVRGLPNDCCQPCACPLISPSNNFSPSCVLEG 1462
QY 1933 GRT-QC-LCKPGVAGASCERCAPGFFGNPLVLGSSCQPCDCSGNGDPNLLFSDCDPLTGA 1990
Db 1463 LEDYRCTACPRGYEQYCERCAPGYTGSPPSGGSCQEC-----ECDP----- 1505
QY 1991 CRGCLRHTTGPRCIBCAPGFYGNALLPGNCTRCDCTPCGTEACDPHSGHCLCKAGVTGRR 2050
Db 1506 -----YGLPVP-----CDRVTGLCTCRPGATGRK 1530

QY 2051 CDRCEGHFGFNGCGCRPCACGPAAGSECHPQSQCHCRPGTMGPQCRPCAPGYWGLP 2110
Db 1531 CDGCEHWH-----AREGAEC----- 1545
QY 2111 EQGRRRCQCPGGRCDPHTGRCNCPPGLSGERCDCDTCQHQHVVPVPGPVGHSHICEVCDHC 2170
Db 1546 -----VFCG--DEC 1552
QY 2171 VVLLDDLERAGAL-----LPATHEQLRGINASSMAWARLHRLNASIADLQSLRS 2221
Db 1553 TGLLLGLARLEQMTNINLTGPLPAPYKILYGLENTT-----QELKH 1595
QY 2222 PLGPRHETAQOQLEVLQOQSTSL-----GQDARRLGGQAVGTRDQ 2260
Db 1596 LLSPORAPERLIQLAEGNVNLTVMETNELLTRATKVTDADGEQTQDARTNSRAESLEEF 1655
QY 2261 ASQLLACTEA-----TLGHAKTLLAAIRAVIDRTLSLMSQTGHLGLANASAPSGE 2310
Db 1656 IKGLVQDAEAINEXAVKLNELTGNQD-----KTAERNLEELQK----- 1693
QY 2311 QLLRTLAEVERLLWEMRARDLCAPOAAAEELAAQRLARVQEQLSLSEENQALATQT 2370
Db 1694 -----EIDRMLKELRSKDLQTKQKEVAEDELVAEGLLKRNVKLFGEPRACQNMEDKDL 1746
QY 2371 RDRLAQHEAGLMDLREALNRAVDATREAOELNSRQERLEELQKQELSRDNATLQATL 2430
Db 1747 QOKLAEYKNDLDDAWDLREATDKTRDANRLSAANQNMNTILETKKEAIEGSKQIENTL 1806
QY 2431 HAARDTLASVFRLLHSLDOAKBELERLAASLDGARTPLLQRMQTFSPAGSKRLVE--A 2487
Db 1807 KEGNDILDEANQLLGEINSVIDYVDDIKTKLPPMSEBELSKIDDLAQEKIDRRLAEKVFQ 1866
QY 2488 AEAHAQQLGQALNLSSIIIDVNQD---RLTORATEASNAYSRILOAVQAAEDAAGQA-- 2542
Db 1867 AESHAAQ-----LNDSSAVLDGILDEAKNISFNATAAFRAYSNIKDYIDEAEKVAREAKE 1921
QY 2543 LQOQADHTWATVVRQGLVDRACQLLANSTALEEAMLEQOORLGLVWALQOQARTQLRDVRA 2602
Db 1922 LAQCATKLATSPQGLLKEDAKGSLQKSFR1---LNEAKKLA---NDVKGNHNDLNDLKT 1974
QY 2603 KKDQLEAH-----IQAAQAMLMDTDETSKKTIAHAKAVAAEAQDTATRVQSQLOAMQE 2655
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Db 2035 NLDGLKQNYNKLADSVAKTNAVVKDPKKNKIIADAGTSVRNLEQEAADRLIDKL-----KP 2089
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QY 2765 YLQGEPEPEPGQGTEDRFVYMGSRQATGDYMGVSLRDKKHVVVY-----QLGEAGPAVLSI 2820
Db 2147 HVK-----TAVADNLLFYLGSAPFI-DFLAEMRKGVKSVFLWIVSGVGRVGFDPDLTI 2198
QY 2821 DEDIGEQAFAVSLDRTLOFGHMSVTV-----ERQMIQETKGDTPVAPGAEGLLNLRPDDFVF 2876
Db 2199 DD---SYWYRIEASRTGRNGSISVRALDGPASMVVSTY-HSVSPPGYVTLDDVANAMLF 2254
QY 2877 YVGYVSTFTPPPLRFPYRGCIEMDTLNEEVVSVLYNFERTFQDPTAVDRPCARSXSTG 2936
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QY 2990 CLAVQEGSLVLLYDFGAGLKKAVPLQPPPLTSASKAIQVFLGGSKRVLVRVERATVY 3049
Db 2364 SVELSDGHVKVSYDLGSGMTSVVSNQ-----NHNKGKWKAFKTLRQKQANISI--VDID 2416
QY 3050 SVEQDN-----DLELADAYYLGGVPPDQLPPLRWLFTFTGGSVR----- 3088

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QY 3089 --GCVKGIK-ALGKYVDLXRLNTTGVSACTADLLVGRAMTFHGHGFLRLALSNAVPLTG 3145
Db 2466 YSGLKXIEISRTYPNLSPPDYVGTGKGSLENV--NTVSFPEGFVLAASVIVGT- 2522
QY 3146 NVYSGFGFHSAQDSALLY--RASPDLGLCQVLSQQGRVSLQL----- 3185
Db 2523 --EINLSFSTRNESGIILLGSGGTLTPPRKRRTQTOAYYAFNLKGRLEVHLSSGTRTM 2580
QY 3186 LRTEVKTQAG-FADGAPHYVAFYSNATGVW-LYVDD-----QLQMKPHR-----GP 3230
Db 2581 RKIVIKPEPNLPHDGRHSV-HVERTRGITFTVQIDEDRRHQNLTEEQPIEVKLFVGA 2639
QY 3231 PPELQPEGPRLILGGLPESGTIYNFSGISNVFVQRLGPRVFDLQNLGSVNVST 3290
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QY 3338 RDSYQFGSLSLHLEFVGILARHNWPSLSMHVLPSSRGLLF-----TARLRP 3387
Db 2735 TGSKQFGLSRNSHIAIVFDDTKVKNRLTIELEVRTEAESGLLFYMGRIHADFGTVQLRN 2794
QY 3388 GSPSLALFLSNGHFVAQMEGLGRLRAQSRQSRPGRWHKVS--VRWEKNRILLVTDGARA 3446
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QY 3447 WSQEGPHRQHQAHPQPH-----TLFVGGLPASSHSSKL-PVTVGSGCVKRLRL 3496
Db 2842 -----SQTISPKKADILDVGGILYVGGLPINVTTRRIGPVTYSLDGCVRNLM 2899
QY 3497 HGRP--LGAPTRMAGVTPCILGPLEAGLFFPGS-----GGVITLPLGATLPDVGLEL 3547
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Db 2941 EFRTRPTGVLLGISSQKMDG-MGIEMIDEKLMFHVNDGAGRFTAIDAEIPGHMNGQW 2999
QY 3606 HRLAVMKSGNVRL-----EVDAGSNHTVGPLLAAAGAPAPLYLGLLP 3649
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RESULT 5

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US-08-460-309-4
; Sequence 4, Application US/08460309
; Patent No. 5837496
; GENERAL INFORMATION:
; APPLICANT: Engvall, Eva
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
; TITLE OF INVENTION: Fragments and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,309
; FILING DATE:
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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/125,077
; FILING DATE: 22-SEP-1993
; APPLICATION NUMBER: US PCT/US 94/10730
; FILING DATE: 21-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/472,319
; FILING DATE: 30-JAN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/919,951
; FILING DATE: 27-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9721
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3111 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-460-309-4
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Query Match 15.4%; Score 3104; DB 2; Length 3111;
Best Local Similarity 23.8%; Pred. No. 2.8e-183;
Matches 974; Conservative 479; Mismatches 1223; Indels 1418; Gaps 137;

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QY 65 GEEAPARGSPRPTEDLYCKLVGGPVAGDPNQITRQYQYCDIC--TAANSNKAHPASNAID 122
Db 59 GERGP-----EMYCKLVEHV-----PGQPVNRPQCRICNQNSNPQRHPITNAID 104
QY 123 GTERWQSPPLSRGLEYNVNTLDLQGVFHVAVYLIKFNANSPRPPDLWVLEERSMDFGRY 182
Db 105 GKNTWQSPSIKNGIEYHYVITLDLQVFOQIAVIVKAANSRPPGNWILERSLD-DVEY 163
QY 183 QPWQFFASSKRDCL-----ERFGPQTLERITRDDAAICTTEYSRIVPLENGEIVVSLVN 236
Db 164 KPQWYHAYVTDTECLTLYNIYPTGPPS---YAKDDEVICTSFYSKIHPLENGEIHISLIN 220
QY 237 GRPGAMNFSYSPLLREFTKATNRLRFLRTNLLGLHLMGKALR-----DPTVTRRYYSI 291
Db 221 GRPSADD--PSPELLEFTSARYIRLRFQIRILNADLMFAHKDPRIDPIVTRRYYSV 278
QY 292 KDISIGRCVCHGHADACADKDPDPF--RLQCTCOHNTCGGTCDRCPCGFNQOPWKPAT 349
Db 279 KDISVGMCIYGHARAC-----PLDPATNKRSECEHNTCGDSCDCCQCPGFHOKPWRAGT 334
QY 350 ANSANEQSCNCYGHATDCYYDPEVDRRRASQSLDGTYYQGGVGCIDCQHTAGVNCERCL 409
Db 335 FLTKTECEACNCHGKAEECYVDENVARNLSLNRKGIYGGVGCINCTQNTAGINCETCT 394
QY 410 PGFYR---SPNHPLDSPHVCRRCNCE--SDFTDGTCE-----LTGRCYCRPNFSG 455
Db 395 DGFFRPKGVSPNY---PRPCQCHCDPIGSLNEVCVKDEKHARRGLAPGSCCHKTGFGG 450
QY 456 ERCDVCAEGFTGFPSCYPTPSSNDTREQVLPAGQIVNCDCSAAGTQGNACRKPVRGRC 515
Db 451 VSCDRCARGYTGYPDCKA-----CNCGLGSK-----NEDPCFGPC 486
QY 516 LCKPNFQGTCHCELCAFGY-----PGCQPCQCSS----- 545
Db 487 ICKENVEGDCSRCKSGFFNLQEDNWKGCDFCSGVSNRQCSSYWTYKIQDMSGWYLT 546
QY 546 --PG---VADDRCDPDTGQCRVGFEGATCDRCAPG--YFHFPLCQLCGCSPA--GTLP 596
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QY 597 -----EGCD-----EAGRLCQPEFAGPH 615
Db FTISYDLEEEEDTERVLQMIILEGNDLSISTAQDEVYLHPSEHTNVLLKBESEFTIH 663
QY 616 CDRCRPGYHGF-----NQACTCDPRGAL 640
Db -----GTH-FPVRRKEFMTVLANKRVLLOITYSFGMDAIFRLSSVNLESAUSYPTDG- 715
QY 641 DQLCGAGGLCRCPGYGTGTACQECSPG-----FHGFPSCVPCHCSAEGSLHA-ACDP 691
Db -SIAAAVEVCQPPGYGTSSCESCWPRHRRVNGTIFGGI--CEPCQCFG-----HAESCD 768
QY 692 RSGQC-SCRPRVTGLRCDTCVPYGAYNFPY-----CEAGSCHPAGLAPVDPALPEAQVP- 743
Db VTGECLNCKDHTGGPYCDKCLPGFYGEPTKGTSEDQPCAC-PLNI-PSNNFSPPTCHLDR 826
QY 744 ----C-MCRAHVEGPSCDRCKPGFWGLSPSNPEG-CTRCSCDLRGLTGGVAECQPGTGQ 796
Db SLGLICDGPVGYTGPCRCAEGYFG-QPSVPGSGCQPCQCNLDNDFSIPGSCDSLGS 885
QY 797 C-FCKPHVCGQACASCKDGFGLDQADYFGCRSCRDIGGALGQSCPEPTGVCRCRPNTQ 855
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Db 945 GQRC----- 948
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Db 949 ----- 948
QY 976 AFITVPQRGFEPFVLNPGTWNALRVEAEGVLLDYVLLPSAYYEAALLQLRVTEACTYRP 1035
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QY 1036 SAQSGDNCLLYTHLPDGFPSAAGLEALCRQDNSLRPCTEQLSPSHPLITCTGSDV 1095
Db 949 -----DKC----- 951
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Db 952 ----- 951
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Db 962 ----- 961
QY 1396 KSYDFISHCAAQGYHISPSSSSLFCRMAAASLSLFYNNGARPCGCHEVGATGPTCEPFGG 1455
Db 962 -----RGCVPCNCNSFGSKSFDCEE-SG 983
QY 1456 QCPCHAVIGRDCSRCATGYWGFP--NCRPCDCG--ARLQDCLTGCICPPTIPPDCLL 1511
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QY 1512 CQPTFGCHPLVGCCECNCSGPGIQELTPTCDTDSGQCKRPNVTGRRCDTCSGPFHGY 1571
Db 1044 CAPNTWGHISITTGCKACNCSTVG---SLDFQCNVNTGQCNCHPKFSGAKCTECSRGHWN 1100

QY 1572 PRCRPCDCHEAGTAPGVC-----DPLTGQCYCKENVQPKCDQCSLGTFFSLDAAN 1621
Db 1101 PRNLCDCLFLPGTDATTCDSSETKKCSCDQTTGQCTCKUNVEGIHCDCRCPGKGLDAKN 1160
QY 1622 PKGTRCFCFGATERCRSSSYTRQBEFVDMEGWLLSTDRQVVP-----HERQPG---- 1670
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QY 1671 -----TEMLRADLRHVPEAVPEAPPELYWQAPPSYGLDRVSSYGGTLRYELHSETQRG 1723
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QY 1724 DVFBMESRPDVLQG--NQMSITFLEPAYPTPHVHRGQLQLVEGNFRH-----TETRN 1776
Db 1266 TGF--STYNPQVIIRGGTPTHARIIVRHMAAPLIGOLTRHEIEMTEKEWKYVGDDPRVHR 1323
QY 1777 TVSREELMMVLASLEQLQIRALFSQISSAVSLRRRVALEVASPAGQAL----ASNVELCL 1832
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QY 1833 CPASYRGDSQCECAPGYR-----DVKGLFLGRVPCQCHGSHDRCLPGSGVCVDCQH 1885
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QY 1886 NTEGAHCERCQAGFMSSRRDPSAPCVSCPCPLSVPSNNAFEGCVLRG-GRTOC-LCKPGY 1943
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Db 1573 -----VFCG--DECTGLLLGLDARLEQ 1592
QY 2184 L-----LPAIHEQLRGINASS-----MAWARLHRLNASIADLQ 2216
Db 1593 MVMSINLTGPLPAPYKMLYGLENNMTQELKHLSPQAPAPBELIQLAEGNLTLVTMNNELL 1652
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QY 2337 AAEALAAQRLARVQEQSLSWEENQALATQTRDRLAQHEAGLMDLREALNRAVDATR 2396
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Db 2088 SKNKIADADATVKNLEQEAADRLDKL-----KPIKELEDNLKKNISEIKELINQARKQA 2142
QY 2731 SKVKVPMKFNRSVQLRTPRDLADLAAYTALKFYLOGPEBPGQGTEDRFVYMGSRQA 2790
Db 2143 NSIKVSVSSGGDC---IRTYKPEIKKGSYNNIVNVK-----TAVADNLLFFYLGSAKF 2192
QY 2791 TGDYMGVSLRDKKVHWYQLGEAGPAV-----LSIDEDIGEQAFAVSLDRTLQFGHMSVTV 2846
Db 2193 I-DFLAIEMRKGVSVFLWDVGVGVRYEPDLTIDDSYWYRIVA---SRTGRNGTISVRA 2248
QY 2847 ---ERQMIQETKGDTPVAPGAEGLLNLRPDDFVYVGGYSPSTFPPLLRFPFGYRGCIEM 2902
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QY 3204 VAFYSNATGVW-LYVDDQLQOM-----KPHR-----GPPPELQPOPEGPPRL1LGL 3249
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Db 2679 PP-----FEGCIWNLVINSV-----PMDFARPVSPK1NADIGRCAHQK1REDEDGAAPAE 2727
QY 3294 -----PALQAQTPGL--GPRGLQATARKASRRSRQPARHPACMLPPHLRTRDSY 3341
Db 2728 IVIQPEPVPTPAFPPTPTPVLTGPCAAS-----EPALLI-----GSK 2765
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QY 3448 SQEGPHRQHQGAHPQP-----HTLFVGLP1ASSHSSKL-PVTVFGSGCVKRLRLHGR 3499
Db 2873 S-----PKKADILDVGM1LYVGLP1NYTRR1IGPVTYSIDGCVRN1LHMAEA 2919
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Db 2920 PADLEQPTSSFHVGTCPAN-AQRGTYFDGTGFAKAVGGFKVGL-----DLLVEFEFATT 2972
QY 3553 AVTGLIFHLGQARTPPYLQLVTEKQVLLRADDGAGEFST--SVTRPSVLCDGQWHRLAV 3610
Db 2973 TTTGVLLGISSQKMDG-MGIEMIDKLMFHVNDGAGRFTAVTDAGVPGHLC1DGQWHKVTA 3031
QY 3611 MKSGNVLRLEVDASQNH1TVG1PL1AA-AAGAPAPLYL1GGLPEPMAVQ1P1PPA--YCGCMRR 3667
Db 3032 NKIKHRIELTV1DGNQV1EASQSPN1PASTAD1NDPVFVGGFDD1LKQFGLT1S1PFRGCIRS 3091
QY 3668 LAVNRSFVAMTRSV 3681
Db 3092 LKLT1KGTASHWRLI 3105

RESULT 6
US-08-125-077-4
; Sequence 4, Application US/08125077
; Patent No. 5872231
; GENERAL INFORMATION:
; APPLICANT: Engvall, Eva
; APPLICANT: Leivo, Ilmo
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
; TITLE OF INVENTION: Fragments and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/125,077
; FILING DATE: 22-SEP-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US 94/10730
; FILING DATE: 21-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/472,319
; FILING DATE: 30-JAN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/919,951
; FILING DATE: 27-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9721
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
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; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3111 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-125-077-4

Query Match 15.4%; Score 3104; DB 2; Length 3111;
Best Local Similarity 23.8%; Pred. No. 2.8e-183;
Matches 974; Conservative 479; Mismatches 1223; Indels 1418; Gaps 137;

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QY 65 GEEAPARGSPRPTEDLYCKLVGGPVAGDPNQTIHQYCDIC--TAANSNKAHPASNAID 122
Db 59 GEKGP-----EMYCKLVEHV-----PGQPVNPNQCRICNQNSSNPORHPITNAID 104
QY 123 GTERWQSPPLSRGLEYNVNVTLDLGQVHFVAYVLKFAANSRPPDLWLWERSMDFGRTY 182
Db 105 GKNTWQSPSIKNGIEYHYVTITLQLQVQFQIAYIVKAANSRPPGNWILERSLD-DVEY 163
QY 183 QPWQFFASSKRDCL-----ERFGPQTLERITRDDAAICTEYSRIVPLENGEIVVSLVN 236
Db 164 KPQYHAVTDECTLYNIYPRTPPS---YAKODEVICTSFYSKIHPLENGEIHISLIN 220
QY 237 GRPGAMNFSYSPLLRREFTKATNVRLRFLRTNTLLGHLMGKALR-----DPTVTRRYYSI 291
Db 221 GRPSADD--PSPELLEFTSARYIRLRFQIRITLNADLMMFAHKDPREIDPIVTRRYYSV 278
QY 292 KDISIGRCVCHGHADACDAKDPDPF--RLQCTCOHNTCGGTCDRCCPGFNGQPWKPAT 349
Db 279 KDISVGMCI CYGHARAC----PLDPATNKSRCCEHNTCGSDCDQCCPGFHQRPWRAGT 334
QY 350 ANSANECQSCNICYGHATDCYYDPEVDRRRASQSLDGTQGGVCIDCQHHTAGVNCERCL 409
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QY 410 PGFYR-----SPNHPLDSPHVCRRNCE--SDFTDGTCE-----LTGRCYCHPNFSG 455
Db 395 DGFFRPKGVSPNY----PRPCQPCCHDPIGSLNEVCVXDEKHARRGLAPGSCCHKTGFGG 450
QY 456 ERCDVCAEGFTGFPSCYPTPSSNDTREQVLPAGQIVNCDCSAAGTQGNACRCKDPRVGR 515
Db 451 VSCDRCARGYTGYDCKA-----CNCISGLGSK-----NEDPCFGPC 486
QY 516 LCKPNFQGTCHCELCAPGFYG-----PGCQPCQCSS----- 545
Db 487 ICKENVEGDCSRCKSGFFNLQEDNWKGCDECFCSGVSNRCQSSYWTYKIQDMSGWILT 546
QY 546 --PG---VADDRCDPDTGQCRRCRVGFEGATCDRCAPG--YFHPPLCOLCGCSPA--GTL 596
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QY 597 -----EGCD-----EAGRCLCQPEFAGPH 615
Db 604 FTISYDLBEEEDTERVLQMIILEGNDLSISTAQDEVYVLPSEHTNVLLKESFTIH 663
QY 616 CDRCRPGYHGPP-----NCQACTCDPRGAL 640
Db 664 -----GTH-FPVRRKEFTVLANKRVLQITYSGMDAIFRLSSVNLESAVSYPDTG- 715
QY 641 DQLCGAGGLCRCRPGYTGTAQCECSPG-----FHGFPSCVPCHCSAEGSLHA-ACDP 691
Db 716 -SIAAAVEVCQPPGYTGSSCESCWPHRRVNGTIFGGI--CEPCQCFG---HAESCDD 768
QY 692 RSGQC-SCRPRVTGLRCDTCVPGAVNFPY-----CEAGSCHPAGLAPVDPALPEAQVP- 743
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Db 827 SLGLICDGCVPYGTGPRCERCAEGYFG-QPSVPGSCQPCQCNNDNLDIFSIPGSCDSLGS 885
QY 797 C-FCKPHVCCQACASCKDGFGLDQADYFGCRSCRCDIGGALGQSCEPRTGVCRCPNTQ 855
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QY 1156 RDTQDHLAVFHLDSASVRLTAEQARFFLHGVTLPVPIEFSEFVEPRVSCISSHGAFGP 1215
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QY 1336 HGYGCRTLVVCEGOALLDVTHSELTVTVRVPPEGRWLWLDYVLVVPENVYSFGYLREEPLD 1395
Db 962 ----- 961
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Db 1044 CAPNTWGHSTITGCKACNCSTVG---SLDFQCNVNTQCNCHPKFSGAKTECSRGHWN 1100
QY 1572 PRCRPPCDCHAGTAGVC-----DPLTGQCYCKENVQGPACDQCSLGTFSLDAAN 1621
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QY 1671 -----TEMLRADLRHVPEAVPEAFPELYQWAPPSYLGDRVSSYGGTLRYELHSETQRG 1723
Db 1215 HPEIVAHDMLREDLHLEP-----FYKWLPEQFEGLKLMAYGGLKYAIYFEAREE 1265
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Db 1266 TGF--STYNPQVIIRGGTPTTHARIIVRHMAAPLIGQLTRHEIEMTEKWKYGGDDPRVHR 1323
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QY 1833 CPASYRGDSCQECAPGFYR-----DVKGLFLGRVCPCQCHGHSRCLPGSGVCVDCQH 1885
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Db 1533 -----YCSLPVP-----CDPVTGCTCRGATGRKCDGCKHWH----- 1565
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Db 1573 -----VFCG--DECTGLLLGLDLARLEQ 1592
QY 2184 L-----LPATHEQLRGINASS-----MAWARLHRLNASIADLQ 2216
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Db 1653 TRATKVTADGEQTQDAERTNTRAKSLGFEIKELARDAEAVNEKAIKL-----NE 1702
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QY 2562 AQOLLANSTALEAMLEQQRGLVWAAALQAGARTQLRDVRAKKDQLEAHIAQAQAMAMD 2621
Db 1975 SFRILNEAKKLANDVKENEDH-----LNLKTRIEADARNGLDRLTLNDTLGKLSAI 2027
QY 2622 TDETSKIAHAKAVAAEAQDTATRVQSOLQAMQENVERWQOQYEGE-----RGQ 2670
Db 2028 PNDTAAKLQAVKDKARQANDTAKDVLAQITELHQNLGLKKNYNKLADSVAKTNVAVKOP 2087
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Db 2088 SKNKIADADATVKNLEQADRLIDKL-----KPIKELEDNLKKNISEIKELINQARKQA 2142
QY 2731 SKVKVPMKFNGRSGVQLRTPRDLADLAAATALKFYLOGPEPEPGQGTEDRFVVMYMSRQA 2790
Db 2143 NSIKVSVSSGGDC---IRYKPEIKKGSYNNIVNVK-----TAVADNLLFYLGSAKF 2192
QY 2791 TGDYMGVSLRDKKVVHVYQLGEAGPAV---LSIDEDIGEQAFAAVSLDRTLQFCHMSVTV 2846
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QY 2847 -----ERQMIQETKGDVAPGAEGLLNLRPDDFFVYVGGYPSFTFTPPPLRFPYRGCIEM 2902
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QY 3106 LNTTGVSACTADLLVGRAMTFHGHGFLRLALSNVAPLTGNTVYSGFGFHSQAQDSALLY- 3164
Db 2513 PDYVGVTKGCSLENVY--TVSFPKPGFVEL---SPVPIDVGTBILNLSFTKNESGIILLG 2567
QY 3165 -----RASPDGLCQVSLQCGRVSLQLLRTEVKTQAG-----FADGAPHY 3203
Db 2568 SGGTPAPPRXRRTQGOAYYVILLNRGRLEVH-LSTGARTMRKIVIRPEPNLFHDGREHS 2626
QY 3204 VAFYSNATGVW-LYVDDQLQOM-----KPHR-----GPPPELQPOPEGPPRLLLGLL 3249
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QY 3553 AVTGLIFHLGQARTPPYLQVTEKQVLLRADDDGAGEFST--SVTRPSVLCDGQWHRLAV 3610
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QY 3611 MKSGNVLRLEVDAQSNHTVGPLLAA-AAGAPAPLYLGLPEPMAVQPNWPPA--YCGCMRR 3667
Db 3032 NKIKHRIELTVDGNOVEAQSPNPASTSADTNDVDFVGGFDDDLKQFGLTTSIPFRGCIRS 3091
QY 3668 LAVNRSPVAMTRSV 3681
Db 3092 LKLTGKTASHWRLI 3105

RESULT 7
US-09-562-702A-6
; Sequence 6, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32


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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 3110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-6

Query Match      15.4%; Score 3103.5; DB 4; Length 3110;
Best Local Similarity 23.8%; Pred. No. 3.1e-183;
Matches 974; Conservative 479; Mismatches 1223; Indels 1417; Gaps 137;

QY 15 GPRGPAPLLLVGLALLGA-----ARAREEAGGGFSLHPPYFNLAEGARIAASATC 64
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QY 292 KDISIGRCVCHGHADACDAKDPDTPF--RLQCTCQHNTCGGTCDCRCCPGFNQOPWKPAT 349
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QY 1725 VFVPMESRPDVVLQG--NQMSITFLEPAYPTPGHVHRGQLQVVEGNFRH----TETRNT 1777
Db 1266 GF--STYNPQVIIRGGTPTHARIIVRHMAAPLIGQLTRHEIEMTEKWKYGGDDPRVHRT 1323
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1834 PASYRGDSQCECAPGYR-----DVKGLFLGRVCPCQCHGSHDRCLPGSGVCVDCQHN 1886
1383 PLGYSGLSCEACLPGFYRLRSQPGGRTPTLGTCTVPCQCHGSHSLCDPETSICQNCQHH 1442
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1532 -----YGSIPVP-----CDPVTGCTCRPGATGRKCDGCKXWH----- 1564
2065 GGCRPCACPAAGSECHPQSGQCHCRPGTMGPQCRECAPGYWGLPEQGCRRCQCPGGRC 2124
1565 -----AREGWEC----- 1571
2125 DPHTGRCNCPGLSGERCDTCSQHQVVPVPGPVGHSIHCEVCHVLLDDDLERAGAL 2184
1572 -----VFCG--DECTGLLGLDLARLEQM 1592
2185 -----LPAIHEQLRGINASS-----MAWARLHRLNASIADLOS 2217
1593 VMSINLTGFLPAPYKMLYGLENTQELKHLSPQAPERLIQLAEGNLTIVTEMNELLT 1652
2218 QLSRPLGRPHETAQOLEVLEQOSTSLGQDARRLGGQAVGTRDQASQLLAGTEATLGHAKT 2277
1653 RATKVTADGEOTQDAERTNTAKSLGEFIKELARDAEAVNEKAIKL-----NET 1702
2278 LLAAIRAVDRITLSELMSQTHGLGLANASAPSGEQLLRLTAEVERLLWEMRARDLGAPOAA 2337
1703 LGTRDEAFERNLEGLQK-----EIDQMIKELRRKNLETKQEI 1739
2338 AEAEALAAQRLRLARVQEBQSLIWEENQALATQTRDLAHEAGLMDLREALNRAVDATRE 2397
1740 AEDELVAEALKKVKKLFGESEGENEEMEKOLREKLADYKNKVDDAWDLREATDKIRE 1799
2398 AQELNSRQERLEBALQKQELSRDQATLQATLHAARDTLASVFRLLHSLDQAKSELERL 2457
1800 ANRLFVAVQKNTALEKKKEAVESGKQRIENTLKEGNDILDEANRLADEINSIIDYVEDI 1859
2458 AASLDGARTPLLQRMQTFSPAGSKLRLVE---AAEAAHQQLGQALNLSIIIDVNQD-- 2512
1860 QTKLPNSEELNDKIDDLSEIKDKRLAEKVSQAEASHAAQ-----LNDSSAVLDGILDEA 1914
2513 -RLTORATEASNAYSRILOVQAABDAAGQALQADHT--WATVVR-----QGLVDRA 2562
1915 KNISFNATAAFKAYSNIKDYIDEAEKVAKEAKDLAHEATKLATGPRGLLKEDAKGCLQKS 1974
2563 QQLLANSTALEEAMLOEQORLGLVWAALQARTQLRDVRAKQDLQLEAHIAQAAMLAMDT 2622
1975 FRILNEAKKLANDVKENEDH-----LNGLKTRIENADARNGDLLRLTNDTLGKLSAIP 2027
2623 DETSKKIAHAKAVAAEAQDTATRVQSQLOAMQENVERWQGYEGL-----RGQD 2671
2028 NDTAKLQAVKDXARQANDTAKDVLAQITELHQNLGDKKNYNKLADSVAKTNAVVKDPS 2087
2672 LGQAVLDAGHSVSTLEKTLQOLLAKLSILENRGVENASLALSASIGRVRELIAQARGAAS 2731
2088 KNKIIADADATVKNLEQADRLIDKL-----KPIKELEDNLKKNISEIKELINQARKQAN 2142
2732 KVKVPMKFNRSRGVQLRTPRDLADLAAYTALKFYLGPEPEPGQGTEDRFVVMGSRQAT 2791
2143 SIKVSVSSGGDC---IRTYKPEIKKGSYNNIVNVVK-----TAVADNLLFYLGSAKEFI 2192
2792 GDYMGVSLRDKKVVHYQIGEAGPAV-----LSIDEDIGEQAFAVSLDRTLQFGHMSVTV- 2846
2193 -DFLAIEMRKKGVSFLWDVSGVGVRVEYXPDLTIDDSYWRIVA---SRTGRNGTISVRAL 2248

RESULT 8

US-09-561-709B-7

; Sequence 7, Application US/09561709B

; Patent No. 6682911

2847 ---EROMIQETKGDIVAPGAEGLLNLRPDDFVYVGGYPSFTFTPPPLLPFGYRGCIEMD 2903
2249 DCPKASIVPSTHSTSPPGYT-ILVDVANAMLF-VGGLTGKLLKADAVRVTFTGCMGET 2306
2904 TLNEEVSLYNFERTFQDITAVDRPCARSKSTGDPWLTDGS-YLDGTGFARIS-----FDS 2958
2307 YFDNKPGLWNP-REKEGDC---KGCTVSPQVED---SEGTQPDGEGYALVSRPIRWYP 2359
2959 QISTTKRFEQELRLVSYSGVLFLL--KQSQFCLCLAVQEGSLVLLYDFGAGLKKAVPLQP 3016
2360 NISTVM---FKFRFTSSSALLMYLATRDLRDFMSVELTDGHKIVSYDLGSGMASVVSQN 2416
3017 PPPLTSASKAIOVFLLLGSRKRVLVRVERATVYSV-----EQDN-----DLE 3058
2417 HND-----GKWSFTLSRIQKQANISIVDIDTQENIATSSSGNNFGLDLK 2463
3059 LADAYLGLGVPPDQLPPSLRWLFPPTGGSVR-----GCVKGIK-ALGKYVDLKLRL 3106
2464 ADDKIYFGGL-----PTLRNL-----SMKARPEVNLKKYSGLKDIEISRTPPYNILSSP 2512
3107 NTTGVSAGCTADLLVGRAMTFHGHGFLRLALSNAVPLTGNVSGFGFHSQAQDSALLYV-- 3164
2513 DYVGVTKGCSENVY--TVSFPKPGFVEL---SPVPIDVGTGEINLSFSTKNESGIIILGS 2567
3165 -----RASPDGLCOVSLQOGRVSLQLLRTEVKTQAG-----FADGAPHV 3204
2568 GGTPAPRRKRRTQOAYVYVILLNRGLEVH-LSTGARTWKIVIRPEPNLFHDGREGHSV 2626
3205 AFYSNATGVW-LYVDDQLQOM-----KPHR-----GPPPELOQOPEGPPRLLLGLLP 3250
2627 -HVERTRGIFTVQVDENRRYMONLTVEQPIEVKLVFGVGAPPEFQPS-----LERNIP 2678
3251 ESGTIYFSGCISNVFVQRLLPQVFDLQONLGSNVSTG-CA----- 3293
2679 P-----FEGCIWNLVINSV-----PMDFARPVSFKNADIGRCAKQKLEDEDEGAAPAEI 2727
3294 -----PALQAQTPGL--GPRGLQATARKASRRSRQPARHPACMLPPHLRTRDSYQ 3342
2728 VIQPEVPVTPAFPTPTPVLTHGPCAAES-----EPALLI-----GSKQ 2765
3343 FGGSLSSHLEFVGILARHRNWPSSLMSHVLPRSSRGLLFP-----TARLRPGSPSL 3392
2766 FGLSRNSHIALAFDDTKVKNRLTIELEVRTEAESGLLFYMAAINHADFATVQLRNLGLPYF 2825
3393 ALFLSNG--HFVAQMEGLGLTRLRAQSRQSRPGRWHKVSVRWEKNRILLVTDGA--RAWS 3448
2826 SYDLGSGDTHM-----IPTKI-----NDGQWHKIKIMRSKQEGILYVDGASNRITIS 2872
3449 QEGPHRQHQGAHPQP-----HTLFVGGLPASSHSSKL-PVTVGFSGCVKRLHLKGRP 3500
2873 -----PKKADILDVGMVLYVGLPINYTRRIGPVTYSIDGCVRNLMHMAEP 2919
3501 --LGAPTRMAGVTPCILEAGLFFPGSG-----GVITLDPGATLPDVGLELEVRPLA 3553
2920 ADLEQPTSSPHVGTCFAN-AQRTYFDGTGTFKAVGGFKVGL-----DLLVEFEFATT 2972
3554 VTGLIFHLGQARTPPYLQVTEKQVLLRADDDGAGBFST--SVTRPSVLCGOWHRLAVM 3611
2973 TTGVLLGISQKMDG-MGIEMIDEKLMFHDVNDGAGRPTAVYDAGVPGHLCGOWHKTAN 3031
3612 KSGNVRLLEVDAQSNHTVGPULLAA-AAGAPAPLYLGLPEPMAVQWPWPPA--YCGCMRRL 3668
3032 KIKHRIELTVDGNQVEAQSPNFASTSADTNDPVFVGFPDDLKQFGLTTSIPFRGCIRSL 3091
3669 AVNRSPVAMTRSV 3681
3092 KLTKGTASHWRLI 3104

QY 1623 KGCTRCFCGATERCRSSSYTRQEFVDMEGWVLLSTDRQVVP-----HEROPG----- 1670
Db 1161 LGCSSCYCFGTTCQSEAKGL-----IRTWVTLKAEQTLPLVDEALQHTTKGIVFQH 1214
QY 1671 -----TEMLRADLRHVPEAVPEAPPELYWQAPPSYLGDRVSSYGGTTLRYELHSETQRGD 1724
Db 1215 PEIVAHMDLMREDLHLEP-----FYWKLPEQFEKGKLMAYGGKLYALYFEAREET 1265
QY 1725 VFVPMESRPDVVLQG---NQMSITFLEPAYPTPGHVRHQQLQVGNFRH-----TETRNT 1777
Db 1266 GF--STYNPOVIRGGTPTTHARIIVRHMAAPLIGQLTRHEIEMTEKEWKYVGGDDPRVHRT 1323
QY 1778 VSREELMMVLASLEQLQIRALFQISSAVSLRRVALEVASPAGQAL-----ASNVELCLC 1833
Db 1324 VTREDFLDILYDIHYILIKATYGNEMRQSRSEISMEVAB-QGRGTTWTPPADLIEKDCD 1382
QY 1834 PASYRGDSQECAPGFYR-----DVKGLFLGRVCPQCHGHSRCLPQSGVCVDCQHN 1886
Db 1383 PLGYSGLSCEACLPFGYRLRSQPGGRTPGPTLTGTCVPCQCNHSSSLCDPETSICQNCQHH 1442
QY 1887 TEGAHCERCQAGFMSSRDDPSAPCVSCPPLSVPSNNPABGCVLRG-GRTOC-LCKPGYA 1944
Db 1443 TAGDFCERCALGYGIVKGLPNDCCQACPLISSNNFSPSCVAEGLDDYRCTACPRGYE 1502
QY 1945 GASCERCAPGFFGNPLVLGSSCQPCDCSGNGDPNLLPSDCDPLTGACRGCLRHHTGPRCE 2004
Db 1503 QYCERCAPGYTGSPGPNPGGSCQEC-----ECDEP----- 1531
QY 2005 ICAPGFYGNALLPGNCTRCDCCTPCGTEACDPHSGHCLCKAGVTGRRRCRQCEGHFGNGC 2064
Db 1532 -----YGSPLVP-----CDPVTGFTCTCPGATGRKCKDCGCKHWH----- 1564
QY 2065 GGORPCACGPAAGSECHPQSGQCHCRPGTMGPQCRBAPGYWGLPEQGCRRRCQCPGGR 2124
Db 1565 -----AREGWEC----- 1571
QY 2125 DPHTGRCNCPGLSGERCDCSCQHQVFPVPGPVGHSIHCEVCDHCVVLLDDDLERAGAL 2184
Db 1572 -----VFCC--DECTGLLLGDLEARLEQM 1592
QY 2185 -----LPAIHEQLRGINASS-----MAWARLHRLNASIADLOS 2217
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QY 2218 QLRSPGPRRHETAQOLEVLEBQSTSLGQDARRLGGQAVGTRDQASQLLAGTEATLGHAKT 2277
Db 1653 RATKVTDAGEQTQDAERTNTRAKSLGEFIKELARDAEAVNEKAIKL-----NET 1702
QY 2278 LLAAITRAVDRTLSELMSTGHLGLANASAPSGEQLLRTLAEVERLLWEMRARDLGAPQAA 2337
Db 1703 LGTRDEAFERNLEGLQK-----EIDQMIKELRRKNLETKQEI 1739
QY 2338 AEAELEAAQORLLARVQEQSLSLWEENQALATQTRDRLAHEAGLMDLREALNRAVDATRE 2397
Db 1740 AEDELVAEALLKVKKLLFGEBSRGENEEMEKDLREKLADYKNKVDDAWDLLREATDKIRE 1799
QY 2398 AQELNSRNQERLEEAQORLQKQELSRDNATLOATLHAARDTLASVFRLLHSLDQAKEELERL 2457
Db 1800 ANRUFVAVNQNMNTALEKKEAVESGKRQIENTLKEGNDILDEANRLADEINSIIDYVEDI 1859
QY 2458 AASLDGARTPLLRMQTSPAGSKLRLVE---AAEHAHQQLGQALNLSSIIIDVNOQD-- 2512
Db 1860 QTKLPPMSEELNDKIDDLUSQEIKDRKLAEKVQAESHAQAQ-----LNDSSAVLDGILDEA 1914
QY 2513 -RLTQRAIEASNAYSRILOAVQAAEDAAGALQQAADHT--WATVVR-----QGLVDRA 2562
Db 1915 KNISFNATAAFKAYSNIKDYIDEAEKVAKAEKDLAHEATKLATGPRGLLKEDAKGCLQKS 1974
QY 2563 QOLLANSTALEEAMLEQOORLGLVWAAALQARTQLRDVRAKKDQLEAHIOAAQAMLANDT 2622
Db 1975 FRILNEAKKLANDVKNEDH-----LNLKTRIEADARNGLDRLTNDTLGLKLSAIP 2027
QY 2623 DETSKKIAHAKAVAAEAQDTATRVQSQLOAQENQENVERWQGYEGL-----RGQD 2671

Db 2028 NDTAAKLQAVKDKARQANDTAKOVLAQITELHQNLQDGLKKNYNKLADSVAKTNVVKDPS 2087
QY 2672 LQQAVIDAGHSVSTLEKTLPLLAKLSILENRGVHNASLALSASIGRVRELIAQARGAAS 2731
Db 2088 KNKIIADADATVKNLEQEADELIDKL-----KPIKELEDNLKKNISEIKELINQARKQAN 2142
QY 2732 KVKVPMKFNKRSQVQLRTPRDLADLAAYTALKFYLQPEPEPQCGCTEDRFVYMGSROAT 2791
Db 2143 SIKVSVSSGGDC---IRTYKPEIKKGSYNNIVNVK-----TAVADNLLFYLGSAKFI 2192
QY 2792 GDYMGVSLRDKKXHVYVQLGEAGPAV---LSIDEDIGEQAFAVSLDRTLQFGHMSVTV- 2846
Db 2193 -DFLAIEMRKGVKSVFLWDVGVGVGRVEYDPLTIDDSYWRIVA---SRTGRNGTISVRAL 2248
QY 2847 ---ERQMIQETKGTIVAPGAEGLLNLRPDDFVYVGGYPSFTPPPLLRFPYRGCIEMD 2903
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QY 2904 TLNEEVVSLYNEFRTFQDLDATAVDRPCARSKSTGDPWLTDGS-YLDGTGFARIS----FDS 2958
Db 2307 YFDNKPIGLWNF-REKEGDC--KGCTVSPQVED---SEGTFQDGEYALVSRPIRWYP 2359
QY 2959 QISTTKRFEQELRLVSYSGVLFEL--KQSQOFLCLAVQEGSLVLLYDFGAGLKKAVLPQP 3016
Db 2360 NISTVM--FKERTFSSALLMYLATRDLRDFMSVELTDGHIKVSVDLGLSGMASVVSQON 2416
QY 3017 PPPLTSASKAIQVFLGGSRRKRVLRVERATVYSV-----EQDN-----DLE 3058
Db 2417 HND-----GKWSFTLSRIQKQANISIVDIDTQNEENIATSSSGNNFGLDLK 2463
QY 3059 LADAYVILGVPDPDQLPPSLRWLFFTGGSVR-----GCVKGIK-ALGYVDLKLRL 3106
Db 2464 ADDKIYFGGL-----PTLRNL-----SMKARPEVNLKXSGCLKDIEISRTPNILSSP 2512
QY 3107 NTTGVSAGCTADLLVGRAMTFHGHGFLRLALSNVAPLTGNVYSGFGFHSQAQDSALLY-- 3164
Db 2513 DYVGVTKGCSENVY--TVSFPFGFVEL---SPVPIDVGTINLSFSTKNESGILLGS 2567
QY 3165 -----RASPDGLCQVSLQOQGRVSLQLLRTTEVKYQAG-----FADGAPHYV 3204
Db 2568 GGTAPPAPPRKERTQOAYVILLNRGRLEVH-LSTGARTMKIVIRPEPNLPHDGRHSV 2626
QY 3205 AFYSNATGVW-LYVDDQLQOM-----KPHR-----GPPPELOPQPEGPRLLLGGLP 3250
Db 2627 -HVERTRGITVQVDENRRYMQNLTVQPIEVKLVKLVGGAPPEFQSP-----LRNIP 2678
QY 3251 ESGTIYNFSGCISNVFVQRLGLPQRFVFDLQNLGSLVNVSTG-CA----- 3293
Db 2679 P-----PEGCIWNLVINSV-----PMDFARPVSKNADIGRCAHQKLEDEDDGAAPAEI 2727
QY 3294 -----PALQAOTPGL--GPRGLQATARKASRRSRQPARHPACMLPPLHRTTRDSYQ 3342
Db 2728 VIQPEPVPTPAFTPTPTVLTGHPCAES-----EPALLI-----GSKQ 2765
QY 3343 FGGSLSSHLEFVGILARHNWPSLSMHVLPSSRGULLLF-----TARLRPGSPSL 3392
Db 2766 FGLSRNSHIAIAFDQTKVKNPLTIELEVRTEAESGLLFYMAAINHADFATVQLRNLGPLYF 2825
QY 3393 ALFLSNG--HFVAQMEGLGTRLRAQSRQSRPRGRWHKVSVRWEKNRILLVTGA--RAWS 3448
Db 2826 SYDLGSGDTHM-----IPTKI-----NDGQWHKIKIMRSKQEGILYVDGASNRTIS 2872
QY 3449 QEGPHRQHQGAEPQP-----HTLFVGGPLPASSHSSKL-PVTVFGSGCVKRLRLHGRP 3500
Db 2873 -----PKADILDVVMGLYVGLPINTYTRRIGPVTYSIDGCVRNLMHMAEP 2919
QY 3501 --LGAPTRMAGVTPCILGLEAGLFFPGSG-----GVITLDLPGATLPDVGLELEVRPLA 3553
Db 2920 ADLEQPTSSFHVGTCTFAN-AQRTYFDGTGTGFAKAVGFKVGL-----DLLVEFEFATTT 2972
QY 3554 VTGLIFHLGQARTPPYLQVTEKQVLLRADDDGAGEFST--SVTRPSVLCDGQWHRLAVM 3611

Db 2973 TTGVLGISSQKMDG-MGIEMIDEKLMFHVNDGAGRFTAVIDAGVPGHLCDGQWHKV TAN 3031

Qy 3612 KSGNVLRLEVDQAQSNHTVGPLLAA-AAGAPAPLYLGLPEPMAVQPNPPA--YCGCMRRL 3668

Db 3032 KIKHRIELTVDGNQVBAQSPNPASTSADTNDPVFVGFPDDLKQFGLTTSIPFRGCIRSL 3091

Qy 3669 AVNRSPVAMTRSV 3681

Db 3092 KLTKGTASHWRLI 3104

RESULT 9

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; Sequence 2, Application US/09562702A

; Patent No. 6632790

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; APPLICANT: Yurchenco, Peter

; TITLE OF INVENTION: Laminin 2 and Methods for Its Use

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; LENGTH: 3110

; TYPE: PRT

; ORGANISM: Homo sapiens

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Query Match 15.4%; Score 3101.5; DB 4; Length 3110;

Best Local Similarity 23.8%; Pred. No. 4.le-183;

Matches 973; Conservative 477; Mismatches 1217; Indels 1417; Gaps 137;

Qy 15 GPRGPAPLLLVGLALLGA-----ARAREEAGGFSLSHPYPFNLAEGARIAASATC 64

Db 3 GAAGVLLLLLLSGLVGVAQBPQQORQSOAHQORG----LFPVNLASNALITTNATC 58

Qy 65 GEEAPARGSPRPTEDLYCKLVGPGVAGDPNQITIRGYCDIC--TAANSNKAHPASNAID 122

Db 59 GEKGP-----EMYCKLVEHV-----PGQPVNPQCRICNQNSSNPQNRHPITNAID 104

Qy 123 GTERWQSPPLSRGLEYNVNVNLTDLGQVHVAVYVLIKEANSRPDLVWILERSMDFGRTY 182

Db 105 GKNTWQSPSIKNGIEYHYVTITLDLQQVFQIAYVIVKAANSRPPGNWILERSLD-DVEY 163

Qy 183 QPWQFASCKRDCL-----ERFGPQTLERITRDDAAICTEYSRIVPLENGEIVVSLVN 236

Db 164 KPWQYHVAVTDECLTLNIIYPRTGPPS---YAKODEVICTSFYSKIHPLENGEIHISLIN 220

Qy 237 GRPGANMFSYSPLLREFTKATNVLRFLRTNTLLGHLMGKALR-----DPTVTRRYYSI 291

Db 221 GRPSADD--PSPELLEFTSARYTLRFRQIRTLNADLMFAHKDPREIDPIVTRRYYSV 278

Qy 292 KDISIGRCVCHGHADACADKDPDPP--RLQCTCQNTCGTCDRCCPGFNQOPWKPAT 349

Db 279 KDISVGMGICYG HARAC-----PLDPATNKSRCCEHNTCGDSCDQCCPGFHQKPRAGT 334

Qy 350 ANSANECSCNYGHATDCYDPEVDRRRASQSLDGTQGGGVCIDCQHHTAGVNCERCL 409

Db 335 FLTKTECACHGKAECCYDENVARRNLSLNIIRKYGIGGVGCINCTQNTAGINCETCT 394

Qy 410 PGFYR----SPNHPLDSPHVCRRNCE--SDFTDGTCD-----LTGRVCYCRNFSG 455

Db 395 DGFFRPKGVSFNY----PRPCQCHCDPIGSLNEVCVKDEKHARRGLAPGSCCHCKTGFGG 450

Qy 456 ERCDVCAEGFTGFPSPCYPTPSSSNDTREQVLPAGQIVNCDCSAAAGTQGNACKKDPVRVGR 515

Db 451 VSCDRCARGYTGYPDCKA-----CNCISGLGSK-----NEDPCFGPC 486

Qy 516 LCKPNFQGTCHCELCAPGYG-----PGCQPCQCSS----- 545

Db 487 ICKENVEGGDCSRCKSGFENLQEDNWKGDECFCGVSNRQCSSYWTYTKIQIDMSGWYLT 546

Qy 546 --PG---VADDRCDPDTGQCRCRVFGEGATCDRCAPG--YHFPLCQLCGCSPA--GTL 596

Db 547 DLPGRIRVAPQDDLDSPQ---QISISNAEARQALPHSYYSWAPAPYLGNKLPVAGQOLT 603

Qy 597 -----EGCD-----EAGRCLCQPEFAGPH 615

Db 604 FTISYDLEEEEDTERTVLQMLILEGNDLSISTAQDEVYVLPSEHTNVLLKXESFTIH 663

Qy 616 CDRCPGYHGFP-----NCQACTCDPRGAL 640

Db 664 -----GTH-FPVRRKEFMTVLANKRVLLQITYSFGMDAIFRLSSVNLESASVYPTDG- 715

Qy 641 DQLCGAGGLCRCPGYTGTAQCECPG-----FHGFPSCVPCHCSAEGSLHA-ACDP 691

Db 716 -SIAAAVEVCQPPGYTGSCESCSCWPRHRRVNGTIFGGL--CEPCQCFG---HAESCDD 768

Qy 692 RSGQC-SCRPRVTGLRCDTCVPGAYNFPY-----CSAGSCHPAGLAPVDPALPEAQVP- 743

Db 769 VTGECLNCKDHTGGPYCDKCLPGFYGEPTKGTSEDCCQAC-PLNI-PSNNFSPPTCHLDR 826

Qy 744 -----C-MCRAHVEGPSDCRCKPGFWGLSPSNPEG-CTRCSCDLRGLTGGVAECQDGTGQ 796

Db 827 SLGLICDGCVPVGTGPRCERCAEGYFG-QPSVPGGSCQPCQNDNLDIFSIPGSDLSGS 885

Qy 797 C-FCKPHVCGQACASCKDGFGLDQADYFGCRSQRCDIGGALGQSCERPRTGVCRRENTQ 855

Db 886 CLICKPGTGRYCELCADGYFG-DAVDAKNCQPCRCNAGGSFSEVCHSQTGQCECRANVQ 944

Qy 856 GPTCSEPARDHYLPDLHLHLRLELEBAATPEGHAVRFGFNLEFENFSWRGYAQMVPQPR 915

Db 945 GQRC----- 948

Qy 916 IVARLNLTPDLFWLVFRYVNRGAMSVSGRVSVREGRSAACANCTAQSQPVAFPPSTEP 975

Db 949 ----- 948

Qy 976 AFITVPQRFGEFVLNPGTVALRVEAEGVLLDYVLLPSAYVEAALLQLRVTEACTYRP 1035

Db 949 ----- 948

Qy 1036 SAQSGDNCLLYTHPLDGFPSAAGLEALCRQDNLSPRCPCTEQLSPSHPLITCTGSDV 1095

Db 949 -----DKC----- 951

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Db 952 ----- 951

Qy 1156 RDTQDHLAVFHLDSASVRLTAEQARFHLHGVTLPVPIEEFSEFVEPRVSCISSHGAFGP 1215

Db 952 -----KAGTFGL 958

Qy 1216 NSAAACLPSPFPKPPQPIILRDCQVITLPPGLPLTHAQDLTATSPAGPRPRPTAVDPDA 1275

Db 959 QSA----- 961

Qy 1276 EPTLLREPQATVVFTTHVPTLGRYAFLLHGYQPAHPTFFVEVLINAGRVWQGHANASFCP 1335

Db 962 ----- 961

Qy 1336 HGYGCRTLVCEGQALLDVTHSELVTVRVPEGRWLWLDYLVVPENVYSFGYLREEPLD 1395

Db 962 ----- 961

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Db 962 -----RGCVPCNCSFGSKSFCEEE-SG 983
QY 1456 QCPCHAVIGRDCSRCATGYWGP--NCRPCDCG--ARLDELDTGQCICPPRTIPDCLL 1511
Db 984 QCWCQPGVTGKCDRCAGHYFNFQEGGCTACECSHLGNNDPKTGRICICPPNTIGKCSK 1043
QY 1512 CQPQTFGCHPLVCEECNCSGPGIQLBTDPTDSDGQCKCRPNVTGRRCDTCSGPHGY 1571
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QY 1623 KGCTRCFCFCGATERCRSSSYTRQEFVDMEGWVLLSTDRQVVP-----HERQPG----- 1670
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QY 1671 -----TEMLRADLRHVPEAVPEAFPELYWQAPPSYLGDRVSSYGGTLRYELHSETQRGD 1724
Db 1215 PEIVAHMDLWREDLHLEP-----FYWKLPEQFECKLMAYGGKLYAIYFEAREET 1265
QY 1725 VFVPMESRPDVVLQG---NOMSITFLEPAYPTPGHVRGQLQVNEGFRH---TETRNT 1777
Db 1266 GF--STYNPQVIIRGGTPTTHARIIVRHMAAPLIGQLTRHEIEMTEKEWKYKGDDPRVHRT 1323
QY 1778 VSREELMMVLASLEQLQIRALFQSISAVSLRRVALEVASPAGQAL-----ASNVELCLC 1833
Db 1324 VTREDFLDILYDIHYILIKATYGNFMQRQSRISEISMEVAE--QGRGTTMTPTPADLIEKDC 1382
QY 1834 PASYRGDSQCECAPGFYR-----DVKGLFLGRVCPCQCHGSHDRCLPGSGVCVDCQHN 1886
Db 1383 PLGYSGLSCEACLPGFYRLRSQPGGRTPGPTLGTCTVPCQNGSHSLCDPETSICQNCQH 1442
QY 1887 TEGAHCECQAGFMSSRDDPSAPCVSCPCPLSVPSNFAEGCVLRG--GRTOC--LCKPGYA 1944
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QY 2005 ICAPGFYGNALLPGNCTRCDCPTGTEACDPHSGHCLCKAGVTGRRRCRQCEGHFGNGC 2064
Db 1532 -----YGSPLVP-----CDPVTGCTCRPGATGKCDGCKGWH----- 1564
QY 2065 GGCPRCAGPAAEGSECHPQSGCHCRPGTMGFCRECAPYWGWLPEQSGCRRCQCPGGR 2124
Db 1565 -----AREGWEC----- 1571
QY 2125 DPHTGRCNPPGLSGERCDTCSQHQVVPVPGPVGHSIHCEVCDHCVVLLDDLERAGAL 2184
Db 1572 -----VFCG--DECTGLLGLDLARLEQM 1592
QY 2185 -----LPATHEQLRGINASS-----MAWARLHRLNASIADLQS 2217
Db 1593 VMSINLTGPLPAPYKMLYGLENNMTQELKHLSPORAPERLIQLAEGNLTIVTEMNELT 1652
QY 2218 QLRSPGPRHETAQQLVLEQOSTSLGQDARRLGGQAVGTRDQASQLLAGTEATLGHAKT 2277
Db 1653 RATKVTADGEQTQDAERTNTRAKSLGEFIKELARDAEAVNEKAIKL-----NET 1702
QY 2278 LLAAIRAVDRTLSEMSQTHGLGLANASAPSGEQLLRTLAEVERLLWEMRARDLGAPAA 2337
Db 1703 LGTRDEAFERNLEGLQK-----EIDQMIKELRRKNLETQKEI 1739
QY 2338 AEAEELAAQRLRLARVQELSSLWEENQALATQTRDLRAQHEAGLMDLREALNRAVDATRE 2397
Db 1740 AEDELVAEALKKVKKLFGBSRGENEEMEXDLREKLADYKKNVDDAWDLLREATDKIRE 1799
QY 2398 AQELNSNQERLEEAALQRQELSRDNATLQATLHAARDTTLASVFRLLHSLDQAKELERL 2457

Db 1800 ANRLFAVNQKNMTALEKKKEAVESGKRQIENTLKEGNDILDEANRLADEINSIIDYVEDI 1859
QY 2458 AASLDGARTPLLRMTQTFSPAGSKLRLVE--AAEAHAQQLGQLALNLSIIIDVNQD-- 2512
Db 1860 QTKLPPMSEELNDKIDDLSEIKDKRLABKVSAESHAQ-----LNDSSAVLDGILDEA 1914
QY 2513 -RLTQRAIEASNAYSIRILQAVQAAEDAGQALQQAADHT--WATVVR-----QGLVDRA 2562
Db 1915 KNISFNATAAFKAYSNIKDYIDEAEKVAKEAKDLAHEATKLATGPRGLLKEDAKGCLQKS 1974
QY 2563 QOLLANSTALEEAMLQEQQRLGLVMAALQAGARTQLRDVRAKKDQLEAHIQAAQAAMLAMDT 2622
Db 1975 FRILNEAKKLANDVKENEDH-----LNGLKTRIENADARNGDLLRTLNDTLGKLSAIP 2027
QY 2623 DETSKKIAHAKAVAAEAQDTATRVQSQLOQAMQENVERWQGVQVEGL-----RGQD 2671
Db 2028 NDTAAKLQAVKDKARQANDTAKOVLAQITELHQNLDGLKKNYNKLADSVAKTNVAVKDP 2087
QY 2672 LGQAVLDAGHSYSTLEKTLPLLAKLSILENRGVHNASLASISGRVRELIAQARGAAS 2731
Db 2088 KNKIIADADATVKNLEQEAARLIDKL-----KPIKELEDNLKKNISEIKELINQARKQAN 2142
QY 2732 KVKVPMKFNRSVQLRTPRDLADLAAYTALKFYLOGPEPEPQGTEDRFVYMGSRQAT 2791
Db 2143 SIKVSVSSGGDC---IRTYKPEIKKGSYNNIVNVK-----TAVADNLLFYLGSAKFI 2192
QY 2792 GDYMGVSLRDKKVHWVYQLGEAGPAV---LSIDEDIGEQAASVSLDRTLQFGHMSVTV- 2846
Db 2193 -DFLAIEMRKGVSLWLVGSGVRYEYVDDLTIDDSYWRIVA---SRTGRNGTISVRAAL 2248
QY 2847 ---ERQMIQETKGDTPVAPGAEGLLNLRPPDDFVYVGVYESTFTPPPLRFPYRGCIEMD 2903
Db 2249 DGPKASIVPSTHSTSPPGYT--ILDVDANAMLF--VGGLTGKLLKADAVRVTFTGCMGET 2306
QY 2904 TLNEEVVSLYNFERTFQDLTAVDRPCARSKSTGDPWLTDCS--YLDGTGFARIS-----FDS 2958
Db 2307 YFDNKPIGLWNP--REKGDG---KGCTVSPQVED---SEGTFQDGEYALVSRPIRWYP 2359
QY 2959 QISTTKRFEQELRLVSYSGVLFLL--KQOSQFLCLAVQEGSLVLLYDFGAGLKKAVPLQP 3016
Db 2360 NISTVM---FKFRTFSSSALLMYLATRDLRDFMSVELTDGHKIKVSYDLGSGMASVVSQN 2416
QY 3017 PPPLTSASKAIQVFLGSGSRKRVLRVVERATVYSV-----EQDN-----DLE 3058
Db 2417 HND-----GKWSFTLSRIQKQANISIVDIDTQNEENIATSSSGNNFGLDLK 2463
QY 3059 LADAYYLGVPDPDQLPPSLRWLFTTGGSVR-----GCVKGIK--ALGKYVDLKLRL 3106
Db 2464 ADDKIYFGGL-----PTLRNL-----SMKARPEVNLKKYSGCLKDIERSPTYNILSSP 2512
QY 3107 NTTGVSAGCTADLLVGRAMTFHGHGFLRLALSNVAPLTGNVYSGFGFHSQDSALLY-- 3164
Db 2513 DYVGVTKGCSLENNY--TVSPFKPGFVEL---SPVPIDVGTINLSFSTKNESGILLGS 2567
QY 3165 -----RASPDGLCQVSLQCGRVSLQLLRTEVKTQAG-----FADGAPHYV 3204
Db 2568 GGTAPAPRRKRRTGTQAYVYVILLNRGRLEVH--LSTGARTMRKIVIRPEPNLFHDGHSV 2626
QY 3205 AFYSNATGVW--LYVDDQLQOM-----KPHR-----GPPPELOPQEPGPRLLLGGLP 3250
Db 2627 -HVERTRGIFTVQVDENRRYMNLTVEQPIEVKKLFVCGAPPEFQPS- 2678
QY 3251 ESGTIYFSGCISNVFVQRLGQVRVFDLQNLQSGVNVSTG-CA----- 3293
Db 2679 P-----FEGCIWNLVINSV-----PMDFARPVSKNADIGRCAHQKLEDEDAAPAEI 2727
QY 3294 -----PALQAQTPGL--GPRGLQATARKASRRSQPARHPACMLPPLHTRTDSYQ 3342
Db 2728 VIQPEPVPTPAFTPTPTVLTGHPCAAES-----EPALLI-----GSKQ 2765
QY 3343 FGGSLSSHLEFVGILARHNWPSLSMHVLPSSRGLLLF-----TARLRPGSPSL 3392
Db 2766 FGLSRNSHIAIAFDDTKVKNRULTIELEVRTEAESGULLFYMAAINHADFAIVQLRNLPLPYF 2825

QY 3393 ALFLSNG--HFVAQMEGLGTRLRAQSRORSRPPGRWHKVSVRWEKNRILLVTDGA--RAWS 3448
Db 2826 SYDLGSDTHTM-----IPTKI-----NDGQWHKIKIMRSKQEGILYVDGASNRTIS 2872
QY 3449 QEGPHRQHQGAERPOP-----HTLFVGGILPASSHSSKL-PVTVGFSGCVKRLRLHGRP 3500
Db 2873 -----PKKADILDVVMGLYVGGILPINYTRRIGPVTYSIDGCVNRLHMAEAP 2919
QY 3501 --LGAPTRMAGVTPCILGPLEAGLFFPGSG-----GVITLDLPGLATLPDVGLGLEVRPLA 3553
Db 2920 ADLEQPTSSFHVGTCPAN-AQRGTFFDGTGPAKAVGGFKVGL-----DLLVEFEFATTT 2972
QY 3554 VTGLIFHLGQARTPPYLQVTEKQVLLRADDDGAGEFST--SVTRPSVLCDGQWHLAVM 3611
Db 2973 TTGVLLGISSQKMDG-MGIEMIDEKLMFHDNGAGRFTAVYDAGVPGHLCGQWHLKV TAN 3031
QY 3612 KSGNVLRLEVDQSNHTVGPLLAA-AAGAPAPLYLGLPEPMAVQPPPA--YCGGWRRL 3668
Db 3032 KIKHRIELTVGDNQVEAQSPNPASTSADTNDVFGVGGPDDLKQFGLTTSIPFRGCIRSL 3091
QY 3669 AVNR 3672
Db 3092 KLTk 3095

RESULT 10
US-09-562-702A-8
; Sequence 8, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 3088
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-8

Query Match 15.4%; Score 3099.5; DB 4; Length 3088;
Best Local Similarity 23.8%; Pred. No. 5.4e-183;
Matches 967; Conservative 478; Mismatches 1213; Indels 1407; Gaps 136;
QY 33 ARAREEAGGFSLHPPYFNLAEGARIAASATCGEEAPARGSPRPTEDLCKLVGGPVAGG 92
Db 9 SOAHQORG-----LFPVNLNLSNALITTNATCGEKG-----EMYCKLVEHV----- 51
QY 93 DPNQITIRGOYCDIC--TAANSNKAHPASNAIDGTERWQSPPLSRGLEYNVNVTLDLGQ 150
Db 52 -PGQVNPQCRICNQSSNPQRHPITNAIDGKNTWQSPSIKNGIEYHYVITLTLQ 110
QY 151 VFHVAVYLLIKEANSPPRDLWVLSMDFGRTYQWPQFASCKRDC-----ERFGPQTL 204
Db 111 VFQIAYVIVKAANSPPRGNWILERSLD-DVEYKWPQYHAYVTDTECLTYNIYVFTGPPS- 168
QY 205 ERITRDDAICTEYSRIVPLENGEIVVSLVNGRPGAMNPSYSPLLREFTKATNVRRLFL 264
Db 169 --YAKDDEVICTSFYSKIHPLENGEIHISLINGRPSADD--PSPELLEFTSAPYIRLRFO 224
QY 265 RTNTLLGLHMGKALR-----DPTVTIRYYSIKDISIGRCVCHGHADACDAKDPTDPF- 318

Db 225 RIRTLNADLMMFAHKDPRIDPIVTRRYYSVKDISVGMCMICYGHARAC-----PLDPAT 280
QY 319 -RLQCTQHNTCGTCDRCQPGFNQPKWKPATANSANECQSCNCCYGHATDCYDPEVDRR 377
Db 281 NKSRCCEHNTCGDSCDQCQPGFHQKPRAGTFLTKTECEACNCHGKAECYDENVARR 340
QY 378 RASQSLDGTYYGGGVCIDCQHHTAGVNCERCLPGFYR-----SPNHPLDSPHVCRRCNCE- 432
Db 341 NLSLNRGKYIGGGVCINCTQNTAGINCETCTDFFRPGKGVSPNY-----PRPCQCHCDP 396
QY 433 -SDFTDGTCE-----LTGRCYCRPNFSGERCDVCAEGTGFPPSCYBTPSSSNDTRE 483
Db 397 IGSLNEVCVKDEKHARRGLAPGSCHCKTGFGVGSVCDRCARGYTGYPDCKA----- 446
QY 484 QVLPAGQIVNDCSAAAGTQGNACRKDPRVGRCLCKPNFQGTGTHCELCAPEGFYG-----PG 537
Db 447 -----CNCISGLGSK-----NEDPCFGPCICKENVEGGDCSRCKSGFFNLQEDNWK 492
QY 538 CQPCQCSS-----PG-----VADDRCDPDTGQCRVGFEG 568
Db 493 CDEFCGSGVSNRCQSSYTYGKIQDMGMYLTDLPGRIRVAPQDDLDSPQ-----QISISN 549
QY 569 ATCDRCAPG--YFHFPLCQLCGCSPA--GTLF-----EGCD 600
Db 550 AEARQALPHSYWSAPAPYLGKLPVAVGGQLTFTISYDEEEEDTERVLQMLILEGND 609
QY 601 -----EAGRCLCQPEFAGPHCDRCRPGYHGF----- 627
Db 610 LSISTAQDEVYLPSEHNTVLLKESFTIH-----GTH-FVRRKEFMTVLANKRV 662
QY 628 -----NCQACTCDPRGALDQLCGAGGLCRCPGYTGACQECSPG- 667
Db 663 LLQITYSFGMDAIFRLSSVNLSEAVSYPTDG--SIAAAVEVCQCPGPGYTSSCESCWPRH 720
QY 668 -----FHGFPSVPCVCHSAGSLHA-ACDPRSGQC-SCRPRVTGLRCDTCVPGAYNFP 718
Db 721 RRVNGTIFGGI--CEPCQCFG-----HAESCDDVTGECNLCKDHTGPGYCDKCLPGFYGEP 774
QY 719 Y-----CEAGSCHPAGLAPVDPALPEAQP-----C-MCRAHVEGSPCDRCRPGFWGL 765
Db 775 TKGTSEDCQPCAC-PLNT-PSNNFSPCHLDRSLGLICDGPVGYTGPRCERCAEGYFG- 831
QY 766 SPSNPEG-CTRCSCDLRGLTGGVAECQPGTGQC-FCKPHVCGQACASCKDGFGLDQADY 823
Db 832 QPSVPGSGCQPCQCNLDNDFSIPGSCDLSGLICKPGTGTGRYCELADGYFG-DAVDA 890
QY 824 FGCRSCRDIGGALGQSCBPRTGVCRCRPNTQGTCTSEPARDHYLPDLHLRLELEAAAT 883
Db 891 KNCQPCRCNAGGSFSEVCHSQTQCECRANVQQR----- 926
QY 884 PEGHAVRFGFNPLEFENFNSWRGYAQMVPQPRIVARLNTSPDLFWLFRVYVNRGMSVS 943
Db 927 ----- 926
QY 944 GRVSVREEGRSAAACANCTAQSPVAFPPSTPAFITVPRQGFGEFVLNPGTWALRVEAE 1003
Db 927 ----- 926
QY 1004 GVLLDYVVLPSAYVEAALLQLRVTEACTYRPSAQSGDNCLLYTHPLDGFPSAAGLEA 1063
Db 927 -----DKC----- 929
QY 1064 LCRQDNLPRPCPTQOLSPSHPLITCTGSDVDVQLQVAVPQGRYALVVEYANEDAROE 1123
Db 930 ----- 929
QY 1124 VGVAVHTPQAPQOGLLSLHPCLYSTLCRGRTARDTQDHLAVFHLDSASVRLTAEQARFF 1183
Db 930 ----- 929
QY 1184 LHGVTLPVIEEFSPEFVEPRVSCISSHGAFGPNSAACLPSPRFPKPPQPIILRDCQVILP 1243

Db 930 -----KAGTFGLQSA----- 939
QY 1244 PGLPLTHAQDLTPATSPAGPRPRPTAVDPDAEPTLLREPOATVFTTHVPTLGRYAFLL 1303
Db 940 ----- 939
QY 1304 HGYQPAHPTFPVEVLINAGRVWQGHANASFCPHGYGCRTLVVCEGOALLDVTHSELTVTV 1363
Db 940 ----- 939
QY 1364 RVPEGRWLWLDYVLVVPENVVSFGYLREEPLDKSYDFISHCAAQGYHISPSSSSLFCRNA 1423
Db 940 ----- 939
QY 1424 AASLSLFYNNGARPCGCHEVGATGPTCEPFGGQCPCHAHVIGRDCSRCATGYWGGP--NC 1481
Db 940 -----RGVPCNCSNFGSKSFDCEE-SGQCWCQPGVTGKKCDRCRAHGFNFQEGGC 989
QY 1482 RPCDCG--ARLCELTGQCICPRTIIPDCLLCQPTGCHPLVGCENCSGPGIQELT 1539
Db 990 TACECSHLGNCDPKTGRICICPNTIGCKSKCAPNTWGHISITTGCKACNCSTVG---SL 1046
QY 1540 DPTCDTDSGQCKCRPNVTGRRCDTCSPGFHGYPRCPDCHAEAGTAPGVD----- 1590
Db 1047 DFQCNVNTGQCNCHPKFSGAKTECSRHWNYPRCNLDCFLPGTDATTCDSKCKSCS 1106
QY 1591 PLTGQCYCKENVQPKDCQCSLGTFSLSDAANPKGCTRCFCGATERCRSSSYTRQEFVDM 1650
Db 1107 DQTGQCTKVNVGHIHCDRCRPGKFGDLAKNPLGSSCYCFGTTTQCSAKGL-----I 1160
QY 1651 EGWVLLSTDRQVVP-----HERQPG-----TEMLRADLRHVPEAVPEAFPPEL 1692
Db 1161 RTWVTLKAEQTLPLVDEALQHTTKGIVFQHPHVAHMDLMREDLHEP-----F 1211
QY 1693 YWQAPPSYLGDRVSSYGGTLRYELHSETQRGDVFPVMESSRPDVVLQ---NQMSITFLEP 1749
Db 1212 YWKLPEQEGKLMAYGGKLYAIYFEAREETGF--STYNQVIRGGTPTTHARIIVRHM 1269
QY 1750 AYPTPGHVHRGQLOLVEGNFRH----TETRNVTSEBELMMVLASLEQLQIRALFSQISSA 1805
Db 1270 AAPLIGQLTRHEIEMTEKWKYGGDDPRVHRTVTRDFDLIDLYDIHYLIKATYGNFMRO 1329
QY 1806 VSLRRVALEVASPAGQAL-----ASNVELCLCPASYRGDSCQECAPGEYR-----DVX 1854
Db 1330 SRISEISMEVAE-QGRGTTMTPTPADLIEKDCDPLGYSGLSCEACLPGEYRLRSQPGGRTP 1388
QY 1855 GLFLGRCVPCQCHGHSRDLCPGSGVCDVCOHNTGAHCERCQAGFMSRDDPSAPCVSCP 1914
Db 1389 GPTLGICVPCQCHGSHSLCDPETSICQNCQHHTAGDFCERCALGYIGYVGLPLNDCCQCA 1448
QY 1915 CPLSVPSNNFAEGCVLRG-GRTOC-LCKPGYAGASCERCAPGFFGNPLVLGSSCQPCDCS 1972
Db 1449 CPLISSNNFSPSCVAEGLDDYRCTACPRGYEGYCERCAPGYTGSFNGPGGSCQEC--- 1505
QY 1973 GNGDPNLLFSDCDPLTGACRGCLRHHTTGPRCEICAPGFYGNALLPGNCTRCDCPTCGTEA 2032
Db 1506 -----ECDP-----YGLPVP----- 1516
QY 2033 CDPHSGHCLCKAGVTGRRCDRCQEGHFGFNGCGGCRPCACGPAEESBCHPQSGQCHCRP 2092
Db 1517 CDPVTGFTCRPGATGRKCDGCKHWH-----AREGWEC----- 1549
QY 2093 GTMGPCRECAPGYWGLPEQGCRRRCQCPGGRCDPHTGRCNCPPLSGERCDTCSQHQVP 2152
Db 1550 ----- 1549
QY 2153 VPGGPVGHSHCEVCHCVVLLDDLERAGAL-----LPAIHEQLRGINASS----- 2199
Db 1550 -----VFCG--DECTGLLLGDRLARLEQVMYSINLTGPLPAPYKMLYGLENTQELK 1598
QY 2200 -----MAWARLHRLNASIADLQSLRSPGLPRHETAQOLEVLEQQSTSLGQ 2245
Db 1599 HLLSPQAPERLIQLAEGNLTLTVMENELLTRATKVATADGEQTGQDAERTNTRAKSLGE 1658

QY 2246 DARRLGGQAVGTEDQASQALLAGTEATLGHAKTLLAAIRAVDRTLSELMSQTHGLGLANAS 2305
Db 1659 FIKELARDAEAVNEKAIKL-----NETLGRDEAFERNLEGLQK----- 1697
QY 2306 APSGEQLLRTLAEBVERLLWEMRARDLGAPOAAAEEAELAAQRLARVQEOQLSSLWEENQA 2365
Db 1698 -----EIDQMIKELRRKNLETOKEIAEDELVAEAEALLKVKKLFGESEGENEE 1745
QY 2366 LATQTRDRLAQHEAGLMDLREALNRAVDATREAQELNSRNOERLEEAALQKQELSRDNAT 2425
Db 1746 MEKDLREKLADYKNKVDDAWDLREBATDKIREANRLFVNQKNMTALEKKKEAVESGKRQ 1805
QY 2426 LQATLHAARDTLASVFRLLHSLDOAKEELERLAASLDGARTPLLRMQTFSPAGSKLRV 2485
Db 1806 IENTLKEGNDILDEANRLADEINSIDYVEDIQTCLPWSHEELNDKIDDLSEIKDRKLA 1865
QY 2486 E---AAEAHAQOLGOLALNLSSIILDVNQD---RLTORATEASNAYSRILOAVQAEDAA 2539
Db 1866 EKVSQAESHAAQ---LNDSSAVLDGILDEAKNISFNATAAFKAYSNIKDYIDEAEKVA 1920
QY 2540 GOALQOQADHT--WATVVR-----QGLVDRAQQLLANSTALEEAMLEQEQRLGLVMAAL 2590
Db 1921 KEAKDLAHEATKLATGPRGLLKEDAKGLQKSFRLNEAKKLANDVKENEDH-----L 1973
QY 2591 QGARTQLRDVRAKKDQLEAHIQAAQAMLAMDTDTSKKTIAHAKAVAAEAQDTATRVQSOL 2650
Db 1974 NGLKTRIEADARNGDLLRTLNDTLGKLSAIPNDTAAKLQAVKDKARQANDTAKDVLAQI 2033
QY 2651 QAMQENVERWQOQYEGGL-----RGQDLGQAVLDAGHSVSTLEKTLPLQLLAKLSI 2699
Db 2034 TELHQNLGDKKNYNKLADSVAKTNAVVKDPSKNKIADADATVKNLEQEAADRLIDLK-- 2091
QY 2700 LENRGVHNASLALSASIGRVRELIQAARGAASKVKVPMKFNKRGSGVQLRTPRDLADLAAY 2759
Db 2092 ---KPIKELEDNLKKNISEIKELINQARKQANSIKVSVSSGGDC---IRTYKEIKKGSY 2145
QY 2760 TALKFYLGPEPEPGQGTEDRFVVMYMSRQATGDYMGVSLRDKKWHVYQVGEAGPAV-- 2817
Db 2146 NNIVNVNK-----TAVADNLLFYLGSAKFI-DFLAEMRKGVSVFLWDVSGVGVRVEY 2197
QY 2818 --LSIDEDIGEFAAVSLDRTLQFGHMSVTV---ERQMIQETKGDTPVAPGAELNLRP 2871
Db 2198 PDLTIDDSYWRIVA--SRTGRNGTISVRALDGPKASIVPSTHSTSPPGYT-ILDVDA 2253
QY 2872 DDFVYVGGYPTFTPTPLLRPGYRGCIEMDTLNEEVVSLYNFERTFQLDFAVDRPCAR 2931
Db 2254 NAMLF-VGGLTGKLLKADAVRVTFTGCMGETYFDNKPGLWNF-REKEGDC---KGCTV 2308
QY 2932 SKSTGDPWLTGDS-YLDGTGFARIS---FDSQISTTKRFEQELRLVSYSGVFFL--KQ 2984
Db 2309 SPQVED---SEGTIQFDGEGYALVSRPIRWYPNISTVM---FKRFTFSSALLMYLATRD 2362
QY 2985 QSQFLCLAVQEGSLVLLYDFGAGLKKAVPLQPPPLTSASKAIQVFLLGSKRKRVLRVE 3044
Db 2363 LRDFMSVELTDGHIKVSVDLGSMAVSVSNQNHND-----GKWSFTLSRIQ 2409
QY 3045 RATVYSV-----EQDN-----DLELADAYVYLGVPVPPDQPPSLRWLFPPTGGS 3086
Db 2410 KQANISIVDIDTNQEEENIATSSSGNFGDLKADDKIYFGGL-----PTLRNL-----S 2458
QY 3087 VR-----GCVKGIK-ALGKYVDLKRNLNTTQVSAGCTADLLVGRAMTFHGHGFLR 3134
Db 2459 MKARPEVNLKYSGLCKDIBISRTYPNLSPPDYVGTGKCSLENVY--TVSFPKPGFVE 2516
QY 3135 LALSNAVPLTGNVYSGFGFHSQADSALLY-----RASPDGLCQVSLQQGRV 3181
Db 2517 L---SPVPIDVGTINLSFSTPKNESGIILLGSGGTAPPRRKRRQTQAYVILLNRGL 2573
QY 3182 SLQLLRTEVKTQAG-----FADGAPHYVAFYSNATGVW-LYVDDQLQOM-----K 3225
Db 2574 EVH-LSTGARTMRKIVIRPBPENLFDHGREHVS-HVERTRGIFTQVDENRRYMQNLTVQE 2631

QY 3226 PHR-----GPPPELQPOEGPPRLLLGGLPESGTIYNFSGCISNVFVQRLLPQRFVD 3278
Db 2632 PIEVKXLFVGGAPPEFQSP-----LRNIPP-----FEGCIWNLVINSV-----PMD 2673
QY 3279 LQQLGSVNVSTG-CA-----PALQAQTFGL--GPRGLQA 3310
Db 2674 FARPVSFQNAIDIGRCAHQKLEDEDEGAAPAEIVIQPEVPPTPAFTPTPVLTTHGPCAAES 2733
QY 3311 TARKASRRSRQPARHPACMLPPHLRTTRDSYOFGSSLSHLEFVGLARHRNPWSLSMHV 3370
Db 2734 -----EPALLI-----GSKQFGLSRNSHIAIAFDITKVKRRLTIELEV 2771
QY 3371 LPRSSRGLLLF-----TARLRPGSPSLALFLSNG--HFVAQMEGLGTRLRAQSRQ 3418
Db 2772 RTEAESGLLFYMAAINHADFAFVQLRNGLPYFSDYDLGSGDTHM-----IPTKI----- 2820
QY 3419 RSRPGRWHKVSVRWEKRIILLVTDGA--RAMSQEGPHRQHGAHPQP-----HTLFV 3469
Db 2821 --NDGQWHKIKIMRSKQEGILYVDGASNRTIS-----PKKADILDVVGMLYV 2865
QY 3470 GGLPASSHSSKL-PVTVPFSGCVKRLRLHGRP--LGAPTRMAGVTPCILGPLEAGLFFPG 3526
Db 2866 GGLPINYTRRIGPVTYSIDGCVRNLMHMAEPADLEQPTSSFHVGTGFAN-AQRGTYFDG 2924
QY 3527 SG-----GVITLDLPGATLPDVGLELEVRPLAVTGLIFHLGQARTPPYLQLQVTEKQVLL 3581
Db 2925 TGFAKAVGGFKVGL-----DLIVEFEFATTTTGVLLGISSQKMDG-MGIEMIDEKLMF 2977
QY 3582 RADDGAGEFST--SVTRPSVLCDGQWHRLAVMKSGNVLRLEVDQAQSNHTVGPLLAA-AAG 3638
Db 2978 HVDNAGARFTAVYDAGVPGHLCGQWHKVTANKIKHRIELTVDGNQVEAQSFPNASTSAD 3037
QY 3639 APAPLYLGLPEPMAVQWPPA--YCGCMRRLAVNRSPVAMTRSV 3681
Db 3038 TNDPVFVGGFDDDKQFGLTTSIPFRGCIIRSLKLTGKTASHWRLI 3082

RESULT 11
US-09-562-702A-4
; Sequence 4, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
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; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent In Ver. 2.0
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; LENGTH: 3089
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QY 33 ARAREEAGGGSFSLHPPYFNLAEGARIAASATCGEEAPARGSPRPTEDLYCKLVGGPVAGG 92
Db 9 SQAHQQRG---LPPAVLNLASNALITTNATCGEKGK-----EMYCKLVEHV----- 51
QY 93 DPNQITIRGOYCDIC--TAANSNKAHPASNAIDGTERWQSPPLSRGLEYNVNVTLDLGQ 150

Db 52 -PGQPVNPOCRICNQSSNPQNRHPITNAIDGKNTWQSPSIKNGIEYHVYVITLTLQ 110
QY 151 VFHVAYVLKIFANSRPRDLWLERSMDFGRYQWQFQFASSKRDCL-----ERFGPQTL 204
Db 111 VFQIAYVIVKAANSRPGNWILERSLD-DVEYKWPQYHATVTECLTLNYPRTGPPS- 168
QY 205 ERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRPGAMNFSYSPLLRREFTKATNVRRLRFL 264
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QY 265 RTNLLGLHLMGKALR-----DPTVTRRRYYYSIKDISIGRCVCHGHADACDAKDPTDPF- 318
Db 225 RIRTLNADLMMFAHKDPRIDPIVTRRRYYYSVKDISVGMCMICYGHARAC-----PLDPAT 280
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Db 341 NLSLNIRKXYIGGGVCINCTONTAGINCETCTDGFRRPKGVSPNY---PRPCQPCCHCDP 396
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RESULT 12

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US-08-460-309-5
; Sequence 5, Application US/08460309
; Patent No. 5837496
; GENERAL INFORMATION:
; APPLICANT: Engvall, Eva
; APPLICANT: Leivo, Ilmo
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
; TITLE OF INVENTION: Fragments and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,309
; FILING DATE:
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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/125,077
; FILING DATE: 22-SEP-1993
; APPLICATION NUMBER: US PCT/US 94/10730
; FILING DATE: 21-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/472,319
; FILING DATE: 30-JAN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/919,951
; FILING DATE: 27-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9721
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3075 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-460-309-5
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Query Match 14.2%; Score 2854; DB 2; Length 3075;
Best Local Similarity 23.4%; Pred. No. 9.1e-168;
Matches 941; Conservative 513; Mismatches 1255; Indels 1320; Gaps 140;

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QY 2149 HQVPVGGPVGHSIHCEVCDHCVLLDDLERAGALLPAIHEQLRGINASSMAWARLHRL 2208
Db 1558 -----DECVGVLNLDLDEIGDAVLSLN--LTGI--IPVPYGILSNL 1594
QY 2209 NASIADLQSLRSPGLGPRRHETAQOLEVLEQQSTSLGQDARRLGGQAVGT---RDQASQLL 2265
Db 1595 ENTKYLOESL-----LKENMQDLGK--IKLEGVAEETDNLQKLTML 1637
QY 2266 A-----GTEATLGHAKTLIAAIRAVDRTLSELSMT-----GHLGLANASAPSGEQ 2311
Db 1638 ASTQKVNRAATERIFKESQDLAVAIERLQMSITEIMEKTTLNQTLDDEDFLLPNTLQNMQQ 1697
QY 2312 LLRTLAEVERLLWEMRARDLGAPQAAAEAEALAAQRLARVQEQLSLSEENQALATQTR 2371
Db 1698 NGTSLLEI-----MQIRDFTQLHQNATLELKAEDLLSQIENYQKPLEELEVLKEAAS 1751
QY 2372 DRLAQHEAGLMDLREALNRAVDA-TREAQELNSRNOERLEALQRKQELSRDNATLQATL 2430
Db 1752 HVLSKHNNEL-KAAEALVREAEAKMQESNHLLMVNANLREFSKKLHVQEEQNLTSELI 1810
QY 2431 HAARDTLASVFRLLHSLDQAKEBELE-----RLAASLDGARTPLLQRMQTFSPAG 2479
Db 1811 VQGRGLIDAAAAQTDVQDALEHLEDHQDKLLLSAKIRHHIDDLVHMMSQR----- 1862
QY 2480 SKRLVVEAAEAHAQQLGQLALNLSIILDVNQDRLTQRAIEASNAYSRILOAVQAAEDAA 2539
Db 1863 NAVDLVYRAEDHATEFORLADLVYSGLENIR--NVSLNATSAAYVHNYIQSLIEESEELA 1920
QY 2540 GQALQOQADHTWATVVRQGLVDRAQQLLANSTALEEAMLEQOORLGLVWAALQOQARTQIRD 2599
Db 1921 RDAHRTVTET--SLLSESLVSGKAAVQRSS---REFKEGNNLS---RKLPGIALELSE 1971
QY 2600 VRAXKDQLEAHI-----QAAQAMLAMDT--DETSKTIHAKAVAAEAQDTATRVQSQLQA 2652

QY 141 EVNVTLDLGOVHVAYVLIKFANSRPDLWVLESMDFGRTYQWQFFASSKRDCLERF- 199
Db 106 WVTITDLRQVFOVAYVIIKAANAPRPGNWILERSLD-GTTFSPWQYAYVSDSECLSYN 164
QY 200 ----GPQTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRPGAMNFSYSPLLREFT 254
Db 165 ITPRRGPPTYR---ADDEVICTSYYSRLVPLEHGEIHTSLINGRPSADDL--SPKLLLEFT 219
QY 255 KATNVRLRFLRTNLLGLHMGKALR-----DPTVTRYYYSIKDISIGGRVCVCHGHADAC 309
Db 220 SARYIRLRFERIRINADLMTLSHREPKELDPMLPRIYYYSIKDISVGMCMICYGHASSC 279
QY 310 DAKDPTDPFRLOCTCOHNTCGTCDRCCPGFNQOPWKPATANSANECQSCNICYGHATDCY 369
Db 280 PWDETTK--KLQOCEHNTCGESNRCPCGYHQPPWRPGTVSSGNTCEACNCHNKAADCY 337
QY 370 YDPEVDRRRASQSLDGTYYGGVCIDCQHHTAGVNCERCLPGFYR---SPNHPLDSPHV 425
Db 338 YDESVAKOKKSLNTAGQFRGGVCINCLQNTMGINCETCIDGYYPHVKVSPYE--DEP-- 393
QY 426 CRRNCE-----SDFTDGTCEDLTGRCYCRPNFSGERCDVCAEGFTGFPS 470
Db 394 CRPCNCDPVGSLSSVICKDDLHSDLENG--KQPGQCPCKEGYTGEXKCDRCQLGYKDYPT 450
QY 471 CYPTPSSSNDTREQVLPAGQIVNCDCSAAGTQGNACRKDPVRGRCCLKCKPNFQGTCELCA 530
Db 451 C-----VSCGCPVGSASD---EPCTGPCVCNENVEGKACDRCK 486
QY 531 PGFYG-----PGCQPCQCSSPGVAD-----DRCDP-----D 556
Db 487 PGFYNLKEKNPRGCSCECF--GVSDVCSSLWPLQVNSMSGWLVTDLISPRKIPSQOD 544
QY 557 TQQRRCRVGFEG-ATCDRCAPGYFHFPLCQLCG-----EFAGPHCDR----- 618
Db 545 ALGGRHQVSINNTAVMQR LAPKYWAAPAYLGNKLTAFGGFLKYTVSYDIPVETVDSNL 604
QY 589 CSPAGTLPEG-----CDEAGRCCLQP-----CDEAGRCCLQP----- 618
Db 605 MSHADVIIKGNGLTSLTQAEGLSLQPYEYLVNVRLVPENFQDFHSKRQIDRDQLMTVLA 664
QY 619 -----CRPGYH-----GFPNCACTCD--PRGALDQLCGAG-GLCRCPGYTGTAQCECS 665
Db 665 NVTHLLIRATYNSAKMALYRLSVSLDIASSNAIDLVAADVEHCEPCQGYTGTSCECL 724
QY 666 PGFHGFPSS-----CVPCHC--SAEGSLHAACDPSSGQSCRRPRVTGLRCDTCVPGAYN 716
Db 725 SGYRVVDGILFGGICQPCCHGHAACNVHVC-----IACAHTTGVHCEQCLPGFYG 778
QY 717 FP-YCEAGSCHPA-----GLAPVDPALPEAQVPC-MCRAHVEGPSCDRCKPGFWGL 765
Db 779 EPSRGTFGDCQPCACPLTIASNNFSPPTCHLNDGDEVVDWCAPGYSGAWCERCADGYG- 837
QY 766 SPSNP-EGCTRCSCLDRLTGLGVAECQPGTGQCF-CRPHVCGQACASCKDGFGLDQADY 823
Db 838 NPTVPGESCVPCDCSGNVDPSEAGHCDSTVTEGLCKLGNLTDGAHCERCADGYG-DAVTA 896
QY 824 FGCRSCRDIGGALGQSCPEPTGVCRCPNTOGPTCSBPARDHYLPDLHLRLLELEEAAT 883
Db 897 KNCRACECHVKGSHSAVCHLETGLCDCKPNTGQQC----- 932
QY 884 PEGHAVRFGFNPLEFENFWSRGYQAQMAPVQPRIVARLNLITSPDLFWLVFRYVNRGAMSVS 943
Db 933 ----- 932
QY 944 GRVSVREGRSAACANCTAQSQPVAFPPSTEPAFITVPQRFGEPPVLNPGTWALRVEAE 1003
Db 933 ----- 932
QY 1004 GVLLDYVLLPSAYYEAALLQRLVTEACTYRPSAQQSGDNCLLYTHPLDGFPSAAGLEA 1063
Db 933 -----DQCL----- 936
QY 1064 LCRQDNLPRPCPTEQLSPSHPLLITCTGSDVDVQLQVAVPQPGRYALVVEYANEDARQE 1123

Db 937 ----- 936
QY 1124 VGVAVHTPQRAPOQGLLSLHPCLYSTLCRGTDARTQDHLAVFHLDEASVRLTAEQARFF 1183
Db 937 ----- 936
QY 1184 LHGVTLPVIEEFSPEFVEPRVSCISSHGAFGPNAACLPSRFPKPPQPIILRDCQVPLP 1243
Db 937 -----HGYYGILDS----- 944
QY 1244 PGLPLTHAQDLTPATSPAGPRPRPTAVDPDABPTLLREPQATVVTTHVPTLGRYAFL 1303
Db 945 ----- 944
QY 1304 HGYQPAHPTFPVEVLINAGRVWQHANASFCPHGYGCRTLVVCEGOALLDVTHSELTVTV 1363
Db 945 -----GHGC----- 948
QY 1364 RVPEGRWLWLDYVLVVPENVYSFGYLREEPLDKSYDFISHCAAQYHISPSSSSLFCRNA 1423
Db 949 ----- 948
QY 1424 AASLSLFYNNGARPCGCHVEVGATGPTCEPFGGQCPCHAHVIGRDCSRCATGYWGF--NC 1481
Db 949 -----RPCNCSVAGSVSDGCTD-EGQCHCVPGVAGKRCDCRCAHGFAYQDGC 995
QY 1482 RPCDC--GARLDELTCGICCPPTIPTPDCLLCQPTTFGCHPLVGEECNCSGPIQELT 1539
Db 996 TPCDCPHTQNTCDPETGECVCPHTQGVKCEECEDGHWGYDAEVGCQACNCSLVG--ST 1052
QY 1540 DPTCDTDSGQCKCRPNVTGRRCDTCSPGFHYGPRCPDCDCHAGTAPGVCD----- 1590
Db 1053 HHRCDVVTGHCQCKSKFGGRACVQCSLGYRDFPDCVPCDCLRGTSGDACNLEQGLCGCV 1112
QY 1591 PLTGQCYCKENVQGPCKDCQCSLGTFSLDAANPKGCTRCFCFGATERCRS--SSYTRQEFVD 1649
Db 1113 EETGACPCKENVFGPQCNECREGTALRADNPLGCSPCFCSCGLSHLCSELEDYVTP-- 1169
QY 1650 MEGWVLLSTDQVVPHERQPGTEMLRADLRHVPEAVPEAFPE-----LY 1693
Db 1170 ----VTGSDQPLL-----RVVSQSNLRTGTEGVYQAPDFLLDAATVRQHRAEPFY 1218
QY 1694 WQAPPSYLGDRVSSYGGTIRYELHSETQRGDVFVPMES-----RPDVVLQGNQM--SIT 1745
Db 1219 WRLPQOFGDQLMAYGKLYSV-----AFYSLDGVGTSNFPQVLIKGGIRKQVI 1270
QY 1746 FLEPAYPTPGHVHRGQLQVVEGNF--RHTETRNTVSRRELMVMVASLEQLQIRALFSQI 1802
Db 1271 YMDAPAPENG-VRQEQEVAMRENFWKYFNSVSEKPVTRFEDFMSVLSIDIEYILIKASYCQG 1329
QY 1803 SSAVSLRRVALEVASPA----GQALASNVLELCLCPASYRGDSCQECAPGYR-----D 1852
Db 1330 LQQSRIISDISMEVGRKAELHPEEBEASLLENCVCPGTVGFSCQDCAPGYHRGKLPAGS 1389
QY 1853 VKG--LFLGRCVPCQCHGHSRCLPGSGVCVDCQHNTEGAHCERCQAGFMSRRDDPSAPC 1910
Db 1390 DRGPRPLVAPCVPCSCNNHSDTCDPNTGKCLNCGDNTAGDCHDVCTSGYYGKVTGSASDC 1449
QY 1911 VSCPCPLSVPSNNFAEGCVLRRGRT-QC-LCKPGYAGASCERCAPGFNGNPLVLGSSCOP 1968
Db 1450 ALCACPHSPPA-SFSPTCVLEGDHDFRCDACLGLYEGKHCECSCSSYYGNPQTPGGSCQK 1508
QY 1969 CDCSGNGDPNLLFSDCDPLTGACRGCLRHTTGPRIEICAPGFYGNALLPGNCTRCDCCTPC 2028
Db 1509 CDCNPHG-----SVHGD----- 1520
QY 2029 GTEACDPHSGHCLCKAGVTGRRCDRCQEGHFGFNGCGGCRPCACGPAAGSECHPQSGQC 2088
Db 1521 ----CDRTSGQCVRLGASGLRCDCEPRHI----- 1547
QY 2089 HCRPGTMGPOCRECAPGYWGLPEQGCRRRCQCPGGRCDPHTGRNCNPPGLSGERCDCSCQ 2148

Db 1548 -----LMETDCVSCD----- 1557
Qy 2149 HQVPVGGPVGSHIHCEVCHVLLDDLERAGALLPAIHEQLRGINASSMAWARLHRL 2208
Db 1558 -----DECVGVLNLDLDEIGDAVLSN--LTGI--IPVYGILSNL 1594
Qy 2209 NASIADLQSLRSPGPRHETAQQLEVLQOQSTSLGQDARRLGGQAVGT---RDQASOLL 2265
Db 1595 ENTTKYLQESL-----LKENMQDLGK--IKLEGVAEETDNLQKLTML 1637
Qy 2266 A-----GTEATLGHAKTLLAAIRAVDRTLSELMSQT-----GHLGLANASAPSGEQ 2311
Db 1638 ASTQKVNRAIERIFKESQDLAVAIERLQMSITEIMEKTTLNQTLDEDFLLPNSTLQNMQQ 1697
Qy 2312 LRLTLAEVERLLWEMRARDLGAPQAAAEALAAQRLARVQEQLSLWEEENOALATQTR 2371
Db 1698 NGTSLLEI-----MQIRDFTQLHQNATLELKAAEEDLLSQIQENYQKPLEELEVLEKEAAS 1751
Qy 2372 DRLAQHEAGLMDLREALNRAVDA--TREAQELNSRNQERLEELQKQELSRLDNATLQATL 2430
Db 1752 HVLSKHNNEL--KAAEALVREAEAKQESNHLLLMVNANLREFSDKLLHVQEEQNLTSELI 1810
Qy 2431 HAARDTLASVFRLLHSLDQAKELE-----RLAASLDGARTPLLQRMQTFSPAG 2479
Db 1811 VOGRGLIDAAAAQTDAVQDALEHLEDHQDKLLWSAKIRHHIDDLVMHMSQR----- 1862
Qy 2480 SKRLVEAAEAHAQQLGQALNLSSIIIDVNQDRLTORAIEASNAYSRILOAVQAAEDAA 2539
Db 1863 NAVDLVYRAEDHATEFORLADVLSGLENIR--NVSLNATSAAYVHYNIQSLIESEELA 1920
Qy 2540 GQALQADHTWATVVRQGLVDRAQQLLANSTALEEAMLEQORQLGLVWAAALQGARTQLRD 2599
Db 1921 RDAHRTVTET--SLLESLSVNGKAAVQRSS---RFLKEGNNLS---RKLPGIALELSE 1971
Qy 2600 VRAKXQDLBAHI-----QAAQAMLAMDT--DETSKKIAHAKAVAAEAQDTATRVQSQLQA 2652
Db 1972 LRKNKTRNFQENAVEITROTNESLLILRAIPEGIRDKGAKTELATSASQSAVSTLRDVAG 2031
Qy 2653 MQENVBRWQGYEGLRG-----QDLGQAVLDAGHSYSTLE---KTLPLQALLAKLSIL 2700
Db 2032 LSQELNLTSAASLSRVNTTLRETHQLLQDSTMATLLAGRKVKDVEIOAKVLFDRKPLKML 2091
Qy 2701 ENRGVHNASLASASIGRVRELIAQARGAASKVKVPMKFNRSQVQLRTPRDLADLAAYT 2760
Db 2092 EEN-----LSRNLSEIKLLISQARKQAASIKVAVSAD-RDCIRAYQPQ--JSSNTYN 2140
Qy 2761 ALKFVLCQPEPEPGQGTEDRFVMYMGSRQATGDMYMGVSLRDKKVVHVYQLGEACPAVLSI 2820
Db 2141 TLLTNVKTQEP-----DNLLFYLSSTAS-DFLAVENRRGRVAFWLWDLGSGSTRLEFP 2192
Qy 2821 DEDIGE-QFAAVSLDRTLQFGHMSVTVEROMIQETKGT---VAPGAEGLLNLRPDDFVF 2876
Db 2193 DFPIDNRWHSIHVARFNGNIGLSV---KEMSSNQKSPTKTSKSPGTANVLDVNNSTLMF 2249
Qy 2877 YVGYPSTFTPPPLLRFPGYRGCIEMDTLNEEVVSLYNF-ERTFQLDТАVDRPCARSKST 2935
Db 2250 -VGGLGGQIKKSPAVKVTHFKGCLGEAFLNGKISGLWNVIEREGKC-----RGCFGSSQN 2303
Qy 2936 GDPWLTGSGYLDGTGFARISFDSQISTTKRFEQELRLVSYSGVLFFLKQ--QSQFLCLAV 2993
Db 2304 EDP----SFHFDGSGYSVVE-KSLPATVTQIIMLNTFSPNGLLLYLGSYGTDFLSIEL 2358
Qy 2994 QEGSLVLLYDFGAGLKKAVPLQPPPLTSAKAIQVFLGGSRKRVLVRVERATVYSV-- 3051
Db 2359 FRGRVKWMTDLGSG-----PITLLTDR-----RYNNGTWYKIAF 2392
Qy 3052 ---EQNDLELADAY-----YLGVPFPDQLPESLRWLF 3081
Db 2393 QRNRKQGVLAVIDAYNTSNKQETPGAGSSDLNRLDKDPYVVGGLPRSRV---VRRGV 2449
Qy 3082 PTGGSVRGCVKGKIKALGKYVDLKRINTTGVSACTADLLVGRAMTFHGHGFLRLALSVA 3141
Db 2450 TTKSFV-GCIKNLEISRSTFDLLR-NSYGVKKGCLLEPI--RSVSFLKGGYELPPKSLS 2505

Qy 3142 PLTGNVYSGFGFHSAQDSALLYRASPDGLCQVSLQOGRV---SLQLL--RTEVXTQAG- 3195
Db 2506 PESEWLVT---FATTNSSGIILAAALGGDVEKRGDREAHVFFFSVMLIGGNIEVHVNPBGD 2562
Qy 3196 -----PADGAPHYVAFYSNATGVWLYVDQLQOMKPHRGPPPEL----- 3234
Db 2563 GTGLRKALLHAPTGTCSDDGQAHSLSVNRRIITVQLDE-----NNPVMKLGTLV 2613
Qy 3235 QPQPEGPPRLLLGGLE-SGTIY-----NFGSCISNVFQRLLPQRPVLDLQONLGSVVV 3288
Db 2614 ESRTINVSNLVVGIPGEGEGTSLLTMRSSFHGCIGNL-----IFNLE--LLDFNS 2661
Qy 3289 STGCAPALQAOQTPGLGPRGLQATARKASRRSRQPARHP-ACWLPPLHRLTRTDSYQFGGSL 3347
Db 2662 AVG-HEQVDLDTCLWLSERPKLAPDAEDSKLLREPRAFPEQCQVYDAALEYVPGAHQFGLTQ 2720
Qy 3348 SSH--LEFVGILARHNRNWPSSLMHVLPRSSRGLLLFTARLPSPSLALFLSNG--HFVA 3403
Db 2721 NSHFILPFNQSAVRKLSVELSIRTL--ASSGLIYYMAHQNDQADYAV-LQLHGGRLHFMF 2777
Qy 3404 QMEGLGTRLRAQSRQSRPRGRWHKYSVRWEKNRILLVTDGARAWSQEGPHRQ--HQGAEH 3461
Db 2778 DL-GKG-RTKVSHPALLSDGKWHVTVKTDYVVRKGFITVDG-----RESPMVTVVGDGTML 2830
Qy 3462 POPHTLFGGLPASSHSSKL-PVTVGFSGCVKRLRLHGRPL--CAPTRMAGVTPCILGPL 3518
Db 2831 DVEGLFYGLGLPQYQARKIGNITHSIPACIGDVTVNSKQDKDSPVSAFTVNRQ-YAVA 2889
Qy 3519 EAGLFFPGSGGVITLDPGATLPDVGLELEVRPLAVTGLIFHLGQARTPPYLQLVTEKQ 3578
Db 2890 QEGTYFDGSGYAAALVKEGYKVQSDVNITLFTSSQNGVLLGISTAKVDA-IGLELVGDK 2948
Qy 3579 VLLRADDGAGEFSTSVTRP---SVLCDGQWHRLAVMKSGNVLRLEVD-----AQSNHTVG 3630
Db 2949 VLFHVNNAGARI-TPAYEPKTATVLCDGKWHITLQANKSKHRTITLIVDGNVAGAESPHT-- 3005
Qy 3631 PLLAAAGAPAPLYLGLPEPMAVQ--PWPPAYCGCMRRRLAVNRSP-----VAMTRSVEVH 3684
Db 3006 --QSTSVDTNNPIYVGYYPAGVKQKCLRSTQTSFRGCLRKLALIKSPQVQSLDFSRFELH 3063
Qy 3685 GAVGASGCP 3693
Db 3064 G-VFLHSCP 3071

RESULT 14
US-08-600-982-24
; Sequence 24, Application US/08600982
; Patent No. 6120991
; GENERAL INFORMATION:
; APPLICANT: Carter, William G.
; APPLICANT: Gil, Susanna A.
; APPLICANT: Ryan, Maureen C.
; TITLE OF INVENTION: Epiligrin, an Epithelial Ligand for
; TITLE OF INVENTION: Integrins
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson, and Kindness
; STREET: 1420 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101-8100
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/600,982
; FILING DATE: 02-SEP-1994
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-8100
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INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1713 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: E170 protein as translated from sequence
DESCRIPTION: OF FIGURES 15A-15F, and as shown also in FIGURES
DESCRIPTION: 19A-19R
US-08-600-982-24

Query Match 11.2%; Score 2260.5; DB 3; Length 1713;
Best Local Similarity 31.5%; Pred. No. 2.6e-131;
Matches 612; Conservative 296; Mismatches 711; Indels 321; Gaps 48;

QY 1818 PAGQAL-ASNVELCLPASRGDSCQECAPGFYRDVKGFLGRVCPCQCHGSHDRCLPG 1876
D 1818 PAGQAL-ASNVELCLPASRGDSCQECAPGFYRDVKGFLGRVCPCQCHGSHDRCLPG 1876
D 29 PPGSQLQASYVEF-----RPSQCSPGYRDHKGLYTGRVPCNCGNSQCQDG 79
QY 1877 SGVVCDCQNTGHAHCERCAQAGFMSSRDDPSAPCVSCPCPLSVPSNPAEGCVLRGGRTQ 1936
D 1877 SGVVCDCQNTGHAHCERCAQAGFMSSRDDPSAPCVSCPCPLSVPSNPAEGCVLRGGRTQ 1936
D 80 SGICVNCQHTAGEHCERCEGYGNAVHGS--CRACPCP---HTNSPATGCVVNGGDVR 134
QY 1937 CLKPGYAGASCERCAPGFGNPLVLGSSCQPCDCSNGDPRNLLFSDCDPLTGACRGCLR 1996
D 1937 CLKPGYAGASCERCAPGFGNPLVLGSSCQPCDCSNGDPRNLLFSDCDPLTGACRGCLR 1996
D 135 CSCKAGYGTQCERCAPGFGNPKQFGGSCQPCSCNSNGQ---LGSCHPLTGDGIN--- 187
QY 1997 HTTGPRCEICAPGYGNALLPGNCTRCCTPCGTEACDPHSGHCLCKAGVTGRRCDRCQE 2056
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D 188 -----PKDSSPAEE-----QE 189
QY 2057 GHFGNCGGCRPCACGPAAGSECHPQSGQCHCRPGTMGPQCRECAPGYWGLPEQGCR 2116
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D 190 -----PKDSSPAEE----- 198
QY 2117 CQPGRCRDPHTGRNCPPGLSGERCCTCSQHQVVPVPGPVGHSIHCEVCDHCVVLLD 2176
D 2117 CQPGRCRDPHTGRNCPPGLSGERCCTCSQHQVVPVPGPVGHSIHCEVCDHCVVLLD 2176
D 199 -----CDDCDSVMTLLN 211
QY 2177 DLERAGALLPAIHEQLRGINASSMAWARLHRLNASIADLQSLRSLGPRHETAQQLVL 2236
D 2177 DLERAGALLPAIHEQLRGINASSMAWARLHRLNASIADLQSLRSLGPRHETAQQLVL 2236
D 212 DLATMGELRLVKSQGLSASAGLLEQMRHMETQAKLRNLNRYSAISNHGSKIEGL 271
QY 2237 EQQSTSLGQDARRLGGQVTRDQASQLLAGTEATLGHAKTLAAIRAVDRTLSEMSQ- 2295
D 2237 EQQSTSLGQDARRLGGQVTRDQASQLLAGTEATLGHAKTLAAIRAVDRTLSEMSQ- 2295
D 272 ERELTLNQEFTLQEKAVNSRKAQTLNNNNVNRATQSAKELDKVIRNVIRNHLKQI 331
QY 2296 TGHGLANASAPSGEQLLFTLAEVERLLWEMEARDLGAPQAAAEALAAQRLARVQEQ 2355
D 2296 TGHGLANASAPSGEQLLFTLAEVERLLWEMEARDLGAPQAAAEALAAQRLARVQEQ 2355
D 332 SGTDBEGN-NVPSGD-FSEWAEAAQRMRELNRNFGKHLREAEADKRESQLLNRIWT 389
QY 2356 LSSLWEENQALATQTRDLAQHEAGLMDLREALNRVADATREAOELNSRNQERLEALQ 2415
D 2356 LSSLWEENQALATQTRDLAQHEAGLMDLREALNRVADATREAOELNSRNQERLEALQ 2415
D 390 QKTHQGENGLANSIRDSINEYEAKLSDLRLRLQEAQAAQAKQANGLNEN-ERALGAIQR 448
QY 2416 K-QELSRDNATLQATLHAARDTLASVFRLLHSLDQAEELERLAASLDGARTPLLRMQT 2474
D 2416 K-QELSRDNATLQATLHAARDTLASVFRLLHSLDQAEELERLAASLDGARTPLLRMQT 2474
D 449 QVKEINSLSQDFTKTLTADSSLLQTNIALQLMKESQKEYEKLAAASLNEARQELSDKVE 508
QY 2475 FSPAGSKRLVEAAEAHAQQLGQALNLSIILDVNDRLTQRAFEASNAYSRILOAVQA 2534
D 2475 FSPAGSKRLVEAAEAHAQQLGQALNLSIILDVNDRLTQRAFEASNAYSRILOAVQA 2534
D 509 LRSAGKTSLEEAEKFAARSLQELAKQLEEKRNASGDELVRCAVDAATAYENILNAIKA 568
QY 2535 AEDAAGQALQADHTWATVVRQGLVDRAQQLANS-TALEEAMIQEQRLGLVWAAQQA 2593
D 2535 AEDAAGQALQADHTWATVVRQGLVDRAQQLANS-TALEEAMIQEQRLGLVWAAQQA 2593
D 569 AEDAANRAASASEALQTVIKEDLPRAKTLSSNSDKLLNEAKMTQKLLKQEVSPALNNL 628

QY 2594 RTQLRDVRAKDKQLEAHIAQAQ-AMLAMDTDETSKIAHAKAVAAEAQDTATRVQSQLOA 2652
D 2594 RTQLRDVRAKDKQLEAHIAQAQ-AMLAMDTDETSKIAHAKAVAAEAQDTATRVQSQLOA 2652
D 629 QOTLNIIVTQKEVIDTNLTTLRDLGHIQORDIDAMISSAKSMVRKANDITDEVLDGLNP 688
QY 2653 MOENVERWQCYEGLRGQDLGQAVLDAGHSVSTLEKTLQQLAKLSILENRGVHNASLA- 2711
D 2653 MOENVERWQCYEGLRGQDLGQAVLDAGHSVSTLEKTLQQLAKLSILENRGVHNASLA- 2711
D 689 IQTDVERIKDTYGRQNEDEKALTDADNSVKNLTNKLPLDLWRKIESI-----NQQLLP 742
QY 2712 ---LSASIGRVRELIAQAARGAASKVKVPMKFNKGRSGVQLRTPRDLADLAAYTALKFYLG 2768
D 2712 ---LSASIGRVRELIAQAARGAASKVKVPMKFNKGRSGVQLRTPRDLADLAAYTALKFYLG 2768
D 743 LGNISDNMDRIELIQARDAASKVAVPMRFGKSGVEVRLPNDLEDLKGYTSLSLFLQR 802
QY 2769 PEPEPGQGTEDRFVNMVMSRQATGDMGVSLRDKKVVWVYQLGEAGPAVLSIDEDIGE- 2827
D 2769 PEPEPGQGTEDRFVNMVMSRQATGDMGVSLRDKKVVWVYQLGEAGPAVLSIDEDIGE- 2827
D 803 PMSRENGGTEIENFMVYLGKNDASRDYIGMAVVDGQLTCVYNLGDG-EAELQVDQILTKE 861
QY 2828 ---FAAVSLDRTLOFGHMSVTVVERQMIQ-ETKG---DTVAPGAEGLLNLRPDDVFYVG 2879
D 2828 ---FAAVSLDRTLOFGHMSVTVVERQMIQ-ETKG---DTVAPGAEGLLNLRPDDVFYVG 2879
D 862 TKEAVMDRVKFORIYQFARLNTYKATSSKPTPGVYDMDGRNSNTLLNLDPENVYFVG 921
QY 2880 GYPSTFTFPPLLRFPFGYRGCIEMDTLNEEVVSLYNEBTFQDLTAVDRPCARSKSTGDPW 2939
D 2880 GYPSTFTFPPLLRFPFGYRGCIEMDTLNEEVVSLYNEBTFQDLTAVDRPCARSKSTGDPW 2939
D 922 GYPDFKLPRLSPFPYKGCIELDDLNLNENVLSLYNFKTKTNLTTEVEPCRRKEE--- 977
QY 2940 LTDGSLDGTGFARISFDSQISTTKRFEQELRLVSVGVFLFKLQSQOFLCLAVQEGSLV 2999
D 2940 LTDGSLDGTGFARISFDSQISTTKRFEQELRLVSVGVFLFKLQSQOFLCLAVQEGSLV 2999
D 978 -SDKNYFEGTGYARVPTQPH-APIPTFGQTIQTTVDRLGLFFAENGDRFISLNIEDGKLM 1035
QY 3000 LLYDFGAGLKK-----AVLPQPPPLTSASKAIQVFLGGSRRKRVLRVERATVYSVEQ 3053
D 3000 LLYDFGAGLKK-----AVLPQPPPLTSASKAIQVFLGGSRRKRVLRVERATVYSVEQ 3053
D 1036 VRYKLNSELPKERGVGDAIN-----NGRDHSIQI-KIGLKQRMWINVD---VQNTII 1084
QY 3054 DNDLELADAYLGGVPPDQLPPLSLRWLFP-TGGSVRGCVKGKIKALGYVLDKRLN-TTGV 3111
D 3054 DNDLELADAYLGGVPPDQLPPLSLRWLFP-TGGSVRGCVKGKIKALGYVLDKRLN-TTGV 3111
D 1085 DGEVDFESTYLLGGI-----PIAIRERFNISTPAPFGCMQVKK---KTSGVVRVRLNDTVGV 1136
QY 3112 SAGCTADLLVGRAMTFHGHGFLRLALSNA-PLTGNVYSGFGFHSQAQDSALLYRASPDG 3170
D 3112 SAGCTADLLVGRAMTFHGHGFLRLALSNA-PLTGNVYSGFGFHSQAQDSALLYRASPDG 3170
D 1137 TKKCEDWKLVSASFSGG--QLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQWTWR 1194
QY 3171 LCQVSLQOGRVSLQLRTE---VKTQAGFADGAPHYAFYFYSNATGVWLYVDDQLQMKPH 3227
D 3171 LCQVSLQOGRVSLQLRTE---VKTQAGFADGAPHYAFYFYSNATGVWLYVDDQLQMKPH 3227
D 1195 NLQVTEDEGYIELSTSDSGGIFKSPQTYMDGLLHVSVISDNLGLRLDLDQLLNS-- 1252
QY 3228 RGPPPELQPEGPPRLILGGLPESGTIYNFSGCISNVFVQRLGLPQRFVLDLQNLGSVN 3287
D 3228 RGPPPELQPEGPPRLILGGLPESGTIYNFSGCISNVFVQRLGLPQRFVLDLQNLGSVN 3287
D 1253 ---KRLKHISRRQSLRGG-----SNFEGCISNVFVQRLSLSPEVLDLTSNLKRD 1301
QY 3288 VST-GCA-----PALQATPGLPGRGLQATARKASRRSRQP 3322
D 3288 VST-GCA-----PALQATPGLPGRGLQATARKASRRSRQP 3322
D 1302 VSLGGCSLNKPPFLMLLKSTFRNKTFTFRINQLQDTTPVASPRSVKW----- 1350
QY 3323 ARHPACMLPPLHRTTRDSYQFGGSLSSHLEF--VGILARHNWPSLSMHVLPSSRGLLL 3380
D 3323 ARHPACMLPPLHRTTRDSYQFGGSLSSHLEF--VGILARHNWPSLSMHVLPSSRGLLL 3380
D 1351 --QDACSPLPKTQANHGALQFGDIPITSHLLFKLPQELLKPRSQAFAVDMQT--TSSRGLVF 1406
QY 3381 FTARLRPGSPSLALFLSNHGFVAQMEGLGTRLRQAQRQSRPGRWHKVSVRWEKNRILV 3440
D 3381 FTARLRPGSPSLALFLSNHGFVAQMEGLGTRLRQAQRQSRPGRWHKVSVRWEKNRILV 3440
D 1407 HTG---TKNSFMALYLSKGRVLPALGTDGKLRKIKSKEKNDGKWTVVFGHDGKGRV 1463
QY 3441 TDGARAWSQEGPHRQHQGAHPQPHLTVG-----GLPASSHSSKLPVTVFGSGCVKRLR 3495
D 3441 TDGARAWSQEGPHRQHQGAHPQPHLTVG-----GLPASSHSSKLPVTVFGSGCVKRLR 3495
D 1464 VDGLRA--REG-----SLPGNSTISIRAPVILGSPSPGKPKSLP-TNSFVGLKXNFQ 1512
QY 3496 LHGRPLCAPTRMAGVTPCILGPLEAGLFFPGSGGVITLDLPGLATLPDVGLELEVRPLAVT 3555
D 3496 LHGRPLCAPTRMAGVTPCILGPLEAGLFFPGSGGVITLDLPGLATLPDVGLELEVRPLAVT 3555
D 1513 LDSKPLYTPSSSGVSSCLGPLEKGIYFSEEGHVLAHSLVLLGPEFKLVFSIRPSLT 1572
QY 3556 GLIFHLGQARTPPYLOLVTEKQVLLRADDGAGFEFSTSVTRPSVLCGQWHLAVMKSGN 3615
D 3556 GLIFHLGQARTPPYLOLVTEKQVLLRADDGAGFEFSTSVTRPSVLCGQWHLAVMKSGN 3615
D 1573 GILIHIG-SQPGKHLGVLEAGKVTASMDSGAGTSTSVTPKQSLCDGOWHSAVTIKQH 1631
QY 3616 VLRLEVDAQSNHTVGVPLLAAGAPAPLYLGLPEPMAVQWP--PAYCGMRRRLAVNRS 3673

Db 1632 ILHLELTDSSYTAGQIPFPASTQEPHLHGGAPANLTLRIPVWKSFFGCLRNHVNHI 1691
QY 3674 PVWATRSVEVHGAVGASGCP 3693
Db 1692 PVPVTEALEVQGPVSLNGCP 1711
RESULT 15
PCT-US94-10261A-24
Sequence 24, Application PC/TUS9410261A
GENERAL INFORMATION:
APPLICANT: Carter, William G.
APPLICANT: Gil, Susanna A.
APPLICANT: Ryan, Maureen C.
TITLE OF INVENTION: Epiligrin, an Epithelial Ligand for
TITLE OF INVENTION: Integrins
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson, and Kindness
STREET: 1420 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101-8100
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10261A
FILING DATE: 02-SEP-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-8100
TELEFAX: (206) 224-0779
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1713 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: E170 protein as translated from sequence of
DESCRIPTION: FIGURES 15A-15F, and as shown also in FIGURES 19A-19R
PCT-US94-10261A-24
Query Match 11.2%; Score 2260.5; DB 5; Length 1713;
Best Local Similarity 31.5%; Pred. No. 2.6e-131;
Matches 612; Conservative 296; Mismatches 711; Indels 321; Gaps 48;
QY 1818 PAGOGAL-ASNVELCLCPASYRGDSQECAPGFYRDVKGLFLGRVCVPCQCHGHSRCLPG 1876
Db 29 PPGQSQLQASYVEF-----RPSQGCSPGYRDHKGLYTGRCVPCNCNGHSNQCQDG 79
QY 1877 SGVCVDCQHNTEGAHCERCQAGFVSSRDDPSAPCVSCPCPLSVPSNNFAEGCVLGGRTQ 1936
Db 80 SGICVNCQHTAGEHCERCQEGYVGNVHGS--CRACPCP---HTNSFATGCVVNGGDVR 134
QY 1937 CLCKPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSGNGDPNLLFSDCDPLTGACRGCLR 1996
Db 135 CSCKAGYGTQCERCAPGYFGNPKQKFGGSCQPCSCNSNGQ----LGSCPLTGDGIN--- 187
QY 1997 HTTGPRCEICAPGFYGNALLPGNCTRCDCCTPCGTEACDPHSGHCLCKAGVTGRRCDRCQE 2056
Db 188 -----PKDSSPAEE-----QE 189
QY 2057 GHFGNCGGCRPCACGPAAGSECHPQSGQCHCRPMTGMPQCRECAPGYWGLPEQGCR 2116
Db 190 -----PKDSSPAEE----- 198

QY 2117 CQCPGGRCDPHTGRCNCPPGLSGERCDCSCQHQVVPVGGPVGSHSIHCEVCDHCVVLLLD 2176
Db 199 -----CDDCDSCVMTLLN 211
QY 2177 DLERAGALLPAIHEQLRGINASSMAWARLHRLNASIADLOSQLSRPLGPRHETAQQLEVL 2236
Db 212 DLATMGEOQLRVKSQLOGLSASAGLLEQMRHMETQAKDLRNQLLNYSAISNHSKIEGL 271
QY 2237 EQQSTSLGQDARRLGGQAVGTRDOASQLLAGTEATLGHAKTLLAAIRAVDRTLSELMQ- 2295
Db 272 ERELTDLNQEFETLQEKAOVNSRKAQTLNNVNRATQSAKELDVKIKNVIRNVHILLKQI 331
QY 2296 TGHGLANASAPSGEQLLRTLAEVERLLWEMRARDLGAPOAAAEALAAQRLARVQEQ 2355
Db 332 SGTDGEYN-VNPSGD-FSREWAEARQMMRELNRNFGKHLREAEADKRESQLLNLRITW 389
QY 2356 LSSLWEENQALATQTRDLRAQHEAGLMDLREALNRAVDATPEAQELNSRNOERLEEALQ 2415
Db 390 QKTHQGENNGLANSIRDSLNEYEAKLSDLRLARLQEAQAAQAKQANGLNQEN-ERALGAIQR 448
QY 2416 K-QELSRDNATLQATLHAARDTLASVFRLLHSLDQAKEELERLAASLDGARTPLLQRMQT 2474
Db 449 QVKEINSLOSDFTKYLTADSSLLQTNIALQLMKESQKEYEKLAAASLNEARQELSDKVRE 508
QY 2475 FSPAGSKRLVVEAAEAHAQQLGQLALNLSSIIIDVNQDRLTQRAIEASNAYSRILOAVQA 2534
Db 509 LRSAGKTSLVEEAEKHARSLOELAKOLEEIKRNASGDELVRCAVDAATAYENILNAIKA 568
QY 2535 AEDAAQALQQADHTWATVVRQGLVDRAQQLLANS-TALEEAMLEQEQRLGLVWAAALQA 2593
Db 569 AEDAANRAASASESALQTVIKEDLPKAKTSSNSDKLLNEAKMTQKKLKQEVSPALNLL 628
QY 2594 RTQLRDVRAKDKQLEAHIAAQ-AMLAMDTDETSKIAHAKAVAAEAQDTATRVQSQLOA 2652
Db 629 QQTLNIVTQKEVIDTNLTTLRLDGLHGIQRGDIDAMISSAKSMVRKANDITDEVLDGLNP 688
QY 2653 MQENVERWQOYEGRLGQDLGQAVLDAGHSVSTLEKTLPLQLLAKLSILENRGVHNASLA- 2711
Db 689 IQTDVERIKDTYGRNQNEDEFFKALTDADNSVNKLTNKLPLDWRKIESI-----NQQLLP 742
QY 2712 ---LSASIGRVRELIAQAARGAASKVKVPMKFNKRGVSVLRDKKVHVYQIGEAGPAVLSIDEDIGE- 2768
Db 743 LGNISDNMDRIRELIQQARDAASKVAVPMRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQR 802
QY 2769 PEPEPGQGTEDRFVVMYMGSRQATGYMGVSVLRDKKVHVYQIGEAGPAVLSIDEDIGE- 2827
Db 803 PMSRENGGTENMFVYMLGNKDSRDYIGMAVVDGQLTCVYNLGD-RAELQVDQILTKSE 861
QY 2828 -----FAAVSLDRTLQFGHMSVTVERQMIQ-ETKG--DTVAPGAEGLLNLRPDDFVYVG 2879
Db 862 TKEAVMDRVKFORIYQFARLNYTKGATSSKPTPGVYDMDGRNSNTLLNLDPENVVYVG 921
QY 2880 GYPSTFTTTPPLLRFPYRGCIEMDTLNEEVSVLYNFERTFOLDTAVDRPCARSKSTGDPW 2939
Db 922 GYPDFKLPRLSFPYKGCIELDDLNNENVLNLYNFKTNLTTEVEPCRRRKEE---- 977
QY 2940 LTDGSLDGTGFARISFDSQISITKRFQELRLVSVSGVLFELKQSQFLCLAVQEGSLV 2999
Db 978 -SDKNYFEGTGYARVPTQPH-APIPTFGQTIQTTVDRLGLLFAENGDRFISLNIEDGKLM 1035
QY 3000 LLYDFGAGLKK-----AVPLOPPPLTSASKAIOVFLGGSRKRVLRVERATVYSVEQ 3053
Db 1036 VRYKLNSELPKERGVDGIN-----NGRDHSIQI-KIGLKQKRMWINVD---VQNTII 1084
QY 3054 DNDLELADAYLGGVPPDQLPPSLRWLFP-TGGSVRGCVKGIKALGKYVDLKRNL-TTGV 3111
Db 1085 DGEVDFSTYYLGGI-----PIAIRERFNISTPAFRGCMKNLK---KTSGVRLNDTVGV 1136
QY 3112 SAGCTADLLVGRAMTFHGHGFLRLALSIVA-PLTGNVYSGFGFHSQAQDSALLYRASP 3170
Db 1137 TKKCEDWKLVRASASFSRGG--QLSFTDLGLPPTDHLQASFGFTQFPQSGILLDHQIWT 1194

